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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

May 18, 2004, 11:21:33 ; Search time 24.9726 Seconds (without alignments) 5623.200 Million cell updates/sec

US-08-353-485-2

2641 1 MRKINSLFSLAVILSLLCWG.....QNITGSAVGQKVTLKWDAPN 497 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:* geneseqp2003as:*geneseqp2003bs:* geneseqp2001s:* geneseqp2002s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

ion	P. qingiv	Haemagglu	P. gingiv	Haemagglu	PrtR anti	Arg-gingi	Arg-gingi	Arg-gingi	P. gingiv	P. gingiv		P. gingiv	Haemagglu	P. gingiv	PrtK anti	Haemagglu	P. gingiv	Haemagglu	P. gingiv	P. gingiv	P. gingiv	Haemagglu	P. gingiv	P. gingiv	Haemagglu
Description	Aar96025	Aaw69483	Aar96030	Aaw69488	Aaw24786	Aar70188	Aaw34843	Aay67396	Aau08938	Aar96033	Aaw69495	Aar96032	Aaw69494	Aar96029	Aaw24787	Aaw69487	Aar96028	Aaw69486	Aau03572	Aau03574	Aar96021	Aaw69489	Aar96023	Aar96022	Aaw69491
	AAR96025	AAW69483	AAR96030	AAW69488	AAW24786	AAR70188	AAW34843	AAY67396	AAU08938	AAR96033	AAW69495	AAR96032	AAW69494	AAR96029	AAW24787	AAW69487	AAR96028	AAW69486	AAU03572	AAU03574	AAR96021	AAW69489	AAR96023	AAR96022	169491
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Aaw69490 Haemagglu	Aar72458 Porphyrom	Aar77313 Porphyrom	Aar96024 P. gingiv	Aaw69492 Haemagglu	Aau03575 P. gingiv	Aay34359 Porphorym	Aay34484 Porphorym	Aay34522 Porphorym	Aay34521 Porphorym	Aay34520 Porphorym	Aay34392 Porphorym	Aab14942 Porphyrom	Aay34483 Porphorym	Aay34358 Porphorym	Aau03573 P. gingiv	Abp55081 Porphyrom	Aab49217 Peptide u	Aaw34805 Arg-speci	Adc01014 Enterohae
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546.5	522	495.5	458.5	458.5	457.5	425.5	379	337	337	337	337	272.5	213.5	213.5	188.5	177.5	176.5	175	153
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Haemagglutinin; hagA; periodontal disease; vaccine; antibody
                                                       Porphyromonas gingivalis; strain 381.
        AAR96025 standard; protein; 497 AA.
                                     P. gingivalis haemagglutinin hagA.
                         (revised)
(first entry)
                         16-OCT-2003
04-SEP-1996
                 AAR96025;
   AAR96025
RESULT 1
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WO9617936-A2

95WO-US016108. 11-DEC-1995; 13-JUN-1996.

94US-00353485. (UYFL) UNIV FLORIDA. (UABR-) UAB RES FOUND 09-DEC-1994;

Lantz M. Han N, Lepine G, Tumwasorn S, WPI; 1996-287181/29. Progulske-Fox A, N-PSDB; AAT30649.

Patti JM;

- used in the detection and Porphyromonas gingivalis genes and proteins vaccination against periodontal disease.

Claim 5; Page 47-51; 153pp; English.

A portion (AAR96025) of P. gingivalis 381 haemagglutinin hagA (see also AAR96030) was identified as the product of clone ST2 (AAT30649) isolated from a P. gingivalis 318 genomic library. The haemagglutinin can be obted from transformed host cells and used as a vaccine to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of a live vaccine. The haemagglutinin can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)

Sequence 497 AA;

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This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagA haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
    encoding haemagglutinin and/or
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100.0%; Score 2641; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.5e-194;
Matches 497; Conservative 0; Mismatches 0;
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                                            Claim 1; Col 37-44; 101pp; English
    Isolated Porphyromonas gingivalis
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                  poly:peptide(s)
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    Length
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Score 2641; DB 2;
Pred. No. 2.5e-194;
Mismatches 0;
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09-DEC-1994;
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                                                                                                                                                                                                                                                 P. gingivalis 381 haemagglutinin hagA (AAR96030) was identified as the product of the hagA gene (AAT30654) isolated as an EcoRV fragment of genomic DNA. The haemagglutinin, or portions of it (see also AAR96021-24), can be obtd. from transformed host cells and used as a vaccine to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of a live vaccine. The haemagglutinin can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-0CT-2003 to standardise OS field)
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                                                                                                                                                                                                detection and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDPFEYKVPVNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQRQGPGDAASVVVTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPASDKRTYVLNESFDTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 VORQGPGDAASVVVTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPASDKRTYVLNESFDTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLPNGWIMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTP
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                                                                                                                                                                                                - used in the
                                                                                                                                        Lantz
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                              Score 2641; DB 2;
Pred. No. 2.9e-193;
0; Mismatches 0;
                                                                                                                                      Han N,
                                                                                                                                                                                             Porphyromonas gingivalis genes and proteins vaccination against periodontal disease.
                                                                                                                                      Lepine G,
                                                                                                                                                                                                                                Claim 6; Page 93-101; 153pp; English.
                                                                                                                                     Progulske-Fox A, Tumwasorn S,
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100.0%;
                                                      95WO-US016108
                                                                            94US-00353485
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497; Conservative
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                                                                                                                                                           WPI; 1996-287181/29.
                                                                                                                                                                                                                                                                                                                                                                         Sequence 2628 AA;
                                                                                                                                                                       N-PSDB; AAT30654
                                                                                                   UNIV
         WO9617936-A2
                                                                            09-DEC-1994;
                                                      11-DEC-1995;
                               13-JUN-1996
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Best Local S:
Matches 497
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61 ARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDPFEYKVPVNA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoding haemagglutinin and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lepine G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTP
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                                                                                                                                                                                                                                                     Haemagglutinin protein; periodontal disease; vaccine; hagA.
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100.0%; Pred. No. 2.9e-193;
ive 0; Mismatches 0;
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AAW69488 standard; protein; 2628 AA
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91US-00647119.
94US-00353485.
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                                                                                                                                                                                          Haemagglutinin protein hagA
                                                                                                                            (first entry)
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Best Local Similarity 100.
Matches 497; Conservative
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                                                                                                                                                                                                                     Periodontal disease; cell surface protein; thiol protease; endopeptidase;
PrtR; PrtR45; PrtR44; PrtR15; PrtR17; PrtR27; haemagglutinin; adhesin;
therapy; diagnosis; vaccine; antigen.
                                                                        480
                       420
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KVIVPENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDKPAPMNLVK 360
                                  SEGVKLPAPYQERTIDLSAYAGQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTV
                                                       YRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL
                                                                       YRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL
                        SEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTV
                                                                                                                                                                                                                                                                                                            /label= PrtR45
/note= "45 kDa Arg-specific thiol protease"
719. .720
                                                                                                                                                                                                                                                                             1. .227
/label= Pro-pro_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "27 kDa adhesin"
                                                                                                                                                                                                                                                                                                                                                                                    /note= "15 kDa adhesin"
1273. .1274
                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "17 kDa adhesin'
                                                                                                                                                                                                                                                                                                                                                     'note= "44 kDa adhesin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYME ) UNIV MELBOURNE.
(VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Slakeski N;
                                                                                                                                                                                                                                                     Porphyromonas gingivalis; strain W50.
                                                                                                                                               AAW24786 standard; protein; 1706 AA.
                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                      PrtR antigenic protein complex.
                                                                                                                                                                                                                                                                                                                                    720. .1138
/label= PrtR44
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/label= PrtR15
                                                                                        TGSAVGOKVTLKWDAPN 497
                                                                                                                                                                                                                                                                                                                                                                                                            label= PrtR17
                                                                                                                                                                                                                                                                                                                                                                                                                                           'label= PrtR27
                                                                                                        TGSAVGQKVTLKWDAPN 497
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                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                             227. .228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-272112/24.
N-PSDB; AAT78850.
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Protein
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                                                                                                                                                                              17-OCT-2003
25-NOV-1997
                        361
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         301
                                                                                                                                                                                                                                                                              Peptide
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comprises a 300 kDa complex composed a 45 kDa arginivalis (PG) comprises a 300 kDa complex composed a 45 kDa arginine-specific thiol protease and 44, 15, 17 and 27 kDa adhesins encoded by the ptrR gene (AAT78850), and a 148 kDa lysine-specific thiol protease and 39, 15 and 44 kDa adhesins (see AAW24787) encoded by the ptrR gene (AAT78851). A claimed antigenic complex comprises at least one multimeric protein complex comprises at least one adhesin domain, the complex baving a mol. wt. of over 2000 kDa, and preferably comprises all 9 proteins of the PtrR-PtrK complex (see also AAW24780-85). It can be used in a claimed composition to elicit an immune response directed against PG, and in a claimed method of reducing the prospect of PG infection and/or severity of disease. Antibodies directed against the complex are primed for use in treating PG infection. Unlike whole PG cells or other previously prepared antigens based on fimbriae or the capsule, the PtrR-PtrK complex or component parts are safe and effective antigens. (Updated on 17-OCT-2003 to standardise OS field)
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New antigenic protein complex from Porphyromonas gingivalis - comprising Arg- and Lys- specific thiol endo-peptidase(s), used in the detection, prevention and treatment of periodontal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   671 TATTOGOKVTLKWDAPSTKTNATTNTARSVDGIRELVLLSVSDAPELLRSGQAEIVLEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 DVWEDGIGYOMLWDADHNQYGASIPEE--SFWFANGTIPAGLYDPFEYKVPVNADASFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 TAAAQG-----GPKTAPSVTHQAVQK--GIR---TSKVKDLRDPIPAGMARIILEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.0%; Score 951.5; DB 2; Length 1706; 31.9%; Pred. No. 1.3e-63; ive 74; Mismatches 156; Indels 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----VIGEGGNEFAPVONLOWSVSGQTVILIWQAPAS--
                                                                                                                                                   Example 1; Fig 8b; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 PGDAASVV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1706 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352 KPAPM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1086
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STO E-NGIPASWKTIDADGDGHGW-KPGNAPGIAGYNSNGCVYSESF-GLGGIGV-LIPDNYL 1025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         671 TATTQGQKVTLKWDAPSTKTNATTNTARSVDGIRELVLLSVSDAPELLRSGQAEIVLEAH 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 YRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVÇKDVTVEGSNEFAHVQNL 480
                                                                                                                                                                                                                               850 SGDGTELTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVATGNHEYCVEVKYTAGVS 909
                                                                                   790 TNMIMDGTASVNIPAGTYDFAIAAPQANAKIWIAGQGPTKEDDYVFEAGKKYHFLMKKAMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GPKTAPSVTHQAVQK--GIR---TSKVKDLRDPIPAGMARIILEAH
                                                                DVWEDGTGYQMLWDADHNQYGASIPEE--SFWFANGTIPAGLYDPFEYKVPVNADASFSP
                                                                                                                                                                                                                                                                  ------DKRTYVLNESF
                                                                                                                                                                                                                                                                                           910 PKVCKDVTVEGSNEFAPVQNLTGSAVGQKVTLKWDAPNGTPNPNPNPNPNPGTTTLSESF
                                                                                                                                                                                                                                                                                                                                 238 DIQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYTYTV
                                                                                                                               INFVLDGTASADIPAGTYDYVIINPNPGI-IYIVGEGVSKGNDYVVEAGKTYHFTVQRQG
                                                                                                                                                                                                                                                                                                                                                                                                    298 VTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --KSEGVKL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arg-specific gingipain protease; gingivalis; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arg-gingipain high molecular weight prepolyprotein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LSAYAGQQV----
                                                                                                                                                                                                                                                               ----VTGEGGNEFAPVONLOWSVSGOTVTLTWOAPAS--
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1. .227
/note= "precursor protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----DKPAPMNLV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW34843 standard; protein; 1704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGSAVGQKVTLKWDAPN 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PAPYQERTID-
                                                                                                                                                                                                  186 PGDAASVV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; infection
 22 TAAAQG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9734629-A1
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Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A low mol.wt. arginine-specific gingipain (AG-1) and high mol.wt. AG (AG-2) were isolated from P. gingivalis strains H66 (ATCC 33277) and W50 (ATCC 53973). The sequences of the proteins were used to design PCR primers and probes to isolate AG DNA. Lambda DASH and lambda ZAP libraries were screened with a probe based on amino acids 11-22 of the AG protein to obtain DNA encoding AG-1 (AAQ83484) and AG-2 (AAQ83489). AG-2 is a prepolyprotein incorporating AG-1. (Updated on 25-MAR-2003 to
                    YTYTVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding Arg-gingipain proteins - used to develop prods. for detection, treatment and prevention of periodontal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1704;
                                                                                                                                                                                                                                                                                                                                 Arg-gingipain-2; gingivalis; periodontal disease; vaccine; arginine-specific protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arg-gingipain-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.8%; Score 944.5; DB 2; 31.9%; Pred. No. 4.4e-63; iive 75; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pavloff N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "corresponds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 720. .1091
/label= Hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1092. .1429
/label= Hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1430. .1704
/label= Hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 70-77; 89pp; English
                                                                                  |:||-
|382 PVKNLKAQPDGGDVVLKWEAPS 1403
                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                              HVQNLTGSAVGQKVTLKWDAPN 497
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                                                                                                                                                                                standard; protein; 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                       228. .719
/label= Protease
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                                                                                                                                                                                                                                                                                                    Arg-gingipain-2 prepolyprotein
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94US-00265441.
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                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                    Porphyromonas gingivalis
                                                                                                                                                                                                                                                 (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potempa J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-123373/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 235; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1704 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ83489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9507286-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-OCT-1993;
24-JUN-1994;
                                                                                                                                                                                                                                               25-MAR-2003
21-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Travis J,
                               1323
                                                              476
                                                                                                                                                                                                                 AAR70188;
 416
                                                                                                                                                                                AAR70188
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1325
1326 YRDGTXIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVAVTI NPTOFNPVKNL 1384
                                                                                                                                                                                  420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arginine specific proteinase; Arg-gingipain; gingipain-2; haemagglutinin; immunogenic component; vaccine; inflammatory response; tissue damage; periodontal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a Porphyromonas gingivalis arginine-specific proteinase known as Arg-gingipain/gingipain-2 amino acid sequence. Gingipain-2 consists or a SORD protease component non-covalently associated with a 44kD haemagolutinin component. The proteinase is stimulated by glycine containing peptides and glycine analogues. It is inhibited by cysteine protease group specific inhibitors. The protease preparation can be used in immunogenic compositions and vaccines against inflammatory response and tissue damage caused by P. gingivalis in periodontal disease. It can also be used to screen for agents that
                                                                                                                                                                                                                720. .1185
/note= "Amino acids 720-1185 are specifically claimed"
                                                                                                                            1206 KDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLST
                                                                                                                                                                                ------YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYTYTV
                                                                                                                                                                                                                                                                                    YRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Porphyromonas gingivalis arginine-specific protease preparation useful for preparing vaccines against periodontal disease and for screening for Arg-gingipain inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229. .719
/note= "Amino acids 229-719 are specifically
720. .1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arg-gingipain-2 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY67396 standard; protein; 1704 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYGE-) UNIV GEORGIA RES FOUND INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1385 KAQPDGGDVVLKWEAPS 1401
                                                                                                                                                                                                                                                                                                                                                                                     481 TGSAVGQKVTLKWDAPN 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-136659/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ60181.
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                                                                                                                                                                                                                                                                                    421
                                                                                                                                                                             386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS------DKRTYVLNESF 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIQILPNGWIMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68
                                                                                                                                                                                                                                                                                                                                                                             Porphyromonas gingivalis Arg-specific gingipain protease peptide(s) -
useful for protecting animals and humans from gingivalis and periodontal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 TAAAQG------GPKTAPSVTHQAVQK--GIR---TSKVKDLRDPIPAGMARIILEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVWEDGIGYOMLWDADHNQYGASIPEE--SFWFANGTIPAGLYDPFEYKVPVNADASFSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence represents an arginine-specific protease of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.8%; Score 944.5; DB 2; Length 1704; 31.9%; Pred. No. 4.4e-63; ive 75; Mismatches 160; Indels 267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 68-73; 95pp; English
                                                                                                                                                                          RES FOUND INC.
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                                                                                                                                                                                             (MORE-) MOREHOUSE SCHOOL MEDICINE.
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                                                                   97WO-US004635.
                                                                                                                       96US-0013945P.
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                                                                                                                                                                                                                                                   Travis J,
                                                                                                                                                                  (UYGE-) UNIV GEORGIA
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N-PSDB; AAT93872.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1704 AA;
                                                                   21-MAR-1997;
                                                                                                                    22-MAR-1996;
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                  25-SEP-1997
                                                                                                                                                                                                                                                 Potempa J,
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Best Local
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/note= "Region of homology with cysteine proteases"
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/label= HGP_44kDa
/note= "Haemagglutinin protein component"
                                                                                                                                                          = HGP_17kDa
"Haemagglutinin protein component"
                                                                                                                                                                                                   = HGP_27kDa
"Haemagglutinin protein component"
                                                                       670. .674
/label= Proteolytic_component
                                                                                                                                                                                                                                                                                                                                                                          Pavloff N;
                                1. .227
/label= Prepro_peptide
                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Col 29-41; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                          Barr PJ,
                                                                                                                                                                                   /label= HGP_2./note= ""-
                                                                                                                                                                                                                                                                                                93US-00119361.
94US-00265441.
94WO-US010283.
94US-00336308.
                                                                                                                                           /label= HGP
/not
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                                                     .619
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Les 235; Conservative
   Porphyromonas gingivalis
                                                                                                                                                                       note=
                                                                                                                                                                                                                                                                                                                                                                         Potempa JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            hemaglutinin component.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is Arg-gingipain-2
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                                                                                              Cleavage-site
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                                                                                                                                                                                                                                                                            25-JAN-2000;
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08-NOV-1994;
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                                                                                                                                                                                                                                   JS6274718-B1
                                                                                                                                                                                                                                                                                                 10-SEP-1993;
                                                                                                                                                                                                                                                                                                            24-JUN-1994;
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                                                                                                                                                789
                                                                                                                                                                  TNFVLDGTASADIPAGTYDYVIINPNPGI-IYIVGEGVSKGNDYVVEAGKTYHFTVQRQG 185
                                                                                                                                                                                                                                    909
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                                                                                                                                      TAAAQG------GPKTAPSVTHQAVQK--GIR---TSKVKDLRDPIPAGMARIILEAH
                                                                                                                          DVWEDGTGYQMLWDADHNQYGASIPEE--SFWFANGTIPAGLYDPFEYKVPVNADASFSP
                                                                                                                                                                                                                                 SGDGTELTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVATGNHEYCVEVKYTAGVS
                                                                                                                                                                                                                                                       -- DKRTYVLNESF
                                                                                                                                                                                                                                                                          910 PKVCKDVTVEGSNEFAPVQNLTGSAVGQKVTLKWDAPNGTPNPNPNPNPNPGTTTLSESF
                                                                                                                                                                                                                                                                                              DIQTLPNGWIMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYL
                                                                                                                                                                                                                                                                                                                                        VIPKVIVPENGKLSYWVSSQ-VPWINEHYGVFLSTIGNEAANFTIKLLEETLGS-----
                                                                                                                                                                                                                                                                                                                                                                                                      BAIRGRIQGTWROKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1206 KDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYTYTV
                                                                                                                                                                                                                                                                                                                                                                                    ---- KSEGVKL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Periodontitis; antiinflammatory; Arg-gingipain-2; AG-2; immunogen.
                                      35.8%; Score 944.5; DB 3; Length 1704; 31.9%; Pred. No. 4.4e-63; ive 75; Mismatches 160; Indels 267;
 modulate Arg-gingipain proteinase activity inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P. gingivalis high molecular weight Arg-gingipain-2.
                                                                                                                                                                                                                                                                                                                                                                                                                            ----LSAYAGOOV-
                                                                                                                                                                                                                                                       ----VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS--
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                                                                                                                                                                                                                                                                                                                                                                                  --- DKPAPMNLV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1385 KAQPDGGDVVLKWEAPS 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 TGSAVGOKVTLKWDAPN 497
                                                                                                                                                                                                             PGDAASVV-----
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                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            ----PAPYQERTID-
                                                Local Similarity
                   Sequence 1704 AA
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The invention relates to a recombinant DNA molecule encoding high molecular weight (mature) Arg-gingipain (AG) protein, which has an enzymatically active procease component (AG-2) and a haemagglutinin component, from P. gingivalis. The nucleic acid is useful for producing mature Arg-gingipain protein. Immunogenic compositions comprising Arg-gingipain are useful for immunising animals including humans against inflammatory response and tissue damage caused by an archaebacterium Porphyromonas gingivalis, which causes progressive periodonticis. Arg-gingipain is also useful for identifying agents that modulate Arg-gingipain is also useful for identifying agents that modulate Arg-gingipain is curvently, whether by acting on the protein in the or preventing the interaction of the proteinase with the protein in the gingival area, such as complement factors C3 or C5. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
New recombinant DNA molecule which encodes high molecular weight (mature) Arg-gingipain protein, useful for immunization against inflammation and tissue damage, comprises enzymatically active protease component and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126
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31.9%; Pred. No. 4.4e-63;
iive 75; Mismatches 160; Indels 267; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GPKTAPSVTHQAVQK--GIR---TSKVKDLRDPIPAGMARIILEAH
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PI Progulske-Fox A, Tumwasorn S, Lepine G, Han N, Lantz M, Patti JM; XX DR WPI; 1996-287181/29. DR N-PSDB; AAT30656. XX PT Porphyromonas gingivalis genes and proteins - used in the detection and PT Vaccination against periodontal disease. XX XX PT Porphyromonas gingivalis genes and proteins - used in the detection and PT Vaccination against periodontal disease. XX PS Claim 5; Page 138-143; 153pp; English.	C product of a gene (AAT30656) identified in P. gingivalis 318 genomic DNA. C product of a gene (AAT30656) identified in P. gingivalis 318 genomic DNA. C The haemagglutinin can be obtd. from transformed host cells and used as a conscione to protect humans or animals against periodontal disease. C Expression in Salmonella cells allows prodn. of a live vaccine. The haemagglutinin can also be used to detect the presence of anti-P. C pingivalis antibodies and to raise monoclonal antibodies for diagnostic conspiration. (Updated on 16-OCT-2003 to standardise OS field) XX SQ equence 1687 AA;	Query Match 35.7%; Score 943.5; DB 2; Length 1687; Best Local Similarity 31.8%; Pred. No. 5.2e-63; Matches 235; Conservative 75; Mismatches 160; Indels 269; Gaps 20; Qy 22 TARAQGGPKTAPSVTHQAVQKGIRTSKVKDLRDPIPAGMARIILEAH 68			194DKRTYVLNE 235	QY 296 YLVTPKVTVPENGKLSYMVSSQ-VPWTNEHYGVFLSTTGNRAANFTIKLLEETLGS 350	QY 351 366 DD 1067 SPEAIRGRIGGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETF 1126	Qy 367 PAPYQERTID	1187 ISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETFNGINKGGARFGL	1247 STEANGAKPQSVWIERTVDLPAGTKYVARRHYNCSDLNYILLDDIQFTWGGSPTPTDYTY	QY 419 TVYRDNVVIAQNLAATTENQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQ 478
Db 731 DVWNDGSCYQILLDADHDQYGQVIPSDTHTLW-PNCSVPANLFAPFEYTVPENADPSCSP 789 C27 TNFVLDGTASADIPAGTYDYVINPPDGI-IYIVGEGVSKGNDYVVEAGKTYHFTVQRGG 185 C30 TNMIMDGTASVNIPAGTYDFAIAAPQANAKIWIAAGQGPTKEDDYVFEAGKKYHFLMKKWG 849 C47 C4	CY 194UTGEGGNEFAPVONLQMSVSGCTVTLTWQAPASDKRTYVLANESF 237 DD 910 PKVCKDVTVBGSNBFAPVQNLTGSAVGQKVTLKWDAPNGTPNPNPNPRTTLSESF 969 CY 238 DTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYL 297 DD 970 B-NGIPASWKTIDADGGGHW-KPGNAPGIAGYNSNGCVYSESF-GLGGIGV-LTPDNYL 1025 CY 298 VTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNBAANFTIKLLEETLGS 350 DD 1026 IPPALDIPNGGKLFWVVAODANVASSGTGNBASHTMALEETLGS 350	351	386	- п	OY 481 TGSAVGQKVTLKMDAPN 497 Db 1385 KAQPDGGDVVLKWEAPS 1401 RESULT 10 AARS6033	ID AAR96033 standard, protein; 1687 AA. XX AC AAR96033; XX	DT 16-OCT-2003 (revised) DT 04-SEP-1996 (first entry) XX DE P. gingivalis haemagalutinin hacE.	XX KW Haemagglutinin; hagE; periodontal disease; vaccine; antibody. XX XX XX XX XX XX XX		PF 11-DEC-1995; 95WO-US016108. XX PR 09-DEC-1994; 94US-00353485.	XX PA (UMER-) UMB RES FOUND. XX

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        891 PKVCKDVTVEGSNEFAPVQNLTGSAVGQKVTLKWDAPNGTPNPNPNPNPNPNPNFGTTTLSE 950
                                                                                                                                                                                                                                                                                                                                                                                                                    TVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQ 478
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                                                            1007 YLITPALDEPNGGKLTFWVCAQDANYASEHXAVYASSTGNDASNFTNALLEETITAKGVR
                                       SFDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN
                                                                                                   YLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS----
                                                                                                                                                                     --KSEGVKL-----
                                                                                                                                                                                                                                                                                                                                                         -----YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P. gingivalis 381 haemagglutinin hagD (AAR96032) was identified as the product of the second open reading frame of the hagD gene (AAR30655)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patti JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemagglutinin; hagD; periodontal disease; vaccine; antibody
                                                                                                                                                                                                                                ----LSAYAGQQV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Han N,
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                                                                                                                                                                  --DKPAPMNLV-
                                                                                                                                                                                                                              -----PAPYOERTID-----
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    P. gingivalis hagD haemagglutinin.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagE haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated Porphyromonas gingivalis genes - encoding haemagglutinin and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                652 TATTÖGOKVTLKWDAPSTKTNATTNTARSVDGIRELVLLSVSDAPELLRSGQABIVLEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| ||:|||:|| || |||||| || || DVWNDGSGYQILLDADHDQYGQVIPSDTHTLW-PNCSVPANLFAPFEYTVPENADPSCSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               831 SCHCITISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVATGNHEYCVEVKYTAGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 TAAAQG------GPKTAPSVTHQAVQK--GIR---TSKVKDLRDPIPAGMARIILEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVWEDGTGYQMLWDADHNQYGASIPEE--SFWFANGTIPAGLYDPFEYKVPVNADASFSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lepine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.7%; Score 943.5; DB 2; Length 1687; 31.8%; Pred. No. 5.2e-63; ive 75; Mismatches 160; Indels 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Progulske-Fox A,
                                                                                                                                                                                                                                   Haemagglutinin protein; periodontal disease; vaccine; hagE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Col 167-182; 101pp; English.
                                                                                                        AAW69495 standard; protein; 1687 AA
                             NLKAQPDGGDVVLKWEAPS 1384
 NLTGSAVGQKVTLKWDAPN 497
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91US-00647119.
94US-00353485.
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                                                                                                                                                                                                    Haemagglutinin protein hagE
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                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                  Porphyromonas gingivalis
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25-JAN-1991;
09-DEC-1994;
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                                                                                                                                                                                                                       67
derived from P. gingivalis 318 genomic DNA. A first open reading frame coded for hagD protease (see also AAR66031). The protease and haemagglutinin can be obtd. from transformed host cells and used in vaccines to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of live vaccines. The haemagglutinin and protease can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                      HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP
                                                                                                                                                                                                                                                                                                TNFVLDGTASADIPAGTYDYVIINPNP--GIIYIVĢEĢ---VSKGNDYVVEAGKTYHFTV
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                                                                                                                                                                                                                       --PIPAGMARIILEA
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                                                                                                                                                                                         Indels 274;
                                                                                                                                                              Length 1358;
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                                                                                                                                                            30.9%; Score 816; DB 2; L 29.6%; Pred. No. 2.4e-53; ive 75; Mismatches 171;
                                                                                                                                                                                                                  TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD-
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                                                                                                                                                                          Local Similarity 29.6
nes 219; Conservative
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                                                                                                                                  Sequence 1358 AA;
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328 TATTOGOKVTLKWDAPS----AKKAEASREVKRIGDGLFVTIEPANDVRANEAKVVLAA 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding haemagglutinin and/or
                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagb haemagglutinin protein. I polypeptides are used to produce antibodies to organisms associated wiperiodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 DNVWGDNTGYQFLLDADHNTFGSVIPATGPLF-TGTASSNLYSANFEYLIPANADPVVTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEEDGVAAGNHEYCVEVKYT
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                                                                                                                                                                                                                                                                                          Progulske-Fox A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 816; DB 2; L; Pred. No. 2.4e-53; 75; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD
                                                               protein; periodontal disease;
                                                                                                                                                                                                                                                                                          Tumwasorn S,
                                                                                                                                                                                                                                                                                                                                                        gingivalis genes
                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Col 145-158; 101pp; English
                                                                                                                                                                                            88US-00241640.
91US-00647119.
94US-00353485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.9%;
                                                                                                                                                                    95US-00570311
                                                                                                                                                                                                                                                                                      Σ
                                   Haemagglutinin protein hagD
           (first entry)
                                                                                                                                                                                                                                                                                                                                                                   protease poly:peptide(s))
                                                                                        Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                        Han N, Lantz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219; Conservative
                                                                                                                                                                                                                                                                                                                                                        Isolated Porphyromonas
                                                                                                                                                                                                                                                               UAB RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OROGPGDAASVV-
                                                                                                                                                                                                                                                UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                 1998-582627/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1358 AA;
                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV58880
                                                              Haemagglutinin
                                                                                                                                                                    11-DEC-1995;
                                                                                                                                                                                                                      09-DEC-1994;
           22-DEC-1998
                                                                                                                                                                                             08-SEP-1988;
                                                                                                                 US5824791-A.
                                                                                                                                          20-0CT-1998
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Best Local
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21;

Gaps

Indels 274; Length 1358;

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AAW69494

RESULT 13 AAW69494
ID AAW6
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987 ESFE-NGIPASWKTIDADGDGHGW-KPGNAPGIAGYNSNGCVYSESF-GLGGIGV-LTPD 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1343 YIVYRDGTKIKEGLIETIFEEDGVATGNHEYCVEVKYTAGVSPKKCVDVIV-NSTQFNPV 1401
                                                                                                               identified as the product of the prtP gene (ART30653) isolated from P. gingivalis W12 genomic DNA. The porphypain shows homology to the meanagolutinins (see also ARS96026-28 and ARS96030-33) of P. gingivalis 318. It can be obtd. from transformed host calls and used as a vaccine to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of a live vaccine. The porphypain and haemagglutinins can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFG 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1283 LSTEANGAKPOSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIOFTMGGSPTPTDYT 1342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         867 RRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEEDGVAAGNHEYCVEVKYT 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---ASDKRTYVLN 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           927 AGVSPKVCKDVTVEGSNEFAPVQNLIGSSVGQKVTLKWDAPNGTPNPNPNPNPNPGTTLS 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESPDIQILPNGWIMIDADGDGHNWLSIINVYNTAIHIGDGAMFSKSWIASGGAKIDLSPD 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YTVYRDNIVVIAQNLAATIFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHV
                                                                                                                                                                                                                                                                                                                                                      68 HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP
                                                                                                                                                                                                                                                                                                                                                                                                       INFVLDGTASADIPAGTYDYVIINPNP--GIIYIVGEG---VSKGNDYVVEAGKTYHFTV
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                                                                                                                                                                                                                                                                                                                                    -----PIPAGMARIILEA
                                      detection
                                                                                                     gingivalis W12 cysteine protease, porphypain (AAR96029), was
                                                                                                                                                                                                                                                                                                         277;
                                                                                                                                                                                                                                                                              Length 1732;
                                     - used in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -------VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAP--
                                                                                                                                                                                                                                                                            30.8%; Score 812.5; DB 2; 30.0%; Pred. No. 6.4e-53; iive 70; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                    TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD-
                                     Porphyromonas gingivalis genes and proteins vaccination against periodontal disease.
                                                                            Claim 5; Page 76-81; 153pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PAPYQERTID
                                                                                                                                                                                                                                                                               Query Match 30.8
Best Local Similarity 30.0
Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRQGPGDAASVV--
WPI; 1996-287181/29.
                                                                                                                                                                                                                                                      Sequence 1732 AA;
            N-PSDB; AAT30653
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366
                          797
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                       SPEAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETF
                                                                      ESSTHGEAPAEWITIDADGDGQDWLCLSSGQLDWLTAHGGTNVVASFSWNGMALNPDNYL
                                                                                                                                                                           918 STEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLDYILLDDIQFTMGGSPTPTDYTY
                                                                                                                                 858 ISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGL
                                                                                                                                                          -----YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porphypain; haemagglutinin; periodontal disease; vaccine; antibody
-KSEGVKL-
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/note= "Pro-Asn repeat region type 1"
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/note= "Pro-Asn repeat region type 4"
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/note= "Pro-Asn repeat
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/note= "Pro-Asn repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gingivalis; strain W12.
DKPAPMNLV
                                                                                                                                                                                                                                                                                                                                                             AAR96029 standard; protein; 1732 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                           1037 NLKAQPDGGDVVLKWEAPS 1055
                                                                                                                                                                                                                                                                  NLTGSAVGQKVTLKWDAPN 497
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(first entry)
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                                                   -----PAPYOERTID-
                                                                                                                                                                                                                                                                                                                                                                                                                                                       gingivalis porphypain.
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(UABR-) UAB RES FOUND
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04-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A PITR-PITK cell surface protein of Porphyromonas ginivalis (PG) comprises a 300 kDa complex composed a 48 kDa lysine-specific thiol protease and 39. Is and 44 kDa adhesins encoded by the pitk gene (AAT78851), and a 45 kDa arginine-specific thiol protease and 44, 15. 17 and 27 kDa adhesins (see AAM24786) encoded by the pitk gene (AAT78850). A claimed antigenic complex comprises at least one multimeric protein complex of Pitk and Pitk each containing at least one adhesin domain, the complex having a mol.wt. of over 200 kDa, and preferably comprises all 9 proteins of the Pitk-Pitk complex (see also AAM24780-85). It can be used
                                                                                                                                                               endopeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antigenic protein complex from Porphyromonas gingivalis - comprising Arg- and Lys- specific thiol endo-peptidase(s), used in the detection, prevention and treatment of periodontal disease.
                                                                                                                                                           Periodontal disease; cell surface protein; thiol protease; endopeptidas.
PrtK; PrtK48; PrtK39; PrtK15; PrtK44; haemagglutinin; adhesin; therapy;
                                                                                                                                                                                                                                                                                                /note= "48 kDa Lys-specific thiol protease"
                                                                                                                                                                                                                                            .. .228
'label= Pro-pro_peptide
                                                                                                                                                                                                                                                                                                                                                                             /label= PrtK15
/note= "15 kDa adhesin"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "44 kDa adhesin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Slakeski N;
                                                                                                                                                                                                          Porphyromonas gingivalis; strain W50.
                                                           AAW24787 standard; protein; 1732 AA
                                                                                                                                                                                                                                Location/Qualifiers
Example 1; Fig 9b; 68pp; English
                                                                                                                                                                                                                                                                                                                                /label= PrtK39
/note= "39 kDa
                                                                                                                                        PrtK antigenic protein complex.
                                                                                                                                                                                                                                                                            229. .737
/label= PrtK48
                                                                                                                                                                                                                                                                                                                                                                                                                          PrtK44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-AU000673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95AU-00006275
                                                                                                                                                                                     diagnosis; vaccine; antigen.
                                                                                                                                                                                                                                                                                                         737. .738
738. .1156
                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                 228. .229
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/label= 1
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                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1997-272112/24.
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Protein
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Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAY-1997
                                                                                                         17-0CT-2003
                                                                                                                  25-NOV-1997
                                                                                   AAW24787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reynolds
                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AICL-)
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1342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1103 RSPKAIRGRIQGTWRQKTVDLPÅGTKYVAFRHFQSTDMFYIDLDEVBIKANGKRADFTET 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1163 FESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGSNVVSSFSWNGMALNPDNY 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1223 LISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFG 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     867 RRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEEDGVAAGNHEYCVEVKYT 926
                                                                                                                                                                                                                                                                                                                                                                                                    593 TATTÓGOKVTLKWEAPS-----AKKAEGSREVKRIGDGLFVTIEPANDVRANEAKVVLAA 747
in a claimed composition to elicit an immune response directed against PG, and in a claimed method of reducing the prospect of PG infection and/or severity of disease. Antibodies directed against the complex are claimed for use in treating PG infection. Unlike whole PG cells or other previously prepared antigens based on fimbriae or the capsule, the PrtR-PrtK complex or component parts are safe and effective antigens. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      748 DNVWGDNTGYQFLLDADHNTFGSVIPATGPLF-TGTASSNLYSANFEYLVPANADPVVTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 INFVLDGTASADIPAGTYDYVIINPNP--GIIYIVGEG---VSKGNDYVVEAGKTYHFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  927 AGVSPKVCKDVTVEGSNEFAPVQNLTGSSVGQKVTLKWDAPNGTPNPNPNPNPNPGTTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NYLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KSEGVKL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----AVSGEGSSNDYT
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                                                                                                                                                                                                                                                                                                                                                     22 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD------PIPAGMARIILEA
                                                                                                                                                                                                                                                                                                      277;
                                                                                                                                                                                                                                                    Length 1732;
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LSAYAGOOV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAP-
                                                                                                                                                                                                                                                    ; Score 812.5; DB 2;
; Pred. No. 6.4e-53;
70; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----DKPAPMNLV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: May 18, 2004, 11:32:40 Job time : 29.9726 secs
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                                                                                                                                                                                                                                                    30.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QRQGPGDAASVV-----
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                            Local Similarity
es 222; Conserv
                                                                                                                                                                                                     Sequence 1732 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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May 18, 2004, 11:29:09; Search time 9.14177 Seconds (without alignments) 5229:534 Million cell updates/sec Run on:

Title: Perfect score:

US-08-353-485-2 2641 1 MRKINSLFSLAVLLSLLCWG......QNLTGSAVGQKVTLKWDAPN 497 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hemadalutinin A -	qinqipain R (EC 3.	ρ;	-H	arginyl endopeptid	endo-1,4-beta-xyla	hypothetical prote	endo-1,4-beta-xyla	probably celluloso	hypothetical prote	probable secreted	hypothetical prote	endo-1,4-beta-xyla	probable peptidogl	bacillopeptidase F	hypothetical prote	outer membrane pro	hypothetical prote	surface protein pr	internalin protein	cell surface prote		ical	probable RTX famil	- 010	hypothetical prote	exo-poly-alpha-dal	internalin protein	cycloinulo-oligosa
SUMMARIES		286	S49763	A55426	3083	I40229	349	F90696	S72640	C97012	G86643	T36143	A83412	S19011	AI1489	A36734	E97835	JC1340	A90255	T30944	AB1744	AI1476	AH1115	AH2515	B85547	A37052	AE2254	872635	AD1374	T18266
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autotransporter pr	proteinase [import	S-layer protein -	probable peptidogl	hypothetical profe	probable glycosyl	alpha-glucosidase	peptidoglycan anch	levanase/invertase	transferred entry	Subtilase family p	fungal stress prot	probable S-layer p	Chitinase (EC 3.2.	aggregation factor	hypothetical prote
AF3204	H90371	F17884	AD1129	AF1718	T35028	F97177	AH1396	C97080	A55368	A12007	JE0292	D97316	A38368	T08615	B84331
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2 AE	ш.	_	0	7	~	N	~	(1	7	71	Н	~	0	N	7
868 2 AE	ш.	21					1530 2							2205 2	694 2
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2	2	21			4.6 729	4.6 1217		4.6 1142	4.6 587	4.6 1448		4.5 1939	669	2205	118.5 4.5 694 2

ALIGNMENTS

RESULT 1

T28651	hemagglutinin A - Porphyromonas gingivalis	C;Species: Porphyromonas gingivalis	C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 03-Aug-2001	C;Accession: T28651	R; Han, N.; Whitlock, J.; Progulske-Fox, A.	Infect. Immun. 64, 4000-4007, 1996	A; Title: The hemagglutinin gene A (hagA) of Porphyromonas gingivalis 381 contains four	A; Reference number: Z20494; MUID: 97047672; PMID: 8926061	A; Accession: T28651	A;Status: preliminary; translated from GB/EMBL/DDBJ	A; Molecule type: DNA	A;Residues: 1-2628 <han></han>	A; Cross-references: EMBL: U41807; NID: q1552410; PID: q1469916; PIDN: AAB17128.1	C, Genetics:	A;Gene: hagA	Outside Matach
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ö Gaps . 0 Length 2628; Indels Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 2.1e-163;

Matches 497; Conservative 0; Mismatches 0;

δλ	7	MRKINSLFSLAVLLSILCWQQTAAAQGGPKTAPSVTHQAVQKGIRTSKVKDLRDPIPAGM 60	
Пр	н	MRKINSLFSLAVILSLICWGQTAAAQGGPKTAPSVTHQAVQKGIRTSKVKDLRDPIPAGM 60	
δ	61	ARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDPFEYKVPVNA 120	
qu	61	ARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDPFEYKVPVNA 120	
6 6	121	DASFSPTNFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSKGNDYVVBAGKTYHFT 180	
d	121	DASFSPINFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSKGNDYVVEAGKTYHFT 180	
δλ	181	VQRQCPGDAASVVVTGEGGNEFAPVQNLQMSVSGQTVTLTWQAPASDKRTYVLNESFDTQ 240	
QQ	181	VQRQGPGDAASVVVTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPASDKRTYVLNESFDTQ 240	
δy	241	TLPNGWIMIDADGDGHNWLSTINVYNTATHTGDGAMPSKSWTASGGAKIDLSPDNYLVTP 300	
QC	241	TLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTP 300	
ò	301	KVTVPENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDKPAPMNLVK 360	
QQ	301	KUTVPENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDKPAPMNLVK 360	
δλ	361	SEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYYV 420	
Ωp	361	SEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTV 420	
δλ	421	YRDNVVIAQNIAATTFNQENVAPGQXNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL 480	

421 YRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL 480

Db 421 YRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL 480	
QY 481 TGSAVGQKVTLKWDAPN 497	416 YTYTVYRDNVVIAQNLAAITIFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFA 47
Db 481 TGSAVGQKVTLKMDAPN 497	1323
	476 HVQNLTGSAVGQKVTLKWDAPN
XESULT 2 S49763	Db 1382 PVKNLKAQPDGGDVVLKWEAPS 1403
<pre>tin R (EC 3.4.22.37) precursor - Porphyromonas gingivalis (fragmen es: Porphyromonas gingivalis</pre>	RESULT 3
C;Date: U5-Mar-1995 #Bequence_revision 12-May-1995 #text_change 31-Mar-1997 C;Accession: S49763	A55426 gingipain R (RC 3 4 22 37) premireor - Downburomonse gingipalis
is, M.A.	N'Alternate names: 50% high molecular mass arginine-specific cysteine proteinase; HGP; CySpecies: Porphyromonas qinqivalis
A; Description: Cloning, sequence analysis and expression in Escherichia coli of prpR1 of A; Reference number: 849763	C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 08-Oct-1999 C;Accession: A55426; D53113
A,Accession: 849763 A,Status: preliminary	R; Pavloff, N.; Potempa, J.; Pike, R.N.; Prochazka, V.; Kiefer, M.C.; Travis, J.; Barr, J. Biol. Chem. 270. 1007-1010. 1995
A; Molecule type: DNA A; Residues: 1.1526 <adu< td=""><td>A,Title: Molecular cloning and structural characterization of the Arg-gingipain protein A,Reference number: A55426; MUID:95138080; PMID:7836351</td></adu<>	A,Title: Molecular cloning and structural characterization of the Arg-gingipain protein A,Reference number: A55426; MUID:95138080; PMID:7836351
A; Lioss-letences: EMBL: A82680 C; Genetics: A.Gane. nrwDl	A;Accession: A55426 A;Status: preliminary
C; Keywords: cysteine proteinase; hydrolase	1
Query Match 36.0%; Score 950.5; DB 2; Length 1526; Best Local Similarity 31.8%; Pred. No. 1.1e-53;	A)LIOSB-IELETERICES: GB:UlozBz; NID:GD5/06/; FIDN:AAA69539.1; FID:GD5/068 R;Pike, R.; McGraw, W.; Potempa, J.; Travis, J. J. Biol. Chem. 269. 406-411 1004
vative 77	A:Title: Lysim: 201, 101 and argining proteinases from Porphyromonas gingivalis. Isola
QY 22 TAAAQGGPKTAPSVTHQAVQKGIRTSKVKDLRDFIPAGMARIILEAH 68	A) Accession: D53113
Db 671 TATTÓGOKVTLKWDAÞSTKTNATTNTARSVDGIRELVLLSVSDAPELÍRSGQABIVLEAH 730	Ablacuts: prelminary Apolecute type: protein
Qy 69 DVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDPFEYKVPVNADASFSP 126	A) ReBidues: 228-249 cFLK> A) Experimental Source: H6 2.NAte: semistre setting from MGT biglions (WGDTD-14100)
Db 731 DVWNDGSGYQILLDADHDQYGQVIPSDTHTLM-PNCSVPANLFAPFEYTVPENADPSCSP 789	C;Keywords: cysteine proteinase; hydrolase
OY 127 TNFVLDGTASADIPAGTYDYVIINPNEGI-IYIVGEGVSKGNDYVVEAGKTYHFTVQRQG 185	84; Score 944.5; DB 2; Length 1704; 98; Pred. No. 3.2e-53;
PGDAASVV-	ALTON I
Db 850 SGDGTELTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVAAGNHEYCVEVKYTAGVS 909	671 TATTQGQKVTLKWDAPSTKTNATTNYARSVDGIRELVLLSVSDAPELLRSGQAEIVLEAH
Qy 194DYRGEGONEFAPVQNLQMSVSGQTVTLTWQAPASDKRTYVLNE 235	QY 69 DVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDPFEYKVPVNADASFSP 126
Db 910 PKVCKDVTVEGSNEFAPVQNLTGSAVGQKVTLKWDAPNGTPNPNPNPNPNPNPNPNPGTTLSE 969	
QY 236 SFDIQILPNGWIMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN 295	Qy 127 INFVLDGTASADIPAGTYDYVIINPNPGI-IYIVGEGVSKGNDYVVEAGKTYHFTVQRQG 185
Db 970 SFE-NGIPASWKTIDADGDGHGW-KPGNAPGIAGYNSNGCVYSESF-GLGGIGV-LTPDN 1025	Db 790 INMINDGTASYNIPAGTYDFALAAPQANAKIWIAGGGPTKEDDYVFEAGKKYHFLMKKMG 849
296 YLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLEETLGS	Qy 186 PGDAASVV 193
1026	Db 850 SGDGTELTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVATGNHBYCVEVKYTAGVS 909
351	Qy 194UTGEGGNEFAPVQNLQWSVSCQTVTLTWQAFASDKRTVLNESF 237
-	Db 910 PKVCKDVTVEGSNEFAPVQNLTGSAVGQKVTLKWDAPNGTPNPNPNPNPNPNPNPNPNPNPNPNPNPNPNPNPNPN
355	Qy 238 DIQILPNGWIMIDADGDGHNWLSTINVYNTATHIGDGAMFSKSWTASGGAKIDLSPDNYL 297
П	Db 970 E-NGIPASWKTIDADGDGHGW-KPGNAPGIAGYNSNGCVYSESF-GLGGIGV-LIPDNYL 1025
360	Qy 298 VTPKVTVPENGKLSYWVSSO-VPWTNEHYGVELSTTGNEAANFTIKLLEETLGS 350
1206	Db 1026 ITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASNFTNALLEETITAKGVRSP 1085
360KSEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSND	Qy 351 366
C. DD 1206 SIEADGAKEQSVWIERIVDLPAGIK-YVAFRHYNCSDLNYILLDDIQFIMGGSPTPTD 1322	Db 1086 EAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETFES 1145

			RESULT 5 140229 arginyl endopeptidase - Porphyromonas gingivalis C;Species: Porphyromonas gingivalis C;Species: Porphyromonas gingivalis C;Species: Porphyromonas gingivalis C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 08-Oct-1999 C;Accession: 140229 #sequence_revision of argingipain, a novel arginine-specific cysteine A;Reference number: 140229; MUID:95168884; PMID:7864651 A;Reference number: 140229; MUID:95168884; PMID:7864651 A;Reference number: 140229; MUID:95168884; PMID:7864651 A;Residues: 1-991 cRES> A;Residues: 1-991 cRES> A;Residues: 1-991 cRES> A;Residues: 1-991 cRES> A;Cross-references: GB:D26470; NID:9927644; PIDN:BAA05484.1; PID:g927645 A;Cross-references: GB:D26470; MID:g927644; PIDN:BAA05484.1; PID:g927645 A;Cross-references: GB:D26470; MID:g927645; DB 2; Length 991; Best Local Similarity 25.5%; Pred. No. 2.9e-24; Matches 124; Conservative 41; Mismatches 90; Indels 231; Gaps 7;
QY 367PAPYQERTID	RESULT 4 T30836 Iysine-specific cysteine proteinase porphypain (EC 3.4.22) - Porphyromonas gingivalis Iysine-specific cysteine proteinase 1, 60K C;Aderession: 12089: lasquence revision 22-Oct-1999 #text_change 17-Nov-2000 C;Accession: T30836; T30837; T30526; A53113 C;Batte: 22-Oct-1999 #sequence revision 22-Oct-1999 #text_change 17-Nov-2000 C;Accession: T30836; T30837; T30526; A53113 J. Bacteriol. 178, 2734-2741, 1996 A;ATILE: Analysis of the prtP gene encoding porphypain, a cysteine proteinase of Porphyr A;Reference number: 220895; MUID:9613011; PMID:8631659 A;Accession: T30836 A;Accession: T30836 A;Accession: T30836 A;Cross-references: EMBL:U42210; NID:91314325; PID:91314326; PIDN:AAB06565.1 R;Slakeski, N.; Cleal, S. M.; Reynolds, E.C. A;Reference number: 220896 A;Accession: T30837 A;Residues: preliminary; translated from GB/EMBL/DDBJ A;Reference number: 20896 A;Accession: T30837 A;Residues: 1-795,'I',797-1389,'W',1391-1478,'Y',1480-1732 <sla></sla>	A;Tross=reletences: EMBL:U75366; NID:g2182811; PID:g2182812; PIDN:AAB60809.1 N;Lewis, J.P.; Macrina, F.L. Infect. Immun. 66, 3035-3042, 1998 A;Title: IS195, an insertion sequence-like element associated with protease genes in Por A;Reference number: Z20844; MUID:98298016; PMID:9632563 A;Accession: T30526 A;Accession: T30526 A;Actus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA	A. Cross-references in 1352-1363, 'Y', 1355-1447, 'H', 1449-1732 < LEW> A. Cross-references is BMBL-AR017059; NID:92738802; PID:92738803; PIDN:AAC26523.1 S. Pitke, R.; MGCraw, W.; Potempa, J.; Travis, J. J. Biol. Chem. 269, 406-411, 1994 J. Travis, J. A., Title: Lygsine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolat A. Reference number: A53113; MUID:94103245; PMID:8276827 A. Reference number: A53113 A. Residues: Detliminary A. Residues: 229-249 < PIK> A. Residues: 229-249 < PIK> A. Residues: 229-249 < PIK> A. Resperimental source: H66 A. Reperimental source: H66 C. Genetics: Sequence extracted from NCBI backbone (NCBIP:141690) C. Genetics: A. Residues: Sequence extracted from NCBI backbone (NCBIP:141690) C. Genetics: A. Residues: A. Res

Db 28 IRAFADDININLUSNGDETGILDGWIKGGNPTLEVTTEQAIGGYSMKVTGRTQTY 83 Oy 178 HFTVQRQGPGDAASVVVTGB-GGNBFAPVQNLQWSVSGQTV-TLT 220 B4EGPAYSFLGKWQKGESYNVSLKVRLVSGQNSNPFITVTMFREDDNGKHYDTTV 137 Oy 221 WQAPASDKRTYVLNESFDTQTLENGWTMIDADGDGHNMLSTINVYNTATHTGDGAMFSKS 280 138 WQKQVSB	or, secreted, cellulose-bi arova, K.S.; Zeng, Q.; Gib D.R. of the Solvent-Producing 1359325 PID:g15023809; GSPDB:GN00	Query Match 5.7%; Score 150; DB 2; Length 1483; Best Local Similarity 20.2%; Pred. No. 0.14; Matches 127; Conservative 81; Mismatches 213; Indels 208; Gaps 29; QY 27 GGPTAPSVTHQAVGGIRSKVKDLRDPIPAGMARILLEAHDVWEDGTGY-77 Db 522 GTPVVTPSQINVEQGSATDQPVKIDLNONTLKDVVDQSGKTLVQGTDXTVTDTGIT 577 QY 78	QY 119 NADASFSPTNF-VLDGTASADIPAGTYDYVIINPNPGIIYIV 159 DD 636 TISQVSTPVGLICMDISYDASKFTVKDVLPNTDLVKDTDNYSFIVNTSTPGKISITFTDP 695 QY 160GEGVSKGNDYVVBAGKIYHFTVQRQGPGDAASVVVTGEGGNEFAPVQNL 208
Db 3415SAGNSSTQTHNVQNNTAAVSLSVST	RESULT 8 672640 672641 672640	C;Superiamily: Thermcanaerobacterium endo-1,4-beta-xylanase A; S-layer repeat homology; C;Keywords: glycosidase, hydrolase F;1-32/Domain: signal sequence #status predicted <sig> F;1-32/Domain: signal sequence #status predicted <sig> F;33-185/Domain: signal sequence #status predicted csIG> F;33-185/Domain: Thermctoga xylanase A maino-terminal repeat homology <txa1> F;38-185/Domain: Thermctoga xylanase A maino-terminal repeat homology <txa2> F;38-675/Domain: Streptomyces endo-1,4-beta-xylanase A homology <sxy> F;682-853/Domain: Thermctoga xylanase A cellulose-binding repeat homology <txc1> F;857-1042/Domain: Thermctoga xylanase A cellulose-binding repeat homology <txc2> F;055-1108/Domain: S-layer repeat homology <sir></sir></txc2></txc1></sxy></txa2></txa1></sig></sig>	Query Match 5.8%; Score 152; DB 2; Length 1234; Best Local Similarity 20.0%; Pred. No. 0.078; Matches 97; Conservative 66; Mismatches 138; Indels 184; Gaps 23; Qy 118 VNADASFSPTNFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSKGNDYVVEAGKTY 177

Db 825 SGSAKVYEATINKNGTYTLGAEVTSDMGIKIVESKGSVKVEL-PDGSTKAYVLIFETS 881 Qy 304 VPENGKLSYWVSSQVPWINEHYGVFLSTTGNE	PERSULT 11	488 DIEADYDFLYTEVSTDGGANWTAIDGTFDGNPIQRDGSDKPALSATVDAYG-KLVYP 373 RIDLSAYAGQQYYLAFRHFNSTGIRRLYLDDVAVGEGSSNDYTYTYYRDNY
Db 696 TLANYPISYDGILAYLDFIINSNATAGDSALTVDPATLIVADENDKDI 743 QY 209 QMSVSGOTVTLTWQAPASDKRTYVLNBSFDTQTLPNGWTMIDA-DGDGH 256 i i	392 972 972 973 974 975 976 977 976 977 977 977 977 977 977 977	OY 201 -EFAPVONLOWSUSGOTUTLTWQAPASDKRIYVLNESFDTQTLFNGWTMIDADGDGHNWL 259 DD 770 KEFKPIPPPQYNQQK-SGSYNA-TSKKITWTIAANFNQÒELSNA-SITDPISDDQNYV 824 OY 260 STINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTPKVT 303

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A; Accession: A83412
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-2468 <STO>
A; Cross-references: GB:AE004613; GB:AE004091; NID:g9947856; PIDN:AAG05263.1; GSPDB:GN001 C; Genetics:
A; Residues: Strain PAO1
C; Genetics: A; Genetics: A;
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K.; Lim,
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R,Gosalbes, M.J.; Perez-Gonzalez, J.A.; Gonzalez, R.; Navarro, A.
J. Bacteriol. 173, 7705-7710, 1991
A;Title: Two beta-glycanase genes are clustered in Bacillus polymyxa: molecular cloning,
                                                                                                                                                                                          hypothetical protein PA1874 [imported] - Pseudomonas aeruginosa (strain PAO1) C; Species: Pseudomonas aeruginosa (c; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C; Accession: A83412 R; Stover, C: K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 15-Oct-1999
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                                     594 AWTAVGFTRKGASFTKEYAQYYIAENRQYVSYD-KTLKTGPYNF 636
      -VIAQNLAATTFNQENVAPGQYNY
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Best Local Similarity 23.7%
Matches 107; Conservative
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A;Reference number: S19011; MUID:92041687; PMID:1938968
A;Accession: S19011
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-635 <GOS>
A;A;Cross-references: BMB:X57094; NID:948815; PIDN:CAA40378.1; PID:948816
A;Cross-references: BMB:X57094; NID:948815; PIDN:CAA40378.1; PID:948816
A;Note: the authors translated the codon GAA for residue 78 as Gly, CCT for residue 272
C;Function:
A;Description: caralyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans
A;Pathway: xylan degradation
C;Superfamily: Clostridium xylanase A repeat homology
C;Reywords: glycosidase; hydrolase; polysaccharide degradation
F;408-502/Domain: Clostridium xylanase A repeat homology <CXA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 LDDVAVSGEGSSNDYTYTVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TGKTPT 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 SVV--VIGEGGNEFAPVQNLQWSVSGQTVILIWQAPASDKRTYVLNESFDIQILPNGWTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 -QASGGP---ISNLNVTN--IHNGDWIAVGKADFGSAGAKTFKANVATNVGGNIEVRLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : : | | : : | | : : : ETGPLVGSLXVPSTGGMQTWREVETTINNATGVHNIYLVFTGSGSGNLLNLDAMOFTPNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --PGMAGVTWLFDPAVLVDDDGTGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --IDLSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 TAAAQGGPKTAP----SVTHQAVQKGIRTSKVKDLRDPIPAGMARIILEAHDVWEDGTGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 IDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAK---
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                                                                                                                                                                                                                                                                                                                                                                                                        5.2%; Score 137.5; Di 21.2%; Pred. No. 0.27;
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                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 21.2*
Matches 123; Conservative
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probable peptidoglycan bound protein (LPXTG motif) lin0457 [imported] - Listeria innocus Cispecies: Listeria control de Beguence_revision 27-Nov-2001 #text_change 27-Nov-2001
Riglacer, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Jones, L.M.; Karset, U.
Science 294, 849-852, 2001
Aphulbors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makhulbors: Kreft, J.; Kuhn, M.; Tisterias, A.; Waqquez-Boland, J.A.; Voss, H.; Wehland, A; Ritle: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669

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1397 ITPVVDYSKVKWDVLGTYPVTVTATDASGNKATQTVNLRIVDTTSPTILIT-----NN 1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1508 SVKPGQYQVQVNLADSSGNQAIPQTITINVVDTMGPVIKADNVSY-HVNTTKTEAEFFQD 1566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1450 PLIYSIENMRKLIEQELYKAAGLIGGDNYDLAPGQSVQPNKQPMVFISNFS--TIFSDIA 1507
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2013 <GLA>
A;Residues: 1-2013 <GLA>
A;Residues: 1-2013 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                130 VLDGTASADIP---AGTYDYVIINPNPGIIYIVGEGVSKGNDYVVEAGK-TYHFTVQRQG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QA--PASDKRIYVINESFDIQILPNGWIMIDADGDGH-----NWLSTINVYNTATHTGD 273
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                                                                                                                                                                                                                                                                                               74 GTGYQM-LWDADHNQYGASIPEES---FWFANGTIPAGLYDPFEYKVPVNADASFSPTNF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 PGDAASVVVTGEGGNEFAPVQNLQWSV-----SGQTV-----TUTW 221
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                                                                                                                                                                                                                                                       Indels 144;
                                                                                                                                                                                                           5.2%; Score 137; DB 2; Length 2013; 20.9%; Pred. No. 1.5;
                                                                                                                                                                                                                                                     82; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GAMFSK-SW-----TASGGAK----
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TTKEITVQVSKD 1624
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Matches 103;
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bacillopeptidase F (EC 3.4.21.-) precursor bpr [validated] - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: 19-May-2000 #sequence_revision 19-May-2000 #text change 16-Jun-2000
C;Accession: A36734; A35131; A35750; B35750; S08223; UN0335; I39849; B69556; UU0084
B;Sloma, A.; Rufo Jr., G.A.; Rudolph, C.F.; Sullivan, B.J.; Theriault, K.A.; Pero, J.
C;Bacteriol. 172, 5520-5521, 1990
A;Reference number: A36734
A;Contents: erratum
A;Accession: A36734
A;Molecule type: DNA
A;Residuses: 1-1433 <SLO>
A;References: GB:M29035; NID:g143307; PIDN:AAA62679.1; PID:g143308
B;Sloma, A.; Rufo Jr., G.A.; Rudolph, C.F.; Sullivan, B.J.; Theriault, K.A.; Pero, J.
J. Bacteriol. 172, 1470-1477, 1990
A;Title: Bacillopeptidase F of Bacillus subtilis: purification of the protein and clonin A;Reference number: A35131; MUID:90170864; PMID:2106512
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5.1%; Score 135.5; DB 1; Length 1433;

Query Match

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A;Note: the authors translated the codon GAA for residue 545 as Leu

A; Accession: A35131 A; Molecule type: DNA

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A;Status: preliminary;
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A;Status: preliminary;
A;Status: DNA
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A;Cross-references: GB:M22630; NID:g142938; PIDN:AAA22458.1; PID:g551705
B;Kunst, F.; Ogaaawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte:
C; Bron, S; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch.
A; Ehloch, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle: iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holeappel, S.; Hosono, S.; Hullo, M.F.
Koetter, E.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee
Y, M.; Ogawar, A.; Oddega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell.
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Seronlon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters; P.; Wipper, A.; Yamamoto, H.; Yamano, K.; Yata, K.; Yoshida, J.;
A;Title: The complete genome sequence of the Gram-Dositive bacterium Bacillus subtilis. A; Molecule type: DNA A; Residues: 1410-1433 <MAS> A; Residues: 1410-1433 <MAS> A; Cross-references: EMBL:X17344; NID:940165; PIDN:CAA35224.1; PID:9809661 R; Kato, T.; Yamagata, Y.; Arai, T.; Ichishima, E. Biosci. Biotechnol. Biochem. 56, 1166-1168, 1992 A; Title: Purification of a new extracellular 90-kDa serine proteinase with isoelectric J A; Reference number: JN03335; MUID:93005071; PMID:1368833 J. Biol. Chem. 265, 6845-6850, 1990
A.Title: Cloning, genetic organization, and characterization of a structural gene encod: A.Reference number: A35750, MUID:90216713, PMID:2108961 'n. A,Title: Cloning and characterization of Bacillus subtilis homologs of Escherichia coli A,Reference number: 139846; MUID:89008108; PMID:3139638 GB: 299112; GB: AL009126; NID: 92633902; PIDN: CAB13404.1; 168 A; Title: Nucleotide sequence of the sporulation gene spoIIGA from Bacillus subtilis. A; Reference number: S08223; MUID:90174995; PMID:2106671 A;Molecule type: DNA A;Residues: 876-935, CG' <WU2> A;Cross-references: GB-J05400; NID:g142607; PIDN:AAAB3363.1; PID:g119197 A;Note: this sequence has been corrected R;Masuda, E.S.; Anaguchi, H.; Sato, T.; Takeuchi, M.; Kobayashi, Y. A;Molecule type: DNA A;Residues: 1-392,'V',394-828,'NIRTRLYSLKFCRSRHKSV' <WUA> A;Cross-references: CB:J05400; NID:g142607; PIDN:AAA83362.1; PID:g142609 A;Note: this sequence has been corrected A;Accession: B35750 A;Status: nucleic acid sequence not shown; translation not shown A;Map position: 135 (degrees)
C;Superfamily: bacillopeptidase F; subtilisin homology
C;Superfamily: bacillopeptidase F; subtilisin homology
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A,Molecule type: protein
A,Molecule type: 195-218, A' «KAT»
A,Mote: source of this material was Bacillus subtilis (natto)
K,Beall, B., Low, M., Lutkenhaus, J.
J. Bacteriol. 170, 4855-4864, 1988 ;227,274,452/Active site: Asp, His, Ser #status predicted A; Reference number: A69580; MUID: 98044033; PMID: 9384377 X.C.; Nathoo, S.; Pang, A.S.H.; Carne, T.; Wong, Nucleic Acids Res. 18, 657, 1990 A;Residues: 1-1433 <KUN> A;Cross-references: GB:Z99111; A;Experimental source: strain 1 A; Accession: 139849 A; Accession: JN0335 A;Accession: B69596 A; Accession: A35750 A; Accession: S08223 A; Molecule type:

20.6%; Pred. No. 1.1; tive 58; Mismatches 150; Indels 223; Gaps 31;	ASIPEESFWFANGTIPAGLYDPFEYKVPUNADASFSPTNFVLDGTAS 136	SSVPGQTYEDGWDGTSMAGPHVSAVAALLKQANASLSVDEMEDILTSTAEPLTDS 491	ADIPAGTYDYVIINPNPGIIYIVGEGVSKGNDYVVEAGKTYHFTVQRQGPGD 188	TFPDSPNNGYGHGLVNAFDA-VSAVTDGLGKAEGQVSVEGDDQEPPVYQHEKVTEAYEGG 550	AASVVVTGEGGNEFAPVONLOWSVSGOTVTLTWOAPASDKRTY- 231	SIPLTLTAEDNVSVTSVKLDQGEWTEITAKRISGDHLKGTYQAEIPDIKGTKLSVK 610	VINESFDTQTLPNGWTMIDADGDGHNWLSTINVYNT 267	WMIHDFGGHVVSSDVYDVTVKPSITAGYKQDFETAPGGWVASGTNNNW 658	ATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTPKVTVPENGK 309	EWGVPSTGPNTAASGEKVYGTNLT-GNYANSANMNLVMPPLKAPDSGS 705	LSYWVSSQVPWTNEHYG-VFLSTTGNEAANFTIKLLEETLGSDKPAPMNLVK 360	LFLQFKSWHNLEDDFDYGYVFVLPEGEKNWEQAGVYNGK744	SEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTY 418	TSSWIDEEIDLSAYKGQNIQVMFNLQSDESIAKEGWYIDDVVLSDKSAGK 794	442	TVKKNYLGVEKPSGKQKKKRPUNPKKARPSANTAVKHQNKAIQPQVLPLKAQVSVVETGKS 854	PGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNLTGSAVGQKVTL 491	rLKHKAGDYTLMAEAYGYQSKTQKVSL 891			
Best Local Similarity 20.6%; P Matches 112; Conservative 58;	90 ASIPEESFWFANGTIPAG	437 SSVPGQTYEDGWDGTSMAC	137ADIPAGTYDYVIINPNPGI	492 TFPDSPNNGYGHGLVNAFDA-	189 AASVWTGEGGNEFAPVO	: : : : : : : : : : : :	232VLNESFDT	611 WMIHDFGGHVVSSDVYDVTV	268 ATHTGDGAMFSKSW	659EWGVPSTGE	310 LSYWVSSQVPWTNEHYC	706 LFLQFKSWHNLEDDFDYC	361 SEGVKLPAPYQERTIDLSAY	745TSSWTDEEIDLSAY	419 TVYRDNVVI	795 TVKKNKLGVEKPSGKQKKKP	443PGQYNYCVEVKYTA	855 TYSDQSTGQYTLKHKAC	492 KWD 494	892 KTD 894	
Best Loca Matches	Qy	ਹਿ ਪ੍ਰਹ	δλ	, අග	λΌ	qa	δλ	qa	ζζ	qa	δλ	Dβ	Qy	qa	ò	qa	δλ	. qa	λŏ	qa	

Search completed: May 18, 2004, 11:35:56 Job time : 13.1418 secs Н

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Q995h0 homo sapien Q52657 rickettsia P35806 caulobacter P35830 thermus the P76072 escherichia P32637 podospora a Q11176 caenorhabdi P21647 kibbsiella Q91740 xenopus lae P16950 t amylopull P04937 rattus norv Q60053 thermoactin	ALIGNMENTS ALIGNMENTS ALIGNMENTS (GI STANDARD; PRT; 2628 AA. (1000 (Rel. 39, Created) (1000 (Rel. 39, Last sequence update) (100 (Rel. 39, Reprinbate C25-Likt 3) (100 (Rel. 30, Reprinbate C25-Likt 3) (100 (Rel. 30, Reprinbate C26-Likt 3) (100 (Rel. 30, Reprinbate C26-Likt 3) (100 (Rel. 30, Reprinbate C26-Likt 3) (100 (Rel. 30, Rel.	Indels
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MEDLINE-92406812; PubMed-1527017;
Chen Z., Potempa J., Polanowski A., Wikstrom M., Travis J.;
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MEDLINE=95168884; PubMed=7864651;
Okamoto K., Misumi Y., Kadowaki T., Yoneda M., Yamamoto
                                                                                                         Indels
1443 PEPTIDASE C25-LIKE 3.
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                                                                                                         10;
                                                            Score 2583; DB 1;
Pred. No. 4.9e-159;
0; Mismatches 10;
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Bacteria; Bacteroidetes; Bacteroides (
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      DASFSPTNFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSKGNDYVVEAGKTYHFT 180
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                             TLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTP
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Hemagglutinin; Virulence; Hydrolase; Thiol protease; Signal; Repeat;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nelson K.E., Fleischmann R.D., Deboy R.T., Paulsen I.T., Fouts D.E., Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M., Haft D.H., Kolonay J.F., Nelson W.C., Mason T., Tallon L., Gray J., Dewhirst F.E., Fraser C.M.;

"Complete genome sequence of the oral pathogenic bacterium Porphyromonas ginglyals strain W83.";

"Bacteriol. 185:559-5601(2003)

"-: FUNCTION: Agglutinates erythrocytes (By similarity).

-: SIMILARITY: Belongs to peptidase family C25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMAGGLUTININ A.
PEPTIDASE C25-LIKE 1.
PEPTIDASE C25-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE017178; AAQ66831.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGSAVGQKVTLKWDAPN 497
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15-MAR-2004
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P59915;
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                                                                                                                                                                                                                                                                                                                     DASFSPTNFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSKGNDYVVEAGKTYHFT 180
                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 VQRQSPGDAASVVVVTGEGGNEFAPVQNLQMSVSGQTVTLTWQAPASDKRTYVLNESFDTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASSGAKIDLSPDNYLVTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL
                                                                                                                                                        1 MRKINSLFSLAVLLSLLCWGQTAAAQGGPKTAPSVTHQAVQKGIRTSKAKDLRDP1PAGM
                                                                                                                                                                                                                ARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDPFEYKVPVNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVTVPENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDKPAPMNLVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 SEGVKAPAPYÓERTIDLSAYAGÓÓVYLAFRHFGCTGIFRLYLDDVAVSGEGSSNDYTYTV
                                                                                                     1 MRKINSLFSLAVILSLLCWGQTAAAQGGPKTAPSVTHQAVQKGIRTSKVKDLRDPIPAGM
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Arg-gingipain)
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2164;
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Arch. Biochem. Biophys. 316:917-925 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gingivalis).
(class); Bacteroidales;
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us-08-353-485-2.rsp

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-- EGGGSDYTYTVYRDGT 875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     989 AA; 110238 MW; FA85FE8A3AC8944C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fletcher H.M., Schenkein H.A., Macrina F.L.;
Infect. Immun. 62:5707-5707(1994).
-!- FUNCTION: CLEAVES HUMAN COMPLEMENT COMPONENT C3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND IS A VIRULENCE FACTOR.
SUBCELLULAR LOCATION: In membrane vesicles.
SIMILARITY: Belongs to peptidase family C25.
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                                                                                                                                                                                                                                                                                   01-NCV-1995 (Rel. 32, Created)
01-NCV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protease prtH (EC 3.4.22.-).
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Hydrolase, Thiol protease, Repeat, Virulence.
                                                                                                                                                                                                                                                989 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95012612; PubMed=7927685;
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                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                      |::|:
GKTITV 941
                                                                                                                   486 GQKVTL 491
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                                                                                                                                                                                                                                                PRTH PORGI
P46071;
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       860
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PRTH PORGI
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                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68
                                                                                                                         COMPLEMENT C3 and C5.
CATALYTIC ACTIVITY: Cleavage of proteins, including collagens and immunoglobulins, with a preference for Arg in P1, and hydrophobic residues in P2 and D3.
ENTYME REGULATION: Requires cysteine for activation and Ca(2+) and/or Mg(2+) for stabilization. It is stimulated by glycine-containing dipeptides. It is resistant to inhibition by proteinase inhibitors in human plasma.
SIMILMARITY: Belongs to peptidase family C25.
"Purification and characterization of a 50-kba cysteine proteinase (gingipain) from Porphyromonas gingivalis.";
J. Biol. Chem. 267:18896-18901(1992).
-!- FUNCTION: Thiol protease which is believed to participate in intracellular degradation and turnover of proteins. Its proteolytic activity is a major factor in both periodontal tissue destruction and in bacterial host defense mechanisms. Activates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGDAASVVVTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPASDKRTYVLNESFDTQTLPNG
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InterPro; IPR001769; Peptidase C25.
InterPro; IPR00536; Peptidase C25.
InterPro; IPR00536; Peptidase C25.
Pfam; PF03785; Peptidase C25; I.
Pfam; PF03785; Peptidase C25_C; I.
Virulence; Hydrolase, Thiol protease; Calcium; Signal; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 494.5; DB 1; Length 991;
Pred. No. 2e-24;
41; Mismatches 90; Indels 231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GINGIPAIN R1.

PROTON DONOR (BY SIMILARITY).

NUCLEOPHILE (BY SIMILARITY).

RT -> TK (IN REF. 2).

RT 03EE3F43CEBRZ544 CRC64;
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25.5%;
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438
471
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HSSP; P95493; 1CVR.
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471
264
991 AA;
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Matches 124;
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ACT_SITE
CONFLICT
SEQUENCE
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                                                            118 QGWLCLSSGQLDWLTAHGGTNVVSSFSWNG----MALNPDNYLLSKDVTGATKVKYYYA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.GINGIVALIS TO EVADE COMPLEMENT-MEDIATED KILLING DURING THE IMMUNE RESPONSE. PLAYS AN IMPORTANT ROLE IN SOFT TISSUE INFECTIONS
VIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNLTGSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 HWW--LSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTPKVTVPENGKLSYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAY ENABLE
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Bacteria, Bacteroidetes, Bacteroides (class), Bacteroidales;
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                                                                             429
                                                                                                                                                          489
                       287
                                                                                                                                                                               GLTETTFEEDGVAIGNHEYCVEVKYTAGVSPKKCVNVTV-NSTQFNPVKNLKAQPDGGDV 346
VSSQVPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDK-PAPMNL-VKSEGVKLPAPYQ 371
                                                                                                                ERTVDLP -- AGTK-YVAFRHYNCSDLNYILLDDIQFTMGGSPTPTDYTYTVYRDGTKIKE
                                                                             ERTIDLSAYAGOOVYLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYTYTVYRDNVVIAO
                                                                                                                                                        430 NLAATTFNQENVAPGOYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNLTGSAVGQKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xylans.
-!- PATHWAY: Xylan degradation.
-!- INDUCTION: By xylan and xylose.
-!- INDUCTION: By xylan and xylose.
-!- SIMILARITY: Belongs to cellulase family F (family 10 of glycosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93388520; PubMed=8376336;

MEDLINE=93388520; PubMed=8376336;

Lee Y.-E., Lowe S.E., Henrissat B., Zeikus J.G.;

Lee Y.-E., Lowe S.E., Henrissat B., Zeikus J.G.;

Lee S.E., Henrissat B., Zeikus J.G.;

Lee S.E., Henrissat B., Zeikus J.G.;

endoxylanase from Thermoanaerobacterium saccharolyticum B6A-RI.";

J. Bacteriol. 175:5890-5898[1933]

-!- FUNCTION: Endo-acting enzyme that randomly cleaves the internal xylosidic linkages of the xylan backbone, yielding xylosidic linkages of the xylan backbone, yielding xylosidic linkages of the xylan backbone, yielding the hydrolyzed to xylose molecules by beta-xylosidase (B7 3.2.1.37). The temperature and pH optima for this enzyme are 70 degrees Celsius and 5.5, respectively. Requires at least three xylose residues for catalytic activity. Does not have activity against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 34-41.
STRAIN=B6A-RI;
MEDILINE=94028940; PubMed=8215382;
Lee Y.-E., Lowe S.E., Zeikus J.G.;
"Gene cloning, sequencing, and biochemical characterization of endoxylanase from Thermoanaerobacterium saccharolyticum B6A-RI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermoanaerobacter saccharolyticum.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydrolases).
-!- SIMILARITY: Contains 2 S-layer homology (SLH) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                 01-UNN-1994 (Rel. 29, Created)
01-UNN-1994 (Rel. 29, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase
                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1,4-beta-D-xylan xylanohydrolase A)
                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                        490 TLKWDAPN 497
                                                                                                                                                                                                                                                                           347 VLKWEAPS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=28896;
                                                                                                                                                                                                                                                                                                                                                                                XYNA THESA P36917;
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166 GNDYVVEAGKTYHFTVQRQGP-----GDAASV-----VVTGE-GGNEFAPVQNLQ 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 RTANWNGPSYDL-----TGKIVPGQQYNVDFWVK-------FVNGNDTEQIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 AGLYDPPEYKVPVNADASFSPTNFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 YSMKVTGRTQTY-----EGPAYSFLGKMQKGESYSVSLKVRLVSGQNSSNPLITVTMFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 EDDNGKHYDTIVWQKQVSEDSWTTVSGTYTLDYIGTLKTLYMYVESPDPTLEYYIDDVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TQTLPNGWTMIDADGDGHNWLSTIN-----VYNTATHTGDGAMFSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 TIQNPIQVGNVIANETFENGNT-----SGWIGTGSSVVKAVYGVA-HSGDYSLLTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 WTAS-GGAKIDLSPDNYLVTPKVTVPENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAANF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIKLLEETLGSDKPAPM-----NLVKSEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 ASLFSP-----PIRVFADDTNINLVSNG----DFESGTIDGWIKQGNPTLAVTTEQAIGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 WSVSGQTV-TLTWQAPASD--------KRTYVLNESFD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 156; DB 1; Length 1157; ; Pred. No. 0.019; 64; Mismatches 128; Indels 166;
InterPro; IPR003305; CBM_CenC.
InterPro; IPR008999; Gal_bind like.
InterPro; IPR0018999; Gal_bind like.
InterPro; IPR0011847; Glyco_hydro_10.
InterPro; IPR001119; SiH.
InterPro; IPR00119; Glyco_lo; 1.
IPR00118; PR00129; Glyco_lo; 1.
IPR00118; PR00129; Glycosyl, HYDROL_F1; 1.
IPR00118; PR00109; SiH. DOMALTN; 2.
IPR00118; PR00107; SiH. DOMALTN; 2.
IPR00118; PR001072; SiH. DOMALTN; 2.
IPR00118; PR001073; SiH. DOMALTN; 2.
IPR00118; PR00118; PR001073; PR00118; P
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Endo-1,4-beta-xylanase D precursor (EC 3.2.1.8) (Xylanase D)
(1,4-beta-D-xylan xylanohydrolase D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128379 MW; 51FA6004497EC58B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ENDO-1,4-BETA-XYLANASE A. CATALYTIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 STGIFRLYLDDVAVSGEGSSNDYT-----YTVYRD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D->N: LOSS OF ACTIVITY
E->Q: LOSS OF ACTIVITY
D->N: LOSS OF ACTIVITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         635 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOPHILE
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61157 AA;
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P45796;
01-NOV-1995 (
01-NOV-1995 (
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PAEPO
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339

EMBL, M97882; AAA21812.1; ALT_SEQ. HSSP, P10478; 1XYZ. InterPro; IPR008960; CBD9-like.

23;

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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=168;
                                                                                                                                                                                   SUBF BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISIONS
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                                                                                                                                                                        SUBF BACSU
                                                                                                                                                          RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---EGVSKGNDYVVEAGKTY---HFT-VQRQGPGDAA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 TFFGVGGNNHHAVFNFKNEMYVVYHAQTVSKAQ---IGAGKGYRSPHINKLVHKEDGSIS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 EVQGNMTG----1AQLSNMNPYTRVEAETIAWQAGVTTEPT--------397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 IDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAK-------IDLSP 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 -QASGGP---ISNLNVTN--IHNGDWIAVGKADFGSAGAKTFKANVATNVGGNIEVRLDS 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 LEETLGSDKPAPMNLVKSEGVKLPAPYQERTIDLSAYAGQQVYLAFRHF--NSTGIFRLY 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QMLWDADHNQYGASIPEESFWFANGTIPAGLYDPFEYKV-------PVNADA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 LFEDSGIHKYNGKYYYSYCINFA--GTHPQQYPAGEIGYMVSDNPMGPFTYKGHFLKNPY 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 SVV--VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPASDKRTYVLNESFDTQTLPNGWTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---FTIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- PGMAGVTWLFDPAVLVDDDGTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217; Gaps
Paenibacillus polymyxa (Bacillus polymyxa).
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
NCBL_TaxID=1406;
                                                                                                                                                                                   ARABINOFURANOSIDASE ACTIVITY.
CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
                                                                                                                              molecular cloning, expression, and sequence analysis of genes
encoding a xylanase and an endo-beta-(1,3)-(1,4)-glucanase.";
J. Bacteriol. 173:7705-7710(1991)
--- FUNCTION: SHOWS XYLANASE ACTIVITY AS WELL AS ALPHA-L-
                                                                                                      Gosalbes M.J., Perez-Gonzalez J.A., Gonzalez R., Navarro A.; "Two beta-glycanase genes are clustered in Bacillus polymyxa:
                                                                                                                                                                                                                         PATHWÄY: Xylan degradation.
SIMILARITY: Belongs to family 43 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 DNYLVTPKVTVPENGKLSYW--VSSQVPWTNEHYGVFLSTTGNEAAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFSPT-------NFVLDGTASADIPAGTYDYVII-NP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 635 ENDO-1,4-BETA-XYLANASE D. 635 AA; 67914 MW; F9DEC69967323316 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART, SM00606, CBD 1V; 1.
Xylan degradation; Hydrolase; Glycosidase; Signal.
SIGNAL 1 26 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.2%; Score 137.5; Di
21.2%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                          EMBL; X57094; CAA40378.1; -.
PIR; S19011; S19011.
InterPro; PRR005684; CBD_IV.
InterPro; IPR005084; CBM_6.
InterPro; IPR0050879; Gal_bind_like.
PF03422; CBM_6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TADTPIGPWTDPLGKALVTHST---
                                                                                         MEDLINE=92041687; PubMed=1938968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 123; Conservative
                                                                                                                                                                                                                linkages in xylans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                               SEQUENCE FROM N.A.
                                                                             STRAIN=ATCC 842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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RA Kunst F., Ogasawara N., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Razevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Razevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Razevedo V., Bertero M.G., Brans A., Braun M., Brignell S.C., Bron S., A. Brouillet S., Bruschi C.V., Connerton I.F., Cummings N.J., Daniel R.A., RA Brouillet S., Deviner K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Gya B.J., Hagad K., Halech J., Harwood C.R., Henaut A., Guiseppi G., Guy B.J., Hagad K., Halech J., Harwood C.R., Henaut A., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Kuita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C., Robasahi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Ruita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C., Roba B., Mixuno M., Moestl D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Rasecan B., Pulralle B., Ropescan B., Puralle B., Roche B., Rose M., Sadaie Y., Reger M., Rivolta C., Rocha E., Rochoeter R., Scoffone F., Schleich S., Schroeter R., Shin B.S., Soldo B., Ra Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
                                              560
                                                                                                                                       402 LDDVAVSGEGSSNDYTYTVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPK 461
                                                                                                                                                                                                                       -----GVTVGSFNF-----TGKTPT 597
Pero J., "Bacillopeptidase F of Bacillus subtilis: purification of the protein
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01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Bacillopeptidase F precursor (EC 3.4.21.-) (Esterase) (RP-I protease)
(90 kDa serine proteinase).
Bacillus subtilis.
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Wu X.-C., Nathoo S., Pang A.S.-H., Carne T., Wang S.-L.;
"Cloning, genetic organization, and characterization of a structural
gene encoding bacillopeptidase F from Bacillus subtilis.";
J. Biol. Chem. 265:6845-6850(1990).
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                                                                                                                                                                                                                                                                                                                462 VCKDVTVEGSNEFAHVQNLTGSAVGQKVTL-----KWDA 495
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J. Bacteriol. 172:1470-1477(1990).
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Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takenohi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambut R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wiptat A., Yamamoto H., Yamane K., Yoshikawa H.F., Zunstein E., Yoshikawa H.F., Zunstein E., Yoshikawa H., Danchin A., "The complete genome sequence of the Gram-positive bacterium Bacillus
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Rato T., Yamagata Y., Arai T., Ichishima B.;
"Purification of a new extracellular 90-kDa serine proteinase with isoelectric point of 3.9 from Bacillus subtilis (natto) and elucidation of its distinct mode of action.";
Biosci. Biotechnol. Biochem. 56:1166-1168 (1992).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Masuda E.S., Anaguchi H., Sato T., Takeuchi M., Kobayashi Y.;
"Nucleotide sequence of the sporulation gene spolIGA from Bacillus
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SIGNAL 1 30
PROPEP 31 194 POTENTIAL.
                                                                                                                                                                                                                     SEQUENCE OF 1-211 FROM N.A.
MEDLINE=89008108; PubMed=3139638;
Beall B., Lowe M., Lutkenhaus J.;
"Cloning and characterization of Bacillus subtilis homologs of
Escherichia coli cell division genes ftsZ and ftsA.";
J. Bacteriol. 170:4855-4864(1988).
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A -> V (IN REF. 3).
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OPQVLP -> RTRLYS (IN REF. 3).
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InterPro; IPR00209; Peptidase S8.
InterPro; IPR009209; Protease Inhib.
Pfam; PF05547; Peptidase M6; I.
Pfam; PF00082; Peptidase S8; I.
PRINTS; PR0723; SUBTILIASIN,
PROSITE; PS00134; SUBTILIASE ASP; FALSE NEG.
PROSITE; PS00134; SUBTILIASE HIS; I.
PROSITE; PS00134; SUBTILIASE HIS; I.
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STRAIN-168 / Marburg;
MEDLINE-90174995; PubMed=2106671;
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EMBL, U05400; AAA83362.1; --
EMBL, Z99111; CAB13403.1; --
EMBL, M22630; AAA22458.1; --
EMBL, X17344; CAA35224.1; --
EMBL, X17344; CAA35224.1; --
FIR, A36734; A36734.
HSSP, P00782; SSBT.
MEROPS; S08.017; --
SubtiList; BG10233; bpr.
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last suntation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
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                                                                                                                                                                                         58; Mismatches 150; Indels 223;
                                                                                                                                Length 1433;
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Rickettsiaceae; Rickettsleae; Rickettsia.
AUVSVVETG -> FCRSRHKSV (IN REF. MISSING (IN REF. 3)
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1433 AA; 154577 MW; 98DF6846897807C9 CRC64;
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Pred. No. 0.54;
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10-OCT-2003 (Rel. 42, Last sequence update)
Hypotherical protein SSO1033 precursor.
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InterPro; IPR008957; FN III-like.
InterPro; IPR003961; FN III.
InterPro; IPR006652; Kelch_rep.
Pfam; PF00041; fn3; 2.
Pfam; PF01344; Kelch; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires alrease agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Stenos J., Walker D.;
Stenos J., Walker D.;
Stenos J., Walker D.;
The rickettsial outer membrane protein A and B genes of Rickettsia australis, the most divergent rickettsia of the spotted fever group.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-: FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                                                                                                                                                                                                                                       (By similarity).
-!-SUBMERLULYAR LOCATION: Cell wall. This bacterium is covered by a S-layer with hexagonal symmetry (By similarity).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 ANGTIPAGLYDPFEYKVPVNADASFSPTNFV------LDGTASADIPAGTYDYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 IINPNPGIIYIVGEGV---SKGNDYVVEAGKTYHFTVQRQGPGDAASVVVTGEGGNE--F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P -> A (IN STRAIN INDIAN TICK TYPHUS).

G -> S (IN STRAIN INDIAN TICK TYPHUS).

K -> N (IN STRAIN INDIAN TICK TYPHUS).

V -> A (IN STRAIN INDIAN TICK TYPHUS).

N -> D (IN STRAIN INDIAN TICK TYPHUS).

I -> V (IN STRAIN INDIAN TICK TYPHUS).

A -> T (IN STRAIN INDIAN TICK TYPHUS).

R -> L (IN STRAIN INDIAN TICK TYPHUS).

K -> L (IN STRAIN INDIAN TICK TYPHUS).

K -> L (IN STRAIN INDIAN TICK TYPHUS).

K -> D (IN REF. 3).

E -> D (IN REF. 3).

G -> S (IN REF. 3).

G -> S (IN REF. 3).

H -> R (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . Pred. No. 0.7;
53; Mismatches 189; Indels 184; Gaps
                                                                                                                                                                                                                                                                                                                                                        FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
                                                                                  Roux V., Raoult D.; "Phylogenetic analysis of members of the genus Rickettsia using the gene coding the outer-membrane protein rOmpB (ompB)."; Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wall; Complete proteome.
120 kDa SURFACE-EXPOSED PROTEIN.
32 kDa BETA PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1) Score 135, ilarity 19.3%; Pred. No. 0 Conservative 53; Mismatch
                                                     STRAIN=Indian tick typhus, and Malish 7;
MEDLINE=20393643; PubMed=10939649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro, IPR006315; Autotransport.
InterPro; IPR005546; Autotransporter.
Pfam; PF03797; Autotransporter; 1.
TIGRPAMS; TIGR01414; autotrans bar1; 2.
Antigen; S-layer; Cell wall; Complete p:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AE008659; AAL03623.1; -. EMBL, AF123721; AAF34124.1; -. EMBL, AF123726; AAF34129.1; -. EMBL, AF149110; AAD39533.1; -.
                                                                                                                                                                                OF 353-1655 FROM N.A.
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1159 1159
1177 1177
1492 1492
1655 AA; 168342 M
                                  OF 33-1649 FROM N.A.
   Science 293:2093-2098(2001).
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Les 102; Conserv
                                                                                                                                                                                                                                                                                                                                        similarity).
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CHAIN
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                                                                                                                                                             228 KRIYVLNESFDIQTLPNGWIM----IDADGDGHNWLSTINVYNTATHTGDGAMFSKSWT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 ASGGAKIDLSPDNYLVTPKVTVPENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAANFTIK 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    805 VASADGTGIVEFVNTGPITVTINKQAAPVNALKQITVSGPGNVVINEIGNAGNYHGAVTD 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          649 IGNNGAVQFAHNTYLITRTTNAAGQGKIIF----NPVVNNNTTL---ATGTNLGSATNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----VSGTVGGQQGNKFNTVALDNGTTVKFLGNATFNGNTTIAANSTLQIGGNYTADF
                                                                                                                                                                                                                                                        ----GVSPKVCKDVTVEGS-----NEFAHVQNLTG----
534 AALQGITLANDATKTLTLGGANIIGANGGTINFQANGGTIKLTSTQNNIVVDFDLAIATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 YLDDVAVSGE--GSSNDYTYTVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTA-
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OC Bacteria OC NICELTO OX NCBI_TO RN [1] TO RD STEQUENCY RC STEALNEY RA UCHIYAMA RT IMPONICA RI SUDMITCA CC -1- FUN CC -1- FUN CC -1- STEA	1 1		CC the Burd CC use by CC modified CC entities	- ,,,,,	DR InterPrough DR Pfam; Plus DR TIGRFAM KW Antigen	FT CHAIN FT CHAIN FT CHAIN SQ SEQUENCY	Query Matcl Best Local Matches	Qy 10 Db 43	Qy 14.	Qy 19 Db 54	Qy 24.	Qy 29	Db 66.	Oy 41	.57 da	Oy 45
ET SMART; SM00660; FN3; 3. PN3; 3. Repeat; Repeat; Signal; Complete proteome. FT SIGNAL 1 28 POTENTIAL. 1 28 POTENTIAL. FT CHAIN 29 725 HYPOTHETICAL PROTEIN SSO1033. FT REPEAT 59 100 KELCH 1. FT REPEAT 501 145 KELCH 3. FT REPEAT 201 248 KELCH 4. FT REPEAT 250 297 KELCH 5. FT REPEAT 250 297 KELCH 5. FT REPEAT 250 297 KELCH 5. FT POMAIN 323 398 FIBRONECTIN TYPE-III 1. FT DOMAIN 385 652 FIBRONECTIN TYPE-III 3. FT DOMAIN 585 652 FIBRONECTIN TYPE-III 3. SEQUENCE 725 AA; 78465 MW; FEBF1220D013BAB6 CRC64;	Query Match Best Local Similarity 20.4%; Pred. No. 0.4; Matches 112; Conservative 61; Mismatches 134; Indels 241; Gaps 27;	Qy 101 NGTIPAGLYDPFEYKVPVNADASFSPTNFVLDGTASADI 139	QY 140PAGTYDYVIINPN	QY 175 KTYHFTVQRQGFGDAASVVVTGBGGNEFAPVQNLQ 209 DD 262 SGGVNNAILAYYNGNLQRVGYLPVPVYSAGYVQVGNMLYLAGGIGSSLSDVSALQLITFN 321	Qy 210WSVSGQTVTLTWQAPASDKRTYVLNESFDTGTLPNGWTMIDADGDGHNWL 259 1 :	QY 260 STINVYNTATHTGDGAMF 277	QY 278SKSWTASGGAKIDLSPDNYLVTPKVT 303 : :	QY 304 VPENGKLSYWVSSQVPWTNEHYGVFLSTTGNE-AANFTIKLLEETLGSDKPAPMNLVKSE 362 	Qy 363 GVKLPAPYQERTIDLSAYAGQQVYLAFRHPNSTGIFRLYL 402 ::	QY 403DDVAVSGEGSSNDYTYTVYRDNVVIÀQNLAATTFNQENVAPGQYNYCVEV 452 DD 588 SPQVSLIGFGNNLYISWNNEANVITYLVYVNNSLVYEGFSNSIVTNISNGTYLVKV 643	Qy 453 KYTAGVSP 460 : Db 644IGVNP 648		PB_RICJA OMPB_RICJA O06653;	ib-UCI-2001 (Rel. 40, Last amocation update) Outer membrane protein B precursor (168 RDs surface (Surface protein antigen) (Cell surface antigen 5)		
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y similarity).

BCELLUTAR LOCATION: Cell wall. This bacterium is covered by a S-
yer with hexagonal symmetry.

MILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 MNLVKS--EGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGE--G
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                                                                                                                                                                                              na T., defing of the gene encoding the protein rOmp B of Rickettsia and \frac{1}{2}
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ia; Proteobacteria; Alphaproteobacteria; Rickettsiales; tsiaceae; Rickettsieae; Rickettsia.
axID=35790;
                                                                                                                                                                                                                                                                             ted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
NCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
RUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
RULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 120 kDa SURFACE-EXPOSED PROTEIN.
56 32 kDa BETA PEPTIDE.
33 POLY-CLY.
168097 MW; 3132A69C9DD5999F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 SSNDYTYTVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF03797; Autotransporter; 1.
Ms; TIGR01414; autotrans_barl; 2.
in; S-layer; Cell wall.
1 1338 120 kDa SUI
1339 1656 32 kDa BED?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ro; IPR006315; Autotransport.
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1656 AA;
                                                                                                                                   TE FROM N.A.
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817 NTGPINVTLNKQAVPVNALKQITVSGPGNVVVNEIGNAGNYHGA 860

794 AA

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 31:2134-2147(2003).
-!- FUNCTION: Required for the insertion of integral membrane proteins into the membrane. Probably plays an essential role in the integration of proteins of the respiratory chain complexes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Specifically interacts with transmembrane segments of nascent integral membrane proteins during membrane integration (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Involved in integration of membrane proteins that insert dependently and independently of the Sec translocase complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC): examining the role of niche-specific genes in the evolution of the Chlamydiaceae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=GPIC;
MEDILINE-22569155; PubMed=12682364;
MEDILINE-22569155; PubMed=12682364;
Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple B., Khouri H., Federova N.B., Carty H.A.
Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                         Chlamydophila caviae.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the OXA1/oxaA family. Subfamily 1.
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                                                                                                                                      (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_01810; -; 1.
InterPro; IPR001708; 60kDa_innermeb.
Pfam; PF02096; 60KD_IMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE016995; AAP05217.1; -. TIGR; CCA00472; -.
                                                                                                                                                                                                                                              Inner membrane protein oxaA. OXAA OR CCA00472.
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691
740
794 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=83557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity)
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                                                                                                                                             10-OCT-2003
                                                                                                                                                                                                                15-MAR-2004
                                                                      OXAA CHLCV
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                                 OXAA_CHLCV
RESULT 11
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PGDAASVVVIGEGGNEFAPVQNLQWSVSGQTVILIWQAPASD--KRIYVLNESFDIQTLP 243
                                    278 PSEASFPGLPSVGANN-QPVSD----TVGGYYPLLRRGILSDAKKRT---PSSYHALNIV 329
                                                                                                                                               281 WTASGGAKIDLSPDNYLVTP------KVTVPE-----NGKLSYWVSSQ 317
                                                                                                                                                                                                                         --VK 365
                                                                                                                                                                                                                                                 SGRELTNSVASGYR-VSTFNSTMLELESNDGSIKKTYKLPQQQPYAFEVEVGVNRASDDL
                                                                                                                                                                             389 WITSGIPEVEIMSNAF--TPAIKYHVIKKNKGQLDKVKLPKAKDPLALRSGVYPQWILN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=VPI 10463;
von Eichel-Streiber C.;
submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
submitted (JAN-1997) to the enteral delivery of the enterotoxin A refunction: Only after the enteral delivery of the enterotoxin A rethe characteristic disease called pseudomembranous colitis be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular characterization of the Clostridium difficile toxin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium difficile.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                   366 LPAPYQERTIDLSAYAGQQVYLAFR-----HFNSTGIFRLYLDDVAVSG 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- DOMAIN: THE C-TERMINAL PART OF TOXIN A CONSISTS OF A 833 A REPETITIVE STRUCTURE. THIS PART OF TOXIN A IS COMPOSED OF DIFFERENT OLIGOPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=VPI 10463;
MEDIATE=90129305; PubMed=2105276;
Dove C.H., Wang S.Z., Price S.B., Phelphs C.J., Lyerly D.M., Wilkins T.W., Johnson J.L.;
                                                                                                                                                                                                                                                                                                                                      500 LPLPQKEGTHRFLVYAGPLADPTLRVLDKAYTNSKGESPQYLDCITFRG
                                                                                                                                                                                                                           318 VPWINEHYGVFLSTIGNEAANFIIKLLEETLGSDKPAPMNLVKSEG--
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MBDLINE=90221894; PubMed=2109310;
Sauerborn M., von Bichel-Streiber C.;
"Nucleotide sequence of Clostridium difficile toxin A.";
Nucleic Acids Res. 18:1629-1630(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                  2710 AA
                                                                         NGWTMIDADGDGHNWLSTINVYNTATHTGDGAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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SEQUENCE FROM N.A.
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                                                                                                              330
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EMBL; X51797; CAA36094.1; -. EMBL; M30307; AAA23283.1; -.

80 LWDADHNQYGASIPEESFW-FANGTIPAGLYDPFEYK-----VPVNADASFSPTNFVLDG 167 VYNKDSAVÝGTSL---VFWRSGNEYLPLGIÝNSKEERLESLDLPITKAAVFSDSKSANAG

21; 133 223

63; Mismatches 154; Indels 106; Gaps

Conservative

96;

Best Loc Matches

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4.9%; Score 129; DB 1; Length 794; 21.0%; Pred. No. 0.65;

9EDCF05E73709133 CRC64;

POTENTIAL. POTENTIAL. POTENTIAL.

661 713 24 593

POTENTIAL

88951 MW;

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195
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                                                                                                                                                                                                                                                                                                     2334 HLCTINNDKYYFSYDGILQ-NGYITIERNNFYFDANNE-----SKMVIGVFKGPNGFEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----IYIVGEGVSKGNDYVVEAGKTYHFTVQRQGPGDAASVVVTG-----EGGNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAPVQNLQWSVSGQTVT----LTWQAPASDKRTYVLNESFDTQTLPNGWTMIDADGDGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2287 FAPANTHINNIEGQAIVYQNKFLT----LNGKKYYPDNDS----KAVTGWQTI----DGK
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                                                                                                                                                                                                                                                                                                                                                                                                       2174 APANTDANNIEGOAILYONEFLTLNGKKYYFGSDSKAVTGWRIINNKKYYFNPNNAIAAI
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MEDLINE=94374689; PubMed=7522196;
MEDLINE=94374689; PubMed=7522196;
MEDLINE=94374689; Davies 0.;
"Biosynthesis of buttroof in Bacillus circulans NRRL B3312:
identification by sequence analysis and insertional mutagenesis of the butB gene involved in antibiotic production.";
                                                                                                                                                                                                                        66; Mismatches 200; Indels 178;
                                                                                                                                                                            DB 1; Length 2710;
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                                                                                                                                    2710 AA; 308052 MW; 0A6E52CE84C14421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGKLSYWVSSQVPWTNEHYGVFLSTTG------NEAAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 ETLGSDKPAPMNLVKSEGVKLPAPYQERTIDLSAYAGQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 29, Last sequence update)
(Rel. 33, Last annotation update)
                                                                                                                                                                                                   4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1616 AA.
                                                                                                                                                                              4.8%; Score 127;
                                                                                                                                                                                                 Pred. No.
EMBL; X92982; CAA63564.1; -.
InterPro; IPR002479; CW binding.
InterPro; IPR007577; Gly transf sug.
Pfam; PF01473; CW binding_1; 28.
Pfam; PF04488; Gly transf sug; I.
Toxin; Enterotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S-layer related protein precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLAFRH--FNSTGIFRLYL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 475 AH-----VQNLTGSAV 485
                                                                                                                                                                                                                                                                       EDGTGYQMLWDADHNQYGAS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                 20.4%;
                                                                                                                                                                                                   Best Local Similarity 20.4%
Matches 114; Conservative
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01-FEB-1996
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P35824;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      156
                                                                                                                                    SEQUENCE
                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -FRHFNSTG--IFRLYLDDVAVSGEGS-SNDYTYTVYR----DNVVIAQNLAATTFNQEN 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 LPVGHINVNVDAP----POKTNYVALFTS-----GAQVTNSQETDKVFVKKTNTAIAVDKH 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
-!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. MAY PLAY A ROLE IN THE EXPORT OF BUTIROSIN FROM THE ORGANISM.
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-layer with hexagonal symmetry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 IPAGMARIILEAHDVWEDGTGYQMLWDADHNQYGASI----PEESFWFANGTIPAGLYDPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----IINPNPGIIYIVGEGVSKGNDYVVEAGKIYHFTVQRQGPGDAASVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -------QAPASDKRTYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 LNESFDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 PDNYLVTPKVTVPENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GPQITVPQ-----FNVAVQV------DAGSKVTKVVNPSIDGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 PAWTGPIDLEIPSGGYVLVA--QD----ISYAGKNIKKYLATYFKVGDAIKLRKNGFAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 SLHKGGQVVHAGDFLNPDPGLNLVTASGTT-----VTSPDFTVSGQVVRYGSGQGISLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       412 PVKDLMGTGGPIARVTLDNYAMYTETKPSTELSGTITNMDDPSKIALTVNGTPLPFGPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRKLINSLFSLAVLLSLL--CWGQTAAAQGGPKTAPSVTHQAVQKGIRTSKVKDLRD---P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 LRKWNGMMIIALVISLLTPAWGKASAQSLGQESGGV---QPQSAGVTDDVYVLSRDGTFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --DLIEVEAAPIDIT-ISIEGPAHA-IGYVD-QDIAGIDDTVALFINDW------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFKTSYTLAEGINYLDLV-----VTKEGKEQDSKDLVVYSRPGFSTGKKVIL-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214; Indels 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 NGTERALKADGAFQSAVRLTAĞTNAISVKLLKDGREIVSSTVTVTYNDAQQPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 1616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-LAYER RELATED PROTEIN.

W; 1F03FF7A4F113AA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA---PMNL-VKSEGVKLPAPYQERTIDLSAYAGQQV--YLA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 EYKVPVNADASFSPTNFVLDGTASADIPAGTY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.7%; Score 124; DB 20.1%; Pred. No. 3.5; tive 78; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172874 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02368; Big 2; 1.
Pfam; PF00395; SLH; 1.
SMART; SM00635; BID 2; 1.
Signal; Cell wall; Slayer.
SiGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR, 117884, 117884.
InterPro; IPR003343; Big_2.
InterPro; IPR001119; SLH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L20421; AAA62588.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 20.1
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1616
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                                                                                                                                                                   Cycloisomaltooligosaccharide glucanotransferase precursor (EC 2.4.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RYNPGDAVSIRVOAKNGTGSSWSGAARLEIFHLENSVYTSSQSLSLINGQSTTLTFTWTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSWTASGGAKIDLSPDNYLVTPKVTVPENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----HINAWOFYDWMWRHD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 FTIKLLEETLGSDKPAPMNLVKSEGVKLPAPYQERTIDL-----SAYAGQQVYLAFRHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 ---KMIKRTGGSIDSTWLDLFNRE---ISWSTLQNQIDAVHDVNGKAMAYAMIYASRENY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 NSTGI---FRLYLDDVAVS-----GEGSSNDYTYTVYRDNVVIAQNLAATTFNQENVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 RQGPGDAASVVVTGEGGN-----EFAPVQNLQWSVS-----GQ--TVTLTWQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 PASDKRIYVLNESFDIQTLPNGWIMIDADGD-----GHNWLSTINVYNIATHTGDGAMFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 PSTDFRGYFVR--IDAGTLGQGATAIDVSSDFTKYPRYGYISEF-----BSGETALES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                         Oguma T., Kurokawa T., Tobe K., Kobayashi M.;
Submitted (UUL-1955) to the EMBL/GenBank/DDG databases.
-!- FUNCTION: PRODUCES CYCLOISOMALTOOLIGOSACCHARIDE FROM DEXTRAN.
-!- SIMILARITY: Belongs to family 66 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYCLOISOMALTOOLIGOSACCHARIDE GLUCANOTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           444 GQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNLTGSAV 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 NWONY-IHAEYIDSINTAGFDGIHVDOMGORSNVYDYNGNSI 324
                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 972 AA; 107431 MW; 2827BEA61782CC22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.6%; Score 121.5; DB 1; 20.8%; Pred. No. 2.6; iive 51; Mismatches 111;
                                                            5-JUL-1998 (Rel. 36, Created)
[5-JUL-1998 (Rel. 36, Last sequence update)
[5-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      587 AA
972 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase; Glycosyltransferase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D61382; BAA09604.1; -.
InterPro; IPR005084; CBM_6.
InterPro; IPR008979; Gal_bind_like.
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Last sequence update)
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(Rel. 32, (Rel. 32, 1) (Rel. 32, 1) (Rel. 43, 1)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nat. Struct. 180. 8:442-446(2001).
-!- CATALYTIC ACTIVITY: Hydrolysis of the B chain of insulin at 13-
-!- CATALYTIC ACTIVITY: Hydrolysis of the B chain of insulin at 13-
-!- CATALYTIC ACTIVITY: Hydrolysis of the B chain of insulin at 13-
-!- CATALYTIC ACTIVITY: Hydrolysis of the B chain of angiotensin
I at 4-Tyr-!-118-5. A good synthetic substrate is Lys-Pro-Ile-Glu-
Phe-|-Phe(NO(2))-Arg-Leu.
-!- CATALOR Binds I calcium ion per subunit.
-!- SUBCELLUIAR LOCATION: Periplasmic.
-!- FTM: Autocatalytically processed.
-!- SIMILARITY: Belongs to peptidase family S53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS) OF 216-585.
MEDLINE=21614391; PubMed=11747435;
Wlodawer A., Li M., Guetchina A., Dauter Z., Uchida K., Oyama H.,
Goldfarb N.E., Dunn B.M., Oda K.,
"Inhibitor complexes of the pseudomonas serine-carboxyl proteinase.";
Biochemistry 40:15602-15611(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oyama H., Abe S.-I., Ushiyama S., Takahashi S., Oda K.;
"Identification of catalytic residues of pepstatin-insensitive
carboxyl proteinases from prokaryotes by site-directed mutagenesis.";
J. Biol. Chem. 274:27815-27822(1999).
                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 216-224.
MEDLINE-95014496; PubMed=7929375;
MEDLINE-95014496; PubMed=7929375;
MEDLINE-95014496; PubMed=7929375;
MEDLINE-95014496; Tokuda Y., Shibano Y., Takahashi S.;
"Cloming, nucleotide sequence, and expression of an isovaleryl pepstatin-insensitive carboxyl proteinase gene from Pseudomonas sp.
                                                                                                                                                                                                                                                                                                                                                                              primary structure of pepstatin-insensitive carboxyl proteinase
uced by Pseudomonas sp. No. 101.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS) OF 216-587.

WIDGINE-21223584; PubMed=11323721;
WIDGAWE A., Uchida K., Oyama H.,
Dunn B.M., Oda K.;
Pseudomonalisin precursor (EC 3.4.21.100) (Pepstatin-insensitive carboxyl proteinase) (Pseudomonapepsin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Carboxyl proteinase from Pseudomonas defines a novel family of
                                                                                                                                                                                                                                                                                               SEQUENCE OF 216-585.
MEDLINE=96157710; PubMed=8576087;
Hayashi K., Izu H., Oda K., Fukuhara K.-I., Matsuo M., Takano
                                                            (strain 101) (Achromobacter parvulus T1)
                                                                                                                                                                                                                                                          Biol. Chem. 269:26518-26524 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99419069; PubMed=10488127;
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                                                                                                                                                                                                                                                                                                                                                                                                 produced by Pseudomonas sp. No
J. Biochem. 118:738-744(1995).
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                                                                            Bacteria, Proteobacteria.
NCBI_TaxID=33067;
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                                                              Pseudomonas sp.
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4.6%; Score 120.5; DB 1; Length 587;
Best Local Similarity 23.5%; Pred. No. 1.6;
Matches 78; Conservative 33; Mismatches 108; Indels 113; Gaps
  Protease; Serine protease; Zymogen; Periplasmic; Signal;
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352 KPAPMNLVKSEGVKLPAPYQERTIDLSAYAGQ 383
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Slakeski N., Cleal S.M., Reynolds B.C.; "Characterization of a Porphyromonas gingivalis gene prtR that encodes an arginine-specific thiol proteinase and multiple adhesins."; Biochem. Biophys. Res. Commun. 224:605-610(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete nucleotide sequence of a gene prtR of Porphyromonas gingivals WSO encoding a 132 Rba protein that contains an arginine-specific thiol endopptidase domain and a haemagglutinin domain."; Biochem. Biophys. Res. Commun. 207:424-431 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95160709; PubMed=7857299;
Kirszbaum L., Sotiropoulos C., Jackson C., Cleal S., Slakeski N.,
Reynolds E.C.;
                                                                                                                                                                                                                             Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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                                                                                                01, Last sequence update)
25, Last annotation update)
   PRT; 1706 AA
                        Q51839; Q51840;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Arginine-specific thiol protease precursor.
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PRELIMINARY;
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Reynolds E.;
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RA RLL DR DR DR DR DR DR DR DR DR FT FT SQ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 3.1e-50;
77; Mismatches 154; Indels 275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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RISSP, 19543; ICVR.
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Last annotation update)
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BETA-ADHESIN.
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Mol. Microbiol. 23:0-0(1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 INFVLDGTASADIPAGTYDYVIINPNPGI-IYIVGEGVSKGNDYVVEAGKTYHFTVQRQG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVWEDGTGYQMLWDADHNQYGASIPEE--SFWFANGTIPAGLYDPFEYKVPVNADASFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                850 SCDGTELTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVATGNHEYCVEVKYTAGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- DKRTYVLNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 ISKDVIGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----EGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDV--AVSGEGSSND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.0%; Score 951.5; DB 2; Length 1706; 31.9%; Pred. No. 2.7e-50; ative 74; Mismatches 156; Indels 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 1706 ARGININE-SPECIFIC THIOL PROTEASE. 1706 AA; 185626 MW; E8BDF07C9813B844 CRC64;
                                                                                                      GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000534; F:ATP binding; IEA.
GO; GO:000534; F:ATP binding; IEA.
GO; GO:0005316; F:DNA ligase (ATP) activity; IEA.
GO; GO:0005310; F:DNA recombination; IEA.
GO; GO:0006528; P:DNA repair; IEA.
GO; GO:0006508; P:DNA replication; IEA.
GO; GO:0066508; P:DNA replication; IEA.
R InterPro; IPR007710; Ig-Iike.
R InterPro; IPR007710; Ig-Iike.
R InterPro; IPR007759; Peptidase.
R InterPro; IPR00756; Peptidase.
R Pfam; PF01764; Peptidase.
R Pfam; PF01765; Peptidase.
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C Pfam; PF01765; Peptidase.
CZ5.
C Pfam; PF01765; PF01765; PF01765; PF01765; PF01765; PF0
Slakeski N.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases
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                                                      EMBL; L26341; AAC18876.1; -. HSSP; P95493; 1CVR.
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Best Local Simil
Matches 237; 0
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                                                                                                                                                                                                                                                                                            1146 ESSTHGEATAEWTTIDADGDGGWLCLSSGQLDWLTAHGGTNVVSSFSWNGMALNPDNYL 1205
                                                                                                                                                                                                                                                                                                                                           1206 ISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGL 1265
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                                               606
                                                                                                                                                                    YLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS---- 350
                                                                                                                                                                                                                                                                     ---PMNLV 359
TNMIMDGTASVNIPAGTYDFAIAAPQANAKIWIAGQGPTKEDDYVFEAGKKYHFLMKKMG 849
                                                                                     910 PKVCKDVTVEGSNEFAPVQNLTGSAVGQKVTLKWDAPNGTPNPNPNPNPNPGTTTLSB
                                                                                                                                                                                                                                                                                                                                                                  360 --KSEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDV--AVSGEGSSND
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                                             SGDGTELTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVAAGNHEYCVEVKYTAGVS
                                                                                                                     SPDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN
                                                                      -- DKRTYVLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95138080; PubMed=7836351;
MEDLINE=95138080; PubMed=7836351;
MEDLINE=95138080; PubMed=7836351;
Tavis J., Potening J., Pike R.N., Prochazka V., Kiefer M.C.,
Travis J., Barr P.J.;
"Molecular cloning and structural characterization of the Arg-
"Molecular cloning and structural characterization of the Arg-
gingipain proteinase of Porphyromonas gingivalis. Biosynthesis as in proteinase-adhesin polyprotein.",
J. Biol. Chem. 270:1007-1010(1995).
PIRI, A55426; A55426.
HSSP; P95493; ICVR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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GO; GO:0008234; F:Cysteine-type peptidase activity; IEA.
GO; GO:0003910; F:DNA ligase (ATP) activity; IEA.
GO; GO:0006281; P:DNA recombination; IEA.
GO; GO:0006281; P:DNA repair; IEA.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                      ----VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVQNLTGSAVGQKVTLKWDAPN 497
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                      PGDAASWV---
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790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  850 SCHOLTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVATGNHEYCVEVKYTAGVS 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      790 TIMIMDGTASVNI PAGTYDFALAAPQANAKI WIAGQGPTKEDDYVFEAGKKYHFLMKKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVWEDGTGYQMLWDADHNQYGASIPEE--SFWFANGTIPAGLYDPFEYKVPVNADASFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNFVLDGTASADIPAGTYDYVIINPNPGI-IYIVGEGVSKGNDYVVEAGKTYHFTVQRQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 VIPKVTVPENGKLSYWVSSQ-VPWINEHYGVFLSTTGNEAANFIIKLLEETLGS----
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                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                    / Match 35.8%; Score 944.5; DB 2; Length 1704; Local Similarity 31.9%; Pred. No. 7.4e-50; Ass. 235; Conservative 75; Mismatches 160; Indels 267;
                                                                                                                                                                                                                                              MATURE 50-KDA CYSTEINE PROTEINASE
                                                                                                                                                                                                                                                                                                 1704 AA; 185436 MW; 6A34B40131C2A676 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194 ----VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS----
GO; GO:0006260; P:DNA replication; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR00077; DNA ligase.

InterPro; IPR001769; Peptidase.

InterPro; IPR001769; Peptidase.

InterPro; IPR001536; Peptidase.

Pfam; PF01364; Peptidase.

Pfam; PF01364; Peptidase.

Pfam; PF03785; Peptidase.

Pfam; PF03785; Peptidase.

Pfam; PF03785; Peptidase.

CSS. 7.

Pfam; PF03786; Peptidase.

CSS. 7.

CHAIN

CHAIN
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                                                                                                                                                                                                                                                                             GINGIPAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGSAVGQKVTLKWDAPN 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGDAASVV----
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PRT; 1687 AA.

1306 478

418

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1127 ESSTHGEAPAEWITIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASFSWNGMALNPDNYL 1186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Okamoto K., Kadowaki T., Nakayama K., Yamamoto K.; Cloning and sequencing of the gene encoding a novel lysine-specific cysteine proteinase (Lys-gingipain) in Porphyromonas gingivalis: structural relationship with the arginine-specific cysteine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           748 DNVWGDNTGYQFLLDADHNTFGSVIPATGPLF-TGTASSNLYSANFEYLIPANADPVVTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      693 TATTOGOKVTLKWDAPS----AKKAEASREVKRIGDGLFVTIEPANDVRANEAKVVLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP
                                                                                                                                                                                                                                                           419 TVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQ
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                                                                                                                                                  1187 ISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGL
                                                                                                                                                                                                                      -----YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UnterPro; IPRO01769; Peptidase.
InterPro; IPRO01769; Peptidase_C25.
InterPro; IPRO01769; Peptidase_C25.
Pfam; PF01364; Peptidase_C25; I.
Pfam; PF013785; Peptidase_C25; I.
PROSITE; PS00697; DNA LIGASE_A1; 1.
REOURNCE 1723 AA; I87261 MW; 5628963D251493EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D83258; BAA11870.1; -
BMBL; D83258; BAA11870.1; -
BMCDF; C25.00524; F.ATP binding; IEA.
GQ; GQ:0008234; F.CYSteine-type peptidase activity; IEA.
GQ; GQ:0008234; F:DNA ligase (ArP) activity; IEA.
GQ; GQ:0006310; P:DNA recombination; IEA.
GQ; GQ:0006261; P:DNA replair; IEA.
GQ; GQ:0006260; P:Proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1723 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97044756; PubMed=8889827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1366 NLKAQPDGGDVVLKWEAPS 1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  479 NLTGSAVGOKVTLKWDAPN 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Arg-gingipain).";
J. Biochem. 120:398-406(1996)
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P72194;
01-FEB-1997 (TEMBLEEL. 0:
01-FEB-1997 (TEMBLEEL. 0:
01-OCT-2003 (TYEMBLEEL. 2:
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                                                                                                                                                                                                                         386
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               831 SGDGTELTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVATGNHEYCVEVKYTAGVS 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVWEDGTGYQMLWDADHNQYGASIPEE--SFWFANGTIPAGLYDPFEYKVPVNADASFSP
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                                                                                                                                                                                                                                                                                                                                                                                                                 Han N., Dong H., Progulske-Fox A.; "Cloning and characterization of hagE from P. gingivalis 381."; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF026946; AAD01810.1; "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1687;
                                                                                                                                                                                    Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0005234; F:ATP binding; IEA.

R GO; GO:0008234; F:Cysteine-type peptidase activity; IEA.

R GO; GO:0005310; F:DNA ligase (ATP) activity; IEA.

R GO; GO:0006210; P:DNA recombination; IEA.

R GO; GO:0006281; P:DNA repair; IEA.

R GO; GO:0006508; P:DNA replication; IEA.

R GO; GO:0006508; P:DNA replication; IEA.

R InterPro; IPR000977; DNA ligase.

R InterPro; IPR000771; DNA ligase.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR007110; Peptidase C25.

R Pfam; PF01364; Peptidase C25.

R Pfam; PF01364; Peptidase C25.

R Pfam; PF01365; Peptidase C25.

R Pfam; PF013785; Peptidase C25.

R PROSITE; PS00697; DNA_LIGASE_A1; 1.
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                       (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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NCBL_TaxID=837;
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                                                                                                                Hemagglutinin/protease.
HAGE.
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01-MAY-2000
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                                                                                                                                                                        296 YLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS---- 350
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SFDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN
                                                                                                                                                                                     1043 YLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASNFTNALLEETITAKGVR
                                                        867 RRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIQEGLIATTFEEDGVAAGNHEYCVEVKYT
                                                                                -----VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS-----DKRTYVLNE
                                                                                                    927 AGVSPKVCKDVTVEGSNEFAPVONLTGSAVGOKVTLKWDAPNGTPNPNPNPNPGTTTLSE
                                                                                                                                                                                                                   --- KSEGVKL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria, Bacteroidetes, Bacteroides (class); Bacteroidales;
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Submitted (ARR-1996) to the EMBL/GenBank/DDBJ databases.
BMBL; U54691; AA99810.1; -.
REMBL; U54691; AA99810.1; -.
RGO; GO:0005524; F:ATP binding; IEA.
GO; GO:000910; F:Cypteine-type peptidase activity; IEA.
GO; GO:000910; F:DNA ligase (ATP) activity; IEA.
RGO; GO:0006210; P:DNA recombination; IEA.
RGO; GO:0006281; P:DNA repair; IEA.
RGO; GO:0006289; P:DNA replication; IEA.
RGO; GO:0006508; P:DNA replication; IEA.
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NCBI_TaxID=837;
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                                    OROGPGDAASVV-
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KGP.
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                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                           68 HDVWEDGIGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FRYKVPVNADASFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               867 RRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEEDGVAAGNHEYCVEVKYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 SFDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- PMINITA
                                                                                                                                                                                                                                                                                                                                                                                                                                          127 INFVLDGTASADIPAGTYDYVIINPNP--GIIXIVGEG---VSKGNDYVVEAGKTYHFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 YLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS----
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                                                                                                                                                                             Length 1723;
                                                             Pfam; PF01364; Peptidase_C25; I. — Pfam; PF03785; Peptidase_C25; I. — PR03785; Peptidase_C25; I. SRQUENCE 1723 Aa; I.GASE A1; 1. SRQUENCE 1723 Aa; I.B6831 FW; 4508A7E50197CEBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                           31.0%; Score 818; DB 2; L 29.4%; Pred. No. 5.4e-42; iive 78; Mismatches 166;
                                                                                                                                                                                                                                                                 22 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD---
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IPR000977; DNA_ligase.
IPR001769; Peptidase_C25.
IPR005536; Peptidase_C25_
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01-WAY-1997 (TrEMBLrel. 03, 01-WAY-1997 (TrEMBLrel. 03, 101-007-2003 (TrEMBLrel. 25, Hemagglutinin.
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                                                                                                                                                                                               Best Local Similarity 29.49
Matches 218; Conservative
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PRT; 1732 AA.
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                                                                                                             1037 NLKAQPDGGDVVLKWEAPS 1055
                                                                                                                                                                                                                                                                                                                     STRAIN=W12;
MEDLINE=96213011; PubMed=8631659;
                                                                                               479 NLTGSAVGOKVTLKWDAPN 497
                                                                                                                                                                                             (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 25,
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Matches 222; Conservative
                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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01-NOV-1996 (
01-OCT-2003 (
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PRTP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 SPDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             622 SFE-NGIPASWKTIDADGDGHGW-KPGNAPGIAGYNSNGCVYSESF-GLGGIGV-LTPDN 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 YLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS---- 350
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                                                                                                                                                                                                                                                                                                                                                                                                                   68 HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP 126
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                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         738 SPEAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 ESSTHGEAPAEWTTIDADGDGQDWLCLSSGQLDWLTAHGGTNVVASFSWNGMALNPDNYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             858 ISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGL
                                                                                                                                                                                                                                                                                                                                                                        22 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD------PIPAGMARIILEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---KSEGVKL----
                                                                                 Han N., Lepine G., Whitlock J., Wojciechowski L., Progulske-Fox A.; "Cloning, sequenching and characterization of hagb, a member of the HArep multigene family in Porphyromone gingivalis."; submitted (AUG-1996) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                           30.9%; Score 816; DB 2; Length 1358;
llarity 29.6%; Pred. No. 5.1e-42;
Conservative 75; Mismatches 171; Indels 274;
          Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                  SMART; SM00060; FN3; 1. _ _ _ PROSITE; PS00697; DNA_LIGASE_A1; 1. SEQUENCE 1358 AA; 147102 NW; 47FCA0B25B06DED8 CRC64;
                                                                                                                                                    activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --LSAYAGOOV---
                                                                                                                        ---VIGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 QRQGPGDAASVV-----
                                Porphyromonadaceae; Porphyromonas
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                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 219; Conserv
                                                               SEQUENCE FROM N.A.
                                          NCBI_TaxID=837;
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22;
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                                          918 STEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSPTPTDYTY 977
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                                                                                                                                            TVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSFKVCKDVTVEGSNEFAHVQ 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barkocy-Gallagher G.A., Han N., Patti J.M., Whitlock J.,
Progulske-Fox A., Lantz M.S.;
"Analysis of the prtP gene encoding porphypain, a cysteine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          693 TATTOGOKVTLKWEAPS----AKKAEGSREVKRIGDGLFVTIEPANDVRANEAKVVLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      748 DNVWGDNTGYQFLLDADHNTFGSVIPATGPLF-TGTASSNLYSANFEYLVPANADPVVTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.8%; Score 812.5; DB 2; Length 1732; 30.0%; Pred. No. 1.2e-41; rive 70; Mismatches 172; Indels 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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E Bacteriol. 178:2734-2741(1996).

E MBL, 1422101, AAB06565.1; -.

R PIR, T30836, T30836.

R MEROPS; C25.002; -.

R GO; GO:0008234; F:APP binding; IEA.

GO; GO:0008234; F:P:YSteine-type peptidase activity; IEA.

GO; GO:0006281; P:DNA recombination; IEA.

GO; GO:0006281; P:DNA replication; IEA.

R GO; GO:0006281; P:DNA replication; IEA.

R GO; GO:0006281; P:DNA replication; IEA.

R GO; GO:0006281; P:DNA replication; IEA.

R GO; GO:0006581; P:DNA replication; IEA.

R InterPro; IPR00977; DNA Ligase.

R InterPro; IPR00536; Peptidase. C25.

R Pfam; PR03184; Peptidase. C25.

R Pfam; PR03185; Peptidase. C25.

R PROSITE; PS00697; DNA LIGASE_A1; 1.
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Last annotation update)
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1732 AA; 187931 MW; B2337463D5CB5EA5 CRC64;
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                                                                     DB 2;
                                                                30.6%; Score 807.5; DB 2;
ilarity 30.0%; Pred. No. 2.4e-41;
Conservative 69; Mismatches 173;
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last seq
01-JCT-2003 (TrEMBLrel. 25, Last ann
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NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 OROGPGDAASVV-----
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                                                                                            Similarity
                                                                                                                 Matches 222;
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Protease.
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                         SEQUENCE
                                                                     Query Match
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                                                                                                                                             1103 RSPKAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTET 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1163 FESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGSNVVSSFSWNGMALNPDNY 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1223 LISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFG 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 LSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSPTPTDYT 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS--- 350
                                                                                                                                                                                                                                                                                                                                                                                                                    385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417
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                                                             927 AGVSPKVCKDVITVEGSNEFAPVQNLIGSSVGQKVILKWDAPNGTPNPNPNPNPNPGTILS 986
                    --ASDKRTYVLN 234
                                                                                                                                                                                                                                                                                                                  -----DKPAPMNLV------KSEGVKL----
                                                                                                                 ESFDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              element associated with protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Lysine specific cysteine protease.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; C25.002; -...
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008234; F:Cysteine-type peptidase activity; IEA.
GO; GO:0003910; F:DNA ligase (ATP) activity; IEA.
GO; GO:0006281; P:DNA recombination; IEA.
GO; GO:0006281; P:DNA repair; IEA.
GO; GO:0006560; P:DNA replication; IEA.
GO; GO:0006508; P:Proteclysis and peptidolysis; IEA.
                    ------VIGEGGNEFAPVQNLQWSVSGQIVTLTWQAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1732 AA
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InterPro, IPR001769; Peptidase C25.
InterPro, IPR005536; Peptidase C25.C.
Pfam; PP01364; Peptidase C25, I.
Pfam; PF03785; Peptidase C25, I.
PROSITE; PS00697; DNA_LIGASE_A1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lewis J.P., Macrina P.L.,
"IS195, an insertion sequence-like el
genes in Porphyromonas gingivalis.";
Infect. Immun. 66:3035-3042 (1998).
EMBL, AF017059; AAC26523.1;
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NCBI_TaxID=837;
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MEDLINE=98298016; PubMed=9632563;
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987 ESFE-NGIPASWKTIDADGDGGGW-KPGNAPGIAGYNSNGCVYSESF-GLGGIGV-LIPD 1042
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                                                                                                                                                                                                    693 TATTOGOKVTLKWEAPS----AKKAEGSREVKRIGDGLFVTIEPANDVRANEAKVVLAA
                                                                                                                                                                                                                                                                       68 HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP
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                                                                                                                                                                                                                                                                                                              348 DNVWGDNTGYQFLLDADHNTFGSVIPATGPLF-TGTASSNLYSANFEYLVPANADPVVYT
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                                                                                                                                 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD------PIPAGMARIILEA
                                                                  Indels 277;
Length 1732;
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Bacteria, Bacteroidetes; Bacteroides (class); Bacteroidales;
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235 ESFDIQILPNGWIMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPD 294
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                                                                                                                 478 QNLTGSAV--GQKVTLKWDAP 496
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es 219; Conservative
                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                     Slakeski N., Cleal S.M., Bhogal P.S., Reynolds E.C.; "Characterization of a Porphyromonas gingivalis gene prtK that encodes a lysine-specific cysteine proteinase and three sequence-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             807 QNIIVTGQGEVVIPGGVYDYCIINPEPASGXMMIAGDGGNQPARYDFTFEAGKKYTFTM
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GO; GO:0008234; F:ATP binding; IEA.

GO; GO:0008310; F:DMA ligase (ATP) activity; IEA.

GO; GO:0006310; F:DMA ligase (ATP) activity; IEA.

GO; GO:0006210; P:DMA repair; IEA.

GO; GO:0006260; P:DMA replication; IEA.

GO; GO:0006260; P:DMA replication; IEA.

GO; GO:0006260; P:DMA replication; IEA.

InterPro; IPR000977; DNA ligase.

InterPro; IPR001769; Peptidase.

R InterPro; IPR001769; Peptidase.

R Pfam; PF01364; Peptidase.

R Pfam; PF01364; Peptidase.

R PROSITE; PS00669; DNA LIGASE A; 1.

R PROSITE; PS00669; DNA LIGASE A; 1.
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                                                                                                                                                                                      Oral Microbiol. Immunol. 14:92-97(1999).
EMBL; U75366; AAB60809.1; -.
MEROPS; C25.002; -.
                                                                 MEDLINE=99235907; PubMed=10219167;
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Matches 220; Conserv
                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       418 AGVSPKVCKDVTVEGSNEFAPVQNLTGSSVGQKVTLKWDAPNGTPNPNPNPNPNPGTTLS
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Shibata Y., Hayakaw M., Takiguchi H., Shiroza T., Abiko Y.;
"Determination and charcterization of the hemaglutinin-associated
short motifs found in Porphyromonas gingivalis multiple gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Products.";

J. Biol. Chem. 274:5012-5020(1999).

R BMBL; AB019363; BAA34341.1;

GO; GO:000524; F:ATP binding; IEA.

GO; GO:0006234; F:ATP binding; IEA.

GO; GO:0006210; F:DNA ligase (ATP) activity; IEA.

GO; GO:0006210; F:DNA recombination; IEA.

GO; GO:0006210; P:DNA repair; IEA.

GO; GO:0006281; P:DNA replication; IEA.

R GO; GO:0006280; P:DNA replication; IEA.

R HITEPRO; IPRO01977; DNA ligase.

INTERPO; IPRO01977; DNA ligase.

R THERPO; IPRO01597; Peptidase C25.

R Pfam; PF03785; Peptidase C25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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us-08-353-485-2.rspt

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360 ---EXSEGVKL---
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SEQUENCE FROM N.A.
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NYLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS--- 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               892
                                                                                 654 FESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASFSWNGMALNPDNY
                                                                                                                                                                                                                                                                                                                                                                                                 -----KSEGVKL----
                                                                                                                                                                           594 RSPEAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTET
                                                                                                                                                                                                                                                                                                                                  714 LISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFG
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"The tla gene of Porphyromonas gingivalis W50: a homologue of the
"Targinine-specific protease precursor (PrpRI) which shares sequence
similarity to TonB-linked receptors.";

J. Bacteriol. 179:4778-4788(1997).
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MEDLINE=97386416; PubMed=9244265;
Aduse-Opoku J., Slaney J.M., Young K.A., Muir J., Rangarajan M.,
                                                                                                                                                                                                                      -----LSAYAGQQV-----
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Porphyromonadaceae; Porphyromonae.
NCBL TaxID=837;
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(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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                                                                                                                                        ----DKPAPMNLV----
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                                                                                                                                                                                                                367 ------PAPYQERTID------
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01-FEB-1997
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01-OCT-2003
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                                                                                                                    165 KGNDYVVEAGKT---YHFT----VQRQGPGDAASVVVTGEGGNEFAPVQNLQWSVSG
                                                                                                                                                                                                                                         215 QTVTLTWQAP-----ASDKRTYVLNESFDTQTLPNGWTMIDADGDGHNWLSTINVY
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499 HFQSTDMFYIDLDEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   559 QLDWLTAHGGSNVVSSFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        619 SKTGTNAGDFTVVFEETPNGINKGGARFGLSTEANGAKPQSVWIERTVDLFAGTKYVAFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391 HFNSTGIFRLYLDDV--AVSGEGSSNDYTYTYYRDNVVIAQNLAATTFNQENVAPGQYNY
                                                                                                                                                                             267 KGSDYTVATGRIRFGIDFTPEWSLNLYONVFLGDAIPV----GGSNEFAPVONLTGSSVG
                                                                                                                                                                                                                                                                                                                                                          266 NIATHIGDGAMFSKSWTASGGAKIDLSPDNYLVTPKVTVPENGKLSYWVSSQ-VPWTNEH
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                                                           Gaps
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                                                        Indels 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449 CVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNLTGSAV--GQKVTLKWDAP 496
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14.4%; Score 379; DB 2; Length 312;
Best Local Similarity 37.2%; Pred. No. 8.6e-16;
Matches 94; Conservative 44; Mismatches 85; Indels 30;
      Length 1097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical outer membrane protein PG27.
Porphyrononas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----PAPYQERTID-
Query Match 21.3%; Score 561.5; DB 2; Best Local Similarity 29.8%; Pred. No. 2.4e-26; Matches 158; Conservative 48; Mismatches 117;
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	QY 233 INESFDIQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLS 292	Qy 198 GGNEFAPVONLOWSVSGOTVTLTWQAPASD
239 PROVIDENTIAL PROPERTY OF P	- -	219 GQNVGRLTWNYPEDYQPEGKGNEEL
359 SDRZADBNILYXSEGNYLADAYGRATIDANAGOOVIANIMANINGTININGTH	PDNYLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVELSTTGNEAANFTIKLIEETLG	232
168 ILYTPLINERANCEDHOGYTTSVPRDGARTAPOGNINGCAPUTTAGG 279 218 228 SYNCKSNIVANS 240 NCKSNIVANS 240 SYNCKSNIVANS	SDKPAPMNLVKSEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVA ::	257
459 SPKVCKGUYTWRSS 471 144 1528 SYKVCKGUYTWRSS 471 1528 SYKVCKGUYTWRSS 471 1528 SYKVCKGUYTWRSS 471 1528 SYKVCKGUYTWRSS 240 1528 SYKVCKGUTTWRSS 240 1528 SYKVCKGUTTWR	VSGEGSSNDYTYTVYRDNVVIAQNLAATTENQENVAPGQYNYCVEVKYTAGV :	315
14	SPKVCKDVTVEGS 47	3.74 4.34
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REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-58100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PoTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PoTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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US-08-480-604A-7 US-08-405-496A-7 US-08-957-310-7 US-08-957-310-7 US-08-08-180-7 US-08-80-604A-29 US-08-915-136-29 US-08-915-136-29 US-08-915-136-29 US-08-915-136-6 US-08-480-604A-6 US-08-480-604A-6 US-08-957-310-6 US-08-957-310-6 US-08-957-310-6 US-08-957-310-6 US-08-957-310-6 US-08-957-310-6 US-08-957-310-6 US-08-957-310-6 US-08-957-310-6 US-09-965-621A-2 US-09-965-621A-2	ALIGNMENTS		## Sequence 2. Application US/08570311 ## Sequence 2. Application US/08570311 ## Sequence 2. Application US/08570311 ## Sequence 3. Application: ## APPLICANT: Progulske-Fox, Ann ## APPLICANT: Tumwasorn, Somying ## APPLICANT: Lepine, Gaylaine ## APPLICANT: Lepine, Gaylaine ## APPLICANT: Lepine, Gaylaine ## APPLICANT: Ant., Joseph ## TITLE OF INVENTION: Cloned Porphyromonas gingivalis G ## TITLE OF INVENTION: Cloned Porphyromonas gingivalis G ## APPLICANT: and Probes for the Detection of P ## APPLICANTION: And Probes for the Detection of P ## APPLICANTION: And Probes for the Detection of P ## APPLICANTION: Application of P ## CORRESPONDENCE ADDRESS: ## APPLICANTION NUMBER: US/08/570,311 ## APPLICATION NUMBER: US/08/570,311 ## APPLICATION ATA: ## APPLICATION	3/353,485 3/647,119 7/241,640 INPLS C3
8111 1 811 1 8 8111 2 8 8111 4 8 8111 4 8 811 1 4 8 812 1 4 8 812 1 2 7 1 0 0 2 7 7 1 0 0 4 7 7 7 1 0 0 4 7 7 7 1 0 0 4 7 7 7 1 0 0 4 7 7 7 1 0 0 4 7 7 7 1 0 0 4 7 7 7 1 0 0 4 7 7 7 1 0 0 4 7 7 7 1 0 0 4 7 7 7 1 0 0 4 7 7 7 1 0 0 4 7 7 7 1 0 0 4 7 7 7 1 0 0 4 7 7 7 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0			Application US/085703111 5824791 NPCRMATION: NT: Progulske-Fox, Ann NT: Tumwasorn, Somying NT: Tumwasorn, Somying NT: Han, Naiming NT: Han, Naiming NT: Lantz, Marilyn NT: Batti, Joseph T INVENTION: and Probes f F INVENTION: and Probes f SEQUENCES: 29 ONDENCE ADDRESS: SEBE: Ted W. Whitlock T: 2421 N.W. 41st Street, Gainesville F. FL RY: USA 32606 RY: USA 32606 RY: USA TYPE: Ploppy disk TYPE: Ploppy disk TYPE: Ploppy disk TYPE: Ploppy disk TYPE: TBM PC compatible TING SYSTEM: PC-DOS/NS-DO APPLICATION DATA: CATION NUMBER: US/08/570, TETCATION NUMBER: US/08/570	PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/353,481 FILING DATE: 09-DEC-1994 CLASSIFICATION: 424 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/647,111 CLASSIFICATION NUMBER: US 07/241,64(FILING DATE: 25-JAN-1991 CLASSIFICATION DATA: APPLICATION NUMBER: US 07/241,64(FILING DATE: 08-SEP-1988 ATTORNEY/AGENT INFORMATION: NAME: Whitlock, Ted W NAME: Whitlock, Ted W REPERBUCE/DOCKET NUMBER: UFF5-C73
			uence 2, Application Us ent No. 584791 NERAL INFORMATION: APPLICANT: Progulake-F APPLICANT: Tumwasorn, APPLICANT: Tumwasorn, APPLICANT: Han, Naimin APPLICANT: Han, Naimin APPLICANT: Han, Naimin APPLICANT: Han, Naimin APPLICANT: Patti, Jose TITLE OF INVENTION: CI TITLE OF INVENTION: CI TITLE OF INVENTION: CI TITLE OF INVENTION: AN NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSEE: Ted W. Wh STREBT: 2421 N.W. 41 CITY: Gainesville COUNTRY: USA ZIP: 32606 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy COMPUTER: IBM PC COM OPERATING SYSTEM: PC SOFFWARE: PREPRICATION DAT APPLICATION NUMBER: TELLOR DAT APPLICATION NUMBER: TELLOR DAT APPLICATION NUMBER: TELLOR DAT APPLICATION NUMBER: TELLOR DAT APPLICATION NUMBER: TELLOR DAT APPLICATION NUMBER: TELLOR DAT APPLICATION NUMBER: TELLOR DAT APPLICATION NUMBER: TELLOR DAT APPLICATION NUMBER: TELLOR DAT APPLICATION NUMBER: TELLOR DAT APPLICATION DAT APPLICATIO	PRIOR APPLICATION DATA: APPLICATION NUMBER: US O FILING DATE: 09-DEC-1994 CLASSIFICATION: 42-4 PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: FILING DATE: 25-JAN-1991 CLASSIFICATION TO AND ADDITED TO APPLICATION AS O FILING DATE: 08-SEP-1988 ATTORNERY AGENT INFORMATION: NAME: Whitlock, Ted M REGISTRATION NUMBER: 36, REFERRACE/DOCKET NUMBER: 36,
127 127 127 127 127 127 127 127 127 127		1 70-311-2	HIGHORY, ADIRED S. ADIRED S. ADIRED S. ADIRED S. PELICANT: PELICANT: PELICANT: PELICANT: PELICANT: PELICANT: PELICANT: PELICANT: PELICANT: PELICANT: PELICANT: PELICANT: PELICANT: PELICANT: PELICANT: PELICANT: PELICATION COUNTRY: COUNTRY: PERICATION COUNTRY: PERICATION COUNTRY: PERICATION COUNTRY: PERICATION COUNTRY: PELICATION COUNTRY: PERICATION COUNTRY: PELICATION COUNTRY: PELICATION COUNTRY: PELICATION COUNTRY: PELICATION COUNTRY: PELICATION COUNTRY: PERICATION COUNTRY: PERICATI	APPLICATION APPLICATION APPLICATION TILING DATE: OCLASSIFICATION TOR APPLICATION APPLICATION APPLICATION APPLICATION TILING DATE: OR APPLICATION TOR APPLICATION TORNEY/AGATE: TORNEY/AGATE: NAME: WAME: WAME: WAME: WALLOCK NAME WALLOCK NAME WALLOCK NAME WALLOCK NAME WALLOCK REGESTRATION NUM REFERENCE/DOCK R
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61 ARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDPFEYKVPVNA 120
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                       APPLICATION NUMBER: US/08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-529-1988
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION WUMBER: 36,965
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Sequence 14, Application US/08570311
Patent No. 5824791;
GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: UF1.
TELECOMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELERAX: (904) 372-5800
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Tumwasorn, Somying
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
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0
                                                                                                                                                      Length 497;
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                                                                                                                                                ; Score 2641; DB 2;
; Pred. No. 1.4e-205;
0; Mismatches 0;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Patent No. 5830710
GENERAL INFORMATION:
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                                                                                                                                                100.0%;
  497 amino acids
                                                                                                                                         Query Match
Best Local Similarity 100.(
Matches 497; Conservative
                       ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-570-311-2
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LENGIH:
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                       KVTVPENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDKPAPMNLVK 360
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                                                            301 KVTVPENGKLSYMVSSQVPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDKPAPMNLVK
                                                                                                                                        421 YRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 DVWEDGTGYQMLWDADHNQYGASIPEE--SFWFANGTIPAGLYDPFEYKVPVNADASFSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reynolds, Eric C.
APPLICANT: Bhogal, Peter S.
APPLICANT: Slakeski, Nada
TIPLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 36.0%; Score 951.5; DB 4; Length 1706; Best Local Similarity 31.9%; Pred. No. 5.6e-68; Matches 237; Conservative 74; Mismatches 156; Indels 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TILE REFERENCE: Reynolds
CURRENT APPLICATION NUMBER: US/09/066,330A
CURRENT FILING DATE: 1998-09-15
BARLIER APPLICATION NUMBER: PN 6275
BARLIER APPLICATION NUMBER: PN 6275
BARLIER APPLICATION NUMBER: PCT/AU96/00673
BARLIER PILING DATE: 1995-10-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-066-330-10; Sequence 10, Application US/09066330A; Patent No. 6511666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) ORGANISM: Porphyromonas gingivalis US-09-066-330-10
                                                                                                                                                                                                                                                                                        TGSAVGQKVTLKWDAPN 497
                                                                                                                                                                                                                                                                                                                                  481 TGSAVGOKVTLKWDAPN 497
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                APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Jantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
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100.0%; Pred. No. 1.7e-204;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                              3: Ted W. Whitlock
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-UAN-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/570,31:
                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Whitlock, Ted W.
REGISTRATION UNDRER: 36,965
REFERENCE/DOCKET NUMBER: UF15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
Tumwasorn, Somying
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PRIOR APPLICATION DATA:
                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. WD
STREET: 2421 N.W. 41
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                        USA
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	QY 298 VTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNBAANFTIKLLBETLGS 350	351DKPAPMNLV36	DB 859 EAIRGRIGGTWRQKTVDLPAGTRXVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETFES 918 Qy 367PAPYQERTID		VINDER WITTERVEY ATAINED DEPLETATION AND CONTRACT OF THE ACTION OF THE A	DD 9/9 KDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLST 103B OY 386YLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTV 420	1039 EANGAKPQSVWIERTVDLPAGT	421 YRDNVVIAQNLAATTENQENVAPGQXNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL 48	DS 1099 YRDGTKIKBGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVNVTI-NPTQFNFVKNL 1157 Qy 481 TGSAVGQKVTLKWDAPN 497		RESULT 6 US-08-336-308A-10 ; Sequence 10, Application US/08336308A ; Patent No. 6017532	GENERAL INFORMATION: ; APPLICANT: Travis, James		; AFFLICANI: PATOLOI: NACINE; TITLE OF INVENTION: POIDBY PROCESS GINGIVALIS; TITLE OF INVENTION: Arginine-specific Proteinase Coding Sequences	SEQUENCES: ENCE ADDRES E: Greenl 5370 Manh		ДЩ	; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: Patentin Release #1.0, Version #1.30	; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/336,308A ; FILING DATE: 08-NOV-1994	; CLASSIFICATION: 435 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 08/119,361 ; FILING DATE: 10-SEP-1993	\mathcal{L}	ATTORNEY AGENT INFORMATION: NAME: Ferber, Donna M.	ON NUMB DOCKET ATION I	; TELEPHONE; (303) 499-8080 ; TELEFAX: (303) 499-8089
Qy 352 KPAPM 356	DD 1086 SPEAMRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETF 1145 QY 357 361	:		362EGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSND	Db 1266 STEADGAKPQSVWIERTVDLPAGTK-YVAFRHYNCSDLNYILLDDIQFTWGGSPTPTD 1322 Ov 416 YTYTVYRDNVVTAONLAATTFNOFNVADGOYNYCVRVKYTAGVSBKVCKNVTVFGSNFFA 475	111 VITON VIANTAMILIANGENVERGINICORVATIAGOSENGEN 4/ 1323 YIYIVYRDGTKIKEGLIETTFEEDGVATGNHEYCVEVKYTAGVSPKKCVNVTV-NGTQFN 13	Qy 476 HVQNLTGSAVGQKVTLKWDAPN 497	Db 1382 PVKNLKAQPDGGDVVLKWEAPS 1403	RESULT 5 US-09-482-500A-1	Sequence 1, Patent No. (GENERAL INFC	, APPLICANT: Travis, James) APPLICANT: Imamura, Takahisa) APPLICANT: Potempa, Jan ; TAPLICANT: Potempa, Jan ; TILE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION ; FILE REFERENCE: 235.00160101		; PRIOR APPLICATION NUMBER: US 60/115,869 ; PRIOR FILING DATE: 1999-01-13 ; NUMBER OF CFO IN NOC. 4-01	NOTIFIED TO SECULD AND SECULD AND SECULD AND SECULD AND SECULD AND SECULD AND SECULD AND SECULD AND SECURD AND		Query Match 35.8%; Score 944.5; DB 4; Length 1477; Best Local Similarity 31.9%; Pred. No. 1.7e-67; Matches 235; Conservative 75; Mismatches 160; Indels 267; Gaps 20;	22 TAAAQGGPKTAPSVTHQAVQKGIRTSKVKDLRDPIPAGMARIILEAH 6	444 TATTQGQKVTLKWDAPSTKTNATTNTARSVDGIRELVLLSVSDAPELLRSGQAEIVLEAH	OY 69 DVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDFFEYKVFVNADASFSP 126	QY 127 INFVLDGTASADIPAGTYDYVIINPNPGI-IYIVGEGVSKGNDYVVPEAGKTYHFTVQRQG 185		623 SGDGT	QY 194VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPASDKRTYVLNESF 237	PDNYL

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                                                                                                                                                                                                                                                                          TNFVLDGTASADIPAGTYDYVIINPNPGI-IYIVGEGVSKGNDYVVEAGKTYHFTVQRQG 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                      238 DTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYL 297
                                                                                                                                                                                  22 TAAAQG-----GPKTAPSVTHQAVQK--GIR---TSKVKDLRDPIPAGMARIILEAH
                                                                                                                                                                                                                                     -----VIGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS------DKRTYVLNESF
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                                                                                                           35.8%; Score 944.5; DB 3; Length 131.9%; Pred. No. 2.1e-67; ive 75; Mismatches 160; Indels
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                          LENGTH: 1704 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                      235; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                        Similarity
                                                                                US-08-336-308A-10
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Matches 23
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Sequence 6, Application US/08822324
Patent No. 6129917
GENERAL INFORMATION:
APPLICANT: Potency, Jan S.
APPLICANT: Travis, Janes
APPLICANT: Genco, Caroline A.

US-08-822-324-6

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IMMUNOGENIC COMPOSITIONS COMPRISING
PORPHYROMONAS GINGIVALIS PROTEINS AND/OR PEPTIDES AND
METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 TAAAQG------GPKTAPSVTHQAVQK--GIR---TSKVKDLRDPIPAGMARIILEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  671 TATTÇĞQKVTLKWDAPSTKTNATTNTARSVDGIRELVILSVSDAPELIRSĞQAEIVLEAH
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                                                                                                                                                                                                                                                                                                            SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.8%; Score 944.5; DB 3;
31.9%; Pred. No. 2.1e-67;
tive 75; Mismatches 160;
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                                                                                                                SE: Greenlee, Winner and Sullivan, 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,324
FILING DATE: 21-MR-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/013,945
FILING DATE: 22-MR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 498-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 31.9%
Matches 235; Conservative
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TITLE OF INVENTION: IMMU
TITLE OF INVENTION: PORP
TITLE OF INVENTION: METH
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-822-324-6
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                       CITY: Boulder
STATE: CO
COUNTRY: US
                                                                                                                                                                                                                            ZIP: 80303
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                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                  STREET:
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1086 EAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETFES 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 YRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL 480
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APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Janz, Marilyn
APPLICANT: Patti, Joseph
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
CORRESPONDENCES 29
                                                                                                                                                                                 69 DVWEDGTGYQMLWDADHNQYGASIPEE--SFWFANGTIPAGLYDPFEYKVPVNADASFSP
                                                                                                                                                                                                                   731 DVWNDGSGYQILLDADHDQYGQVIPSDTHTLM-PNCSVPANLFAPFEYTVPENADPSCSP
                                                        22 TAAAQG-----GPKTAPSVTHQAVQK--GIR----TSKVKDLRDPIPAGMARIILEAH
                                                                                                                 671 TATTOGOKVTLKWDAPSTKTNAŤINTARSVDGÍRELVLLSVSDAPELLRSGOAEÍVLEAH
                                                                                                                                                                                                                                                                                                      TNFVLDGTASADIPAGTYDYVIINPNPGI-IYIVGECVSKGNDYVVEAGKTYHFTVQRQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 -----VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS------DKRTYVLNESF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 VTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS-----
75; Mismatches 160; Indels 267; Gaps
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2421 N.W. 41st Street, Suite A-1
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APPLICANT: Progulske-Fox, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1385 KAQPDGGDVVLKWEAPS 1401
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235; Conservative
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US-08-570-311-29
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                                                                                  1146 STHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASFSWNGMALNPDNYLIS 1205
                                                                                                                                                                                                       1206 KDVTGATKVKYYYAVNDGPPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLST 1265
                                                                                                                                                                                                                                                                                                                                                                                     -YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYTYTV 420
                                                                                                                                                                                                                                                                                                            Porphyromonas gingivalis
Arginine-specific Proteinase Coding Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
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REGISTRATION NUMBER: 33,878
REFRENCE/DOCKET NUMBER: 21-93C
TELECOMMUNICATION INFORMATION:
TELEPRONE: (303) 499-8089
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER.STICS:
LENGTH: 1704 aming acids
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APPLICATION NUMBER: US 08/265,441
FILING DATE: 24-UUN-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/09490931
Patent No. 6274718
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Barr, Philip J.
APPLICANT: Barr, Philip J.
APPLICANT: Barrinesee:
TITLE OF INVENTION: Porphyromonas grant and applicant and appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/336,308
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31.9%;
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
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: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 5370 Me
CITY: Boulder
STATE: Colorade
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
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E: Ted W. Whitlock
2421 N.W. 41st Street, Suite A-1
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APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-UAN-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/241,640
FILING DATE: 08-SEP-198
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                             1366 NLKAQPDGGDVVLKWEAPS 1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/08570311
Patent No. 5824791
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    479 NLTGSAVGQKVTLKWDAPN 497
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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REFERENCE/DOCKET NUMBER: UF.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 27:
SECUENCE CHARACTERISTICS:
LENGTH: 1358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Gainesville
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                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-08-570-311-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.7%; Score 943.5; DB 2; Length 1687; 31.8%; Pred. No. 2.5e-67; tive 75; Mismatches 160; Indels 269;
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                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                                                                                                                                                                                               FILING DATE: 22 C.C.
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08 SEP-1988
ATTORNEY-AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 372-8100
TELEFAX: (904) 372-8800
TELEFAX: (904) 372-8800
TELEFAX: (904) 372-8800
TELEFAX: (904) 372-8800
SEQUENCE CHARACTERISTICS:
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FILING DATE:
CLASKIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASKIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
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Matches 235, Conservative
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COUNTRY: US.
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1127 ESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASFSWNGMALNPDNYL 1186
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1307 TVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVNVTI-NPTQFNPVK 1365
                                                                                                                                                 1187 ISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGL 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Progulske-Fox, Arn
APPLICANT: Tunwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Oloned Forphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
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1247 STEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDDIQFTMGGSPTPTDYTY
                                                                                                                                                                                                                            --YLAFRHFNSTGIFRLYLDDV---AVSGEGSSNDYTY
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
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127 TNFVLDGTASADIPAGTYDYVIINPNP--GIIYIVGEG---VSKGNDYVVEAGKTYHFTV 181
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Cloned Porphyromonas gingivalis Genes
and Probes for the Detection of Periodontal Disease
29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD------PIPAGMARIILEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 30.8%; Score 812.5; DB 2; Best Local Similarity 30.0%; Pred. No. 1e-56; Matches 222; Conservative 70; Mismatches 172;
                                                                                                                              ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 418t Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION AND ADDRESSING ASSISTANCE AND ADDRESSING ASSISTANCE AND ADDRESSING ASSISTANCE AND ADDRESSING ASSISTANCE AND ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESSING ADDRESS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: RATEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-570-311-10
TITLE OF INVENTION: CI
TITLE OF INVENTION: an
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        Gainesville
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                                                                                                                                                                                                                                        STATE: F
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                          328 TATTÓGQKVTLKWDAPS----AKKAEASREVKRIGDGLFVTIEPANDVRANEAKVVLAA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                             68 HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 QNIIVTGQGEVVIPGGVYDYCIINPEPASGKMWIAGDGDNQPARYDDFTFEAGKKYTFTM 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 SPDIQILPNGWIMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          622 SFE-NGIPASWKTIDADGDGHGW-KPGNAPGIAGYNSNGCVYSESF-GLGGIGV-LTPDN 677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        883 DNVWGDNIGYQFLLDADHNIFGSVIPAIGPLF-IGTASSNLYSANFEYLIPANADPVVTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              738 SPEAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETF
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                                                                                                                                                                  30.9%; Score 816; DB 2; Length 1358;
29.6%; Pred. No. 3.7e-57;
iive 75; Mismatches 171; Indels 274; Gaps
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Patent No. 5824791
GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
APPLICANT: Lepine, Guylaine
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .037 NLKAQPDGGDVVLKWEAPS 1055
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                                                                                                                                                              Query Match 30.99
Best Local Similarity 29.6
Matches 219; Conservative
                                                           , MOLECULE TYPE: protein US-08-570-311-27
       TYPE: amino acid
TOPOLOGY: linear
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US-08-570-311-10
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                                                                                                                                      30.8%; Score 812.5; DB 2; 30.0%; Pred. No. 1e-56; iive 70; Mismatches 172;
                                                                                                                                                                                                             22 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD-
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| ONLTAEQAPNSMDAILKWNAP 1422
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Patent No. 5824791
GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
APPLICANT: Tumwasorn, Somying
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lepine, Guylaine
                                  1732 amino acids
amino acid
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                                                                                                                                                        Best Local Similarity so.or
Matches 222; Conservative
                SEQUENCE CHARACTERISTICS
                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
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US-08-353-485-10
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US-08-570-311-8
                                  LENGTH:
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                                                                                                     1103 RSPKAIRGRIQGTWRQKTVÖLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTET 1162
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NYLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS--- 350
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TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                            1163 FESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGSNVVSSFSWNGMALNPDNY
                                                                                                                                                                                                                                             1223 LISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFG
                                                                                                                                                                                                                                                                               -YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYT
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                                                                   --KSEGVKL--
                                                                                                                                         -LSAYAGOOV-
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,485
FILING DATE: 09-DEC-1994
FILOR APPLICATION A24
PRIOR APPLICATION NUMBER: US/08/353,485
FILING DATE: 07-DEC-1994
FILING DATE: 07-DEC-1994
FILING DATE: 07-DEC-1994
FILING DATE: 07-DEC-1991
CLASSIFICATION NUMBER: US 07/647,119
FILING DATE: 05-JAN-1991
CLASSIFICATION NUMBER: US 07/241,640
FILING DATE: 08-DEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: WhitLock, Ted W.
REGISTRATION NUMBER: UF15-C2
TELECOMMUNICATION INFORMATION:
NAME: WHITLOCK TED W.
REFERENCE (0904) 375-E0000
THELEPHONE: 0303 375-E0000
                                                                     -- DKPAPMNLV-
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5830710
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Progulske-Fox, Ann APPLICANT: Tumwasorn, Somying APPLICANT: Lepine, Guylaine APPLICANT: Han, Naiming APPLICANT: Lantz, Marilyn APPLICANT: Patti, Joseph
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                                                                                                                                         -----PAPYQERTID
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MEDIUM TYPE: Floppy
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1103 RSPKAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTET 1162
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                                                                                                                                                                                                          68 HDVWEDGIGYOMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP
                                                                                                                                                                                                                                         927 AGVSPKVCKDVTVEGSNEPAPVQNLTGSSVGQKVTLKWDAPNGTPNPNPNPNPRGTTLS
                                                                                                      --PIPAGMARIILEA
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Length 1732;
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353 487 547 385 385

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371 GW-KPGNAPGIAGYNSNGCVYSESF-GLGGGIGV-LTPDNYLITPALDLANGGKLTFWVCA 427
                                                                                                                                                                      -PAPYQERTID---- 376
                                                                                                                                                                                                                                                                                                      608 PGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLSTEANGAKPQSVWIERTVDLP 667
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APPLICANT: Tumwasorn, Somying
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Farti, Joseph
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 NVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNLTGSAVGQKVTLKWDAPN 497
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                                                                                                      488 AGTKYVAPRHFQSTDMFYIDLDEVEIKANGKRADFTETPESSTHGEAPABWTTIDADGDG
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,485
FILING DATE: 09-DEC-1994
PRIOR APPLICATION: 424
PRIOR APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION: 244
                                                                       317 Q-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS--
                                                                                                                                                                        ---KSEGVKL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/241,640 FILING DATE: 08-SEP-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 372-8100
TELEFAX: (904) 372-8000
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08353485
Patent No. 5830710
                                                                                                                                                                                                                                                                          --LSAYAGOOV-
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APPLICATION NUMBER: 1
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                                                                                                                                                                      354 APMNLV--
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 GSVIPATGPLF-TGTASSNLYSANFEYLIPANADPVVTTQNIIVTGQGEVVIPGGVYDYC 191
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                       APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 IINPNP--GIIYIVGEG---VSKGNDYVVEAGKTYHFTVQRQGPGDAASVV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 SAKKABASREVKRIGDGLFVTIEPANDVRANBAKVVLAADNVWGDNTGYQFLLDADHNTF
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UNRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.5%; Score 806.5; DB 2; 29.4%; Pred. No. 1.6e-56; tive 76; Mismatches 166;
                                                                                                                                                                      ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE:
CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC_1994
CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY AGENT INFORMATION:
NAME: WAITLOCK TE W.
REGISTRATION NUMBER: 36,965
REPERRENCEY,DOCKET NUMBER: 36,965
REFERENCEY,DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
TELECHONE: (904) 375-8100
TELEPRAX: (904) 375-8100
TELEPRAX: (904) 375-8100
SEQUENCE CHARACTERISTICS:
TENETRY 1007 MINO ACIDS
TENETRY 1007 MINO ACIDS
TENETRY 1007 MINO ACIDS
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
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Matches 211; Conservative
     Han, Naiming
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                                                                                                                                                                                                89 GASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSPTNFVLDGTASADIPAGTYDYV 147
                                                                                                                                                                                                                148 IINPNP--GIIYIVGEG---VSKGNDYVVEAGKIYHFTVQRQGPGDAASVV----- 193
                                                                                                                                                                                                                                                                               251
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                                                                                                                                             39 AVOKGIRISKVKDLRD-----PIPAGMARIILEAHDVWEDGTGYQMLWDADHNQY
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                                                                                                                     Gaps
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APPLICANT: Bhogal, Peter S.
APPLICANT: Bhogal, Nada
TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
FILE REFERENCE: Reynolds
CURRENT APPLICATION NUMBER: US/09/066,330A
CURRENT FILING DATE: 1998-09-15
EARLIER APPLICATION NUMBER: PN 6275
                                                                                                                    265;
                                                                                         DB 2; Length 1087;
                                                                                        30.5%; Score 806.5; DB 2; Length 1
29.4%; Pred. No. 1.6e-56;
ive 76; Mismatches 166; Indels
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Sequence 11, Application US/09066330A

; Patent No. 6511666

; GENERAL INFORMATION:
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            1087 amino acids
                                                                                       Query Match
Best Local Similarity 29.4
Matches 211; Conservative
SEQUENCE CHARACTERISTICS
                                                MOLECULE TYPE: protein
                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 APMNLV-
                                                               US-08-353-485-8
            LENGTH:
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1283 LSTEANGAKPOSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSPTPTDYT 1342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 INFVLDGTASADIPAGTYDYVIINPNP--GIIYIVGEG---VSKGNDYVVEAGKTYHFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                  693 TATTOGOKVILKWEAPS-----AKKAEGSREVKRIGDGLFVTIEPANDVRANEAKVVLAA
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                                                                                                                                                                                                                                                                                                                                   Indels 277;
                                                                                                                                                                                                                                                                                 Length 1732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------PAPYQERTID--------LSAYAGQQV-----
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                                                                                                                                                                                                                                                                                 Query Match 30.5%; Score 806.5; DB 4; Best Local Similarity 29.7%; Pred. No. 3.2e-56; Matches 220; Conservative 72; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                     22 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD-
EARLIER FILING DATE: 1995-10-30
EARLIER APPLICATION NUMBER: PCT/AU96/00673
EARLIER PILING DATE: 1996-10-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 1732
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                                                                                                                                                                                                        ORGANISM: Porphyromonas gingivalis US-09-066-330-11
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us-08-353-485-2.rapb

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Sequence 5, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 27, Appl
Sequence 51483, A
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6, Appli
62947, A
9, Appli
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Sequence 11, App]
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                                                                                            May 18, 2004, 11:32:49 ; Search time 19.8443 Seconds (without alignments) 6969.043 Million cell updates/sec
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Sequence 3,
Sequence 101
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2641
1 MRKLNSLFSLAVLLSLLCWG......QNLTGSAVGQKVTLKWDAPN 497
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| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB_pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB_pep:*
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16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-229-066-11
US-10-174-695-3
US-10-174-695-6
US-10-174-695-6
US-10-174-695-6
US-10-174-695-4
US-10-174-695-4
US-10-282-122A-51483
US-10-282-122A-51483
US-10-282-122A-62947
US-10-387-977-101
US-10-387-977-6
US-10-387-977-97
US-10-387-977-97
US-10-387-977-97
US-10-387-977-97
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seg length: 2000000000
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16	138.5		2468	14	-10-246	Sequence	4, Appli
17	137		25	15	-10-387-977	Seguence	82, App.
18	137		579	15	-10-369-493-9	Sequence	9075, A
13	134		2435	12	-10-282-122A-47	Sequence	47453, 1
20	132	5.0	698	14	-10-156-761-119	Sequence	11953, 7
21	129		973	14	-10-156-761-9	Sequence	9394, AI
22	128	4.8	26	15	-10-387-977-1	Sequence	14
23	127		811	12	10-272	Sequence	7
24	127	•	811	14	-10-011	Sequence	7,
25	127	4.8	811	15	10-354	Seguence	7
26	127	4.8	811	15	US-10-271-012-7	Sequence	7,
27	127		2710	12	10-272	Sequence	-
28	127	4.8	2710	14	10-011-366-	Sequence	6, Appl:
29	127		2710	15	0	Sequence	-
30	127	4.8	2710	15	1-012-	Sequence	6, Appl:
31	126	4.8	1752	14	0-387-	Sequence	2, Appl:
32	125.5		577	15	7	Sequence	21739,
33	124	4.7	2013	12	US-10-282-122A-60608	Seguence	9
34	124	4.7	2358	12	US-10-282-122A-45763	Sequence	45
35	123.5	4.7	1204	12	US-10-282-122A-49627	Sequence	49627,
36	123	4.7	998	14	US-10-222-038-2	Sequence	'n
37	123	4.7	951	σ	US-09-924-097-15	Seguence	15,
38	122		908	15	US-10-369-493-3678	Sequence	367
39	121		25	σ	4	Sequence	46,
40	121		25	10	9-9	Sequence	18,
41	121		25	14	0-2	Sequence	46,
42	121	•	25	14	0-0	Sequence	40,
43	121		25	14	0-372-076-4	Sequence	41,
44	121	4.6	25	15	10-387-977-7	Seguence	76, App.
45	121		25	15	0-3	Sequence	79

ALIGNMENTS

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               Sequence 10, Application US/10229066
Fublication No. US20030157637A1
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric C.
APPLICANT: Reynolds, Eric C.
APPLICANT: Blogal, Peter S.
CURRENT APPLICATION NUMBER: US/0/066,330
PRIOR APPLICATION NUMBER: PCT/AU96/00673
PRIOR APPLICANTION NUMBER: PCT/AU96/00673
PRIOR APPLICANTION NUMBER: PCT/AU96/00673
PRIOR PLING DATE: 1998-10-30
PRIOR FILING DATE: 1998-10-30
SRUOR FILING DATE: 1998-10-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
36.0%; Score 951.5; DB 14; Length 1706;
Best Local Similarity 31.9%; Pred. No. 3.5e-75;
Matches 237; Conservative 74; Mismatches 156; Indels 275; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Porphyromonas gingivalis
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US-10-229-066-10
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                                                                                                                                                                                                                                                                                                                                                                                                        361
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                                                                                                                                                                 910 PKVCKDVTVEGSNEFAPVQNLTGSAVGQKVTLKWDAPNGTPNPNPNPNPNPNPGTTTLSE 969
                                                                                                                                                                                                   SFDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN 295
                                                                                                                                                                                                                                                                     296 YLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETL---GSD 351
                   TIMIMDGTASVNIPAGTYDFALAAPQANAKIWIAGQGPTKEDDYVFEAGKKYHFLMKKMG 849
                                                                                               850 SGÖGTELTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVATGNHEYCVEVKYTAGVS 909
TNFVLDGTASADIPAGTYDYVIINPNPGI-IYIVGEGVSKGNDYVVEAGKTYHFTVQRQG 185
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                                                                                                                                 194 -----VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS------DKRTYVLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/10229066
Publication No. US20030157637A1
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric C.
APPLICANT: Rehogal, Peter S.
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 806.5; DB 14; Length 1732; Pred. No. 3.2e-62;
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CURRENT FILING DATE: 2002-08-28
PRIOR PRILING DATE: 1998-09-15
PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1995-10-30
PRIOR FILING DATE: 1995-10-30
PRIOR FILING DATE: 1995-10-30
PRIOR FILING DATE: 1995-10-30
PRIOR FILING DATE: 1995-10-30
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 11
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; ORGANISM: Porphyromonas gingivalis
US-10-229-066-11
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29.7%;
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Best Local Similarity
                                                               186 PGDAASVV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1223 LISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFG 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417
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                                            67
                                                                                                                                                                        1103 RSPKAIRGRIQGTWRQKTVDLPÅGTKYVAFRHFQSTDMFYIDLDEVBIKANGKRADFTBT
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                                                                                                                                      68 HDVWEDGTGYQMLWDADHNOYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP
                                                                                                                                                                                                                                                                                                                                                                                                                            -ASDKRTYVLN
                                               --PIPAGMARIILEA
                                                                                         693 TATTOGOKVTLKWEAPS----AKKAEGSREVKRIGDGLFVTIEPANDVRANEAKVVLAA
                                                                                                                                                                                                                                       TNFVLDGTASADIPAGTYDYVIINPNP--GIIYIVGEG---VSKGNDYVVEAGKTYHFTV
Indels 277; Gaps
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APPLICANT: Slakeski, Nada
APPLICANT: Slakeski, Nada
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
APPLICANT: Barr, Ian George
TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REFERENCE: 529282000700
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: PCT/AU00/01588
PRIOR PILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/AU00/01588
PRIOR FILING DATE: 1999-12-24
PRIOR PILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
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72; Mismatches 172;
                                               22 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD--
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  Conservative
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179 224 239 284 296 343 355

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344 LEETLGSDKPAPMMLVKSEGVKLP-----APYQERTIDLSAYAGQQVYLAFRHFNST 395
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58 AGMARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKV 116
                                                                              117 PVNADASFSPTNFVLDGTASADIPAGTYDYVIINPNP--GIIYIVGEG---VSKGNDYVV
                                                                                                                                                                                                    120 EAGKKYTFTMRRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEEDGVAAGN
                                                                                                                                                                                                                                                                                   180 HEYCVEVKYTAGVSPKVCKDVTVEGSNEFAÞVONLIGSSVGOKVILKMDAPNGTPNPNPN
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                                                                                                                                                                                                                                                                                                                                                                                                                               80 IMDADHNOYGASIPEESFWFANGTIPAGIYDP-FEYKVPVNADASFSPTNFVLDGTASAD
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                         -----VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAP-----
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17.3%; Score 457.5; DB 15; Length 231;
Best Local Similarity 27.8%; Pred. No. 2.2e-32;
Matches 118; Conservative 22; Mismatches 63; Indels 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stakeski, Nada
APPLICANT: Slakeski, Nada
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
APPLICANT: Barr, Ian George
TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REFERENCE: $25282000700
CURRENT APPLICATION NUMBER: US/10/174,695
CURRENT FILING DATE: 2002-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/AU00/01588
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: AU PQ 4859
PRIOR PLING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                            172 EAGKTYHFTVQRQGPGDAASVV---
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Publication No. US20030232022A1
GENERAL INFORMATION:
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PRT
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| XKYHFLMKKKMGSGDGTELTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVAAGNHEY 179
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                                                                                                                                                                                                                                                                                                                                    58 AGMARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEE--SFWFANGTIPAGLYDPFEYK
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                                                                                                                                           DB 15; Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --VIGEGGNEFAPVONLOWSVSGOTVILIWOAPAS--
                                                                                                                                         30.0%; Score 791.5; DB 15; Length 39.9%; Pred. No. 8e-62; tive 61; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10174695
Publication No US2003023222A1
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric Charles
APPLICANT: Slakeski, Nada
APPLICANT: Chen, Chen, Chen Guang
APPLICANT: Chen, Chen, Chen George
TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REFERENCE: 522820000700
CURRENT APPLICATION NUMBER: US/10/174,695
CURRENT FILING DATE: 2002-06-18
PRIOR FILING DATE: 2002-06-18
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 4.0
    SOFTWARE: FastSEQ for Windows Version
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ORGANISM: Porphyromonas gingivalis
                                                           TYPE: PRT ORGANISM: Porphyromonas gingivalis
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Best Local Similarity 36.0%
Matches 157; Conservative
                                                                                                                                         Query Match
Best Local Similarity 39.9<sup>5</sup>
Matches 174; Conservative
                                        419
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DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH PORPHYROMONAS GINGIVALIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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5.7%; Score 150; DB 15;
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 29; Conservative 0; Mismatches 0;
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: DRABHTROMONAS GINGIVALIS
FILE REFERENCE: 529282000301
CURRENT APPLICATION NUMBER: US/10/387,977
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 09/423,056
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1997-04-30
SOFTWARE: FELING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FELING DATE: 2997-04-30
NUMBER OF SEQ ID NOS: 105
LENGTH: 29
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51483, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILLING DATE: 2003-02-20
PRIOR FILLING DATE: 2000-03-21
PRIOR FILLING DATE: 2000-03-21
PRIOR FILLING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/200, 948
PRIOR PILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230, 335
PRIOR PILLING DATE: 2000-09-09
PRIOR FILLING DATE: 2000-09-09
PRIOR FILLING DATE: 2000-09-09
PRIOR PILLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR APPLICATION NUMBER: 60/253, 625
PRIOR PILLING DATE: 2000-11-27
PRIOR PILLING DATE: 2000-11-27
PRIOR PILLING DATE: 2000-11-27
PRIOR PILLING DATE: 2000-12-22
PRIOR PILLING DATE: 2001-12-22
PRIOR PILLING DATE: 2001-12-22
PRIOR PILLING DATE: 2001-12-22
PRIOR PILLING DATE: 2001-12-22
PRIOR PILLING DATE: 2001-02-09
PRIOR PILLING DATE: 2001-02-09
PRIOR PILLING DATE: 2001-02-09
PRIOR PILLING DATE: 2001-02-09
PRIOR PILLING DATE: 2001-02-09
PRIOR PILLING DATE: 2001-02-09
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Ohlsen, Kari
Zyskind, Judith
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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                                                                                                                                                                                                                                                             374 TIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTVYRDNVVIAQNLAA 433
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                                        254 DGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTPKVTVPENGKLSYW 313
                                                                                                                                               314 VSSQVPWTNEHYGVFLSTTGNBAANFTIKLLBETLGSDKPAPMNLVKSEGVKLPAPYQER 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: APPLICANT: Changes APPLICANT: Changes APPLICANT: Chen, Chao Guang APPLICANT: Chen, Chao Guang APPLICANT: Chen, Chao Guang APPLICANT: Barr, Ian George TITLE OF INVENTION: P. GINGTVALIS ANTIGENIC COMPOSITION FILE REFERENCE: 529282000700 VOIS88 CURRENT FILING DATE: 2002-06-18 PRIOR APPLICATION NUMBER: PCT/AU00/01588 PRIOR FILING DATE: 1209-12-21 PRIOR PILING DATE: 1999-12-24 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4 LENGTH: 196
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APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: Slakeski, Nada
IITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 VIGEGGNEFAPVONLOWSVSGOTVTLIWQAPAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10174695
Publication No. US20030232022A1
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 LPNGWTMIDADGDGHNWL-
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Best Local Similarity
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                                                              TYPE: PRT
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Best Local
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Sequence 3, Application US/10229066

Publication No. US20030157637A1

Sequence 3, Application US/10229066

FULL CANT No. US20030157637A1

APPLICANT: Bhogal, Fetc C.

APPLICANT: Bhogal, Fetc C.

APPLICANT: Sheski, Nada

TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE

FILE REFERENCE: REPUTOLG

CURRENT APPLICATION NUMBER: US/10/229,066

CURRENT FILING DATE: 1998-09-15

PRIOR FILING DATE: 1998-09-15

PRIOR FILING DATE: 1995-10-30

PRIOR FILING DATE: 1995-10-30

PRIOR FILING DATE: 1995-10-30

NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                               27 GGPKTAP-----SVTHQAVQKGIRTSKVKDLRDPIPAGMARIILEAHDVWEDGTGY-
                                                                                                                                                                                                                                                              -QMLWDADHNQYGAS -----IPEESFWFANGTIPAGLYDPFEYKVPV
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                                                                                                                                         Gaps
                                                                                             5.7%; Score 150; DB 12; Length 1483;
20.2%; Pred. No. 0.0011;
tive 81; Mismatches 213; Indels 208;
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; IENGTH: 1483
TYPE: PRT
; GRGANISM: Clostridium acetobutylicum
US-10-282-122A-51483
                                                                                                                  Best_Local Similarity 20.29
Matches 127; Conservative
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161 -YSWNSQVGQPTIKYGMQYYYNQEHGYTDVXNYLKAPYTGCYSHLNTGVSFA-NYTAHGS
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19.1%; Pred. No. 0.00061;
iive 65; Mismatches 155; Indels 21
                                                                                                                                                                                     Length 42;
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                                                                                                                                                                               Score 148; DB 14;
Pred. No. 7.3e-06;
7; Mismatches 7;
                                                                                                                                                                                                                                                                                        58 AGMARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEES
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APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: 0'Brien-Simpson, Neil Martin
TITLE OF INVENTION: SYMPHETIC PEPTIDE CONSTRUCTS
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF F
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
FILE REFERENCE: 529282000301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/387,977
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 09/423,056
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 1990-04-30
PRIOR PILING DATE: 1990-04-30
PRIOR PILING DATE: 1990-04-30
NUMBER: PRIOR FILING DATE: 1997-04-30
NUMBER: PRIOR FILING DATE: 1997-04-30
SEQ ID NO 101
SEQ ID NO 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 101, Application US/10387977
Publication No. US20040005276A1
GENERAL INFORMATION:
                                                                                                     ; ORGANISM: Porphyromonas gingivalis
US-10-229-066-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Porphyromonas gingivalis
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                                                                                                                                                                               ch 5.6%;
1 Similarity 64.1%;
25; Conservative 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 42
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US-10-387-977-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                     | Sequence 6, Application US/10387977 | Sequence 6, Application US/10387977 | Sequence 6, Application US/10387977 | Sequence 6, Application US/2040005276A1 | Senblication No. US20040005276A1 | GENERAL INFORMATION: Exprended Experiment of Period Sequence 6, Applicant of Period Sequence 6, Applicant of Period Sequence 6, Applicant of Period Sequence 6, TITLE OF INVENTION: SYNTHETIC PERIODONTITIS ASSOCIATED WITH TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS | FILE REFRENCE: 529282000301 | TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS | FILE REFRENCE: 52928200301 | CURRENT APPLICATION NUMBER: US 09/423,056 | PRIOR PILING DATE: 2003-07-18 | PRIOR FILING DATE: 2000-03-22 | PRIOR FILING DATE: 1998-04-30 | PRIOR FILING DATE: 1999-04-30 | PRIOR FILING DATE: 1997-04-30 | PRIOR FILING DATE: 1997-04-30 | PRIOR FILING DATE: 1997-04-30 | NUMBER OF SEQ ID NOS: 105 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID NO 6 | SEQ ID N
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339 AGNIGNITHIGAHYYWEAYHVLGDGSVMPYRAMPKINTYTLPASLPQNQASYSIQASAGS 398
                                                                                                 384 QVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTVYRDNVVIAQNLAATTFNQENVAP 443
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-03-21
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Publication No. US20040029129A1

GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Alone, Cheryl
APPLICANT: Olsen, Kari
APPLICANT: Olsen, Kari
APPLICANT: Tyskind, Undith
APPLICANT: Tawick, John
APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Yamanoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                   ---VAISKDG
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US-10-387-977-6
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62947
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/240,347
PRIOR APPLICATION NUMBER: 60/240,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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US-10-282-122A-62947
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Sequence 9, Application US/10387977

Publication No. US20040005276A1

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Reynolds, Eric Charles

APPLICANT: Reynolds, Eric Charles

APPLICANT: SLakeski, Nada

TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE

TITLE OF INVENTION: DIAGNOSIS AND TREATHENT OF PERIODONTITIS ASSOCIATED WITH

TITLE OF INVENTION: DIAGNOSIS AND TREATHENT OF PERIODONTITIS ASSOCIATED WITH

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

FRICK REPLICATION NUMBER: US 04/423,056

PRIOR FILING DATE: 1998-04-30

PRIOR FILING DATE: 1998-04-30

PRIOR FILING DATE: 1997-04-30

PRIOR FILING DATE: 1997-04-30

NUMBER OF SEQ ID NOS: 105

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; Publication No. US20040005276A1
; GENERAL INPORMATION:
; APPLICANT: REYNOLGS, Exic Charles
; APPLICANT: REYNOLGS, Exic Charles
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: O'Brien-Simpson, Neil Martin
; TITLE OF INVENTION: SYNTHERIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DARPHYROMONAS GINGIVALIS
; TITLE OF INVENTION: DARPHYROMONAS GINGIVALIS
; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
; FILE REFERENCE: 529262000301
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 99/423,056
; PRIOR PILICATION NUMBER: PCT/AU98/00311
; PRIOR APPLICATION NUMBER: AU PO 6528
; PRIOR FILING DATE: 1998-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Pred. No. 2.2e-05;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469 EGSNEFAHVQNLTGSAVGQKVTLKWDAPN 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGSNEFAPVONLTGSSVGOKVTLKWDAPN 29
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; ORGANISM: Porphyromonas gingivalis
US-10-387-977-9
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Best Local Similarity
Matches 26; Conserv
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FAPVQNLQWSVSGQTVTLTWQAPASD 26

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RESULT 15

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352 SSVTGN---AEPGAT--VGVDTDGDGQPDTTVVVGPGGSFEVPLN--PPLINGETVTVIV 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 VS-KGNDYVVEAGKTYHFTVQRQGPGDAASVVVTGEGGNEFAPVQNLQWSVSGQTVTLTW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12; Length 2468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 200-02-02-02
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-02-02
PRIOR PILING DATE: 2000-03-02-03
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-27
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-03
PRIOR PILING DATE: 2001-02-03
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
PRIOR PILING DATE: 2001-02-05
Sequence 66335, Application US/10282122A
Publication No. US20040029129A1
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                                                                                                                                                                                                                                                                                      Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                     APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                      Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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Best Local Similarity 23.7%
Matches 107; Conservative
                                                          SENERAL INFORMATION:
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Aaw64787 Pertk anti
Aaw69494 Haemagglu
Aar74488 Porphyrom
Aar7428 Porphyrom
Aar6928 P. gingiv
Aaw64486 Haemagglu
Aaw64486 Pertk anti
Aay67396 Arg-gingi
Aaw6498 P. gingiv
Aar86495 Haemagglu
Aaw44843 Arg-gingi
Aaw44843 Arg-gingiv
Aar66033 P. gingiv
Aar66033 P. gingiv
Aaw64847 Lys-gingiv
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                                                     May 18, 2004, 11:21:33 ; Search time 87.0274 Seconds (without alignments) 5623.200 Million cell updates/sec
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 GenCore version (c) 1993 - 2004
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                                                        Porphyromonas gingivalis genes and proteins vaccination against periodontal disease.
                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 9179;
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                           Claim 5; Page 76-81; 153pp; English.
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Best Local Similarity 100.
Matches 1732, Conservative
                                                      Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                        Sequence 1732 AA;
WPI; 1996-287181,
N-PSDB; AAT30653
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Periodontal disease, cell surface protein, thiol protease, endopeptidase,
PrtK; PrtK48; PrtK39; PrtK15; PrtK44; haemagglutinin, adhesin, therapy;
                                                                                               1. .28

/label= Pro-pro_peptide

228 . .29

229 . .737

/label= PrtK48

/note= "48 kDa Lys-specific thiol protease"

738 . .136

/label= PrtK39

/note= "39 kDa adhesin"
                                                                                                                                                                                                          1292. .1732
/label= PrtK44
/note= "44 kDa adhesin"
                                                                                                                                                                              1157. .1291
/label= PrtK15
/note= "15 kDa adhesin"
                                                                                                                                                                                                                                                                                           (UYME ) UNIV MELBOURNE.
(VICT-) VICTORIAN DAIRY IND AUTHORITY.
                                                                             Porphyromonas gingivalis; strain W50.
                                                                                                                                                                                                                                                                                                                  Slakeski N;
                                                                                          Location/Qualifiers
                                  PrtK antigenic protein complex.
                                                                                                                                                                                                                                                                 96WO-AU000673.
                                                                                                                                                                                                                                                                               95AU-00006275.
                                                              diagnosis; vaccine; antigen.
              (revised)
(first entry)
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Protein
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             17-OCT-2003
25-NOV-1997
                                                                                                                                                                                                                                                  09-MAY-1997,
AAW24787;
                                                                                           Key
Peptide
                                                                                                                                                  Protein
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                                                                                                                                                                              Protein
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New antigenic protein complex from Porphyromonas gingivalis - comprising Arg- and Lys- specific thiol endo-peptidase(s), used in the detection, prevention and treatment of periodontal disease. WPI; 1997-272112/24. N-PSDB; AAT78851.

Example 1; Fig 9b; 68pp; English.

Comprises a 300 kDa complex composed a 48 kDa lysine-specific thiol protesses and 39, 15 and 44 kDa adhesins encoded by the prtK gene (AAT78851), and a 45 kDa adhesins encoded by the prtK gene (AAT78851), and a 45 kDa adresins encoded by the prtK gene (AAT78851), and a 45 kDa adresins encoded by the prtK gene (AAT78850). A claimed antigenic complex comprises at least one multimeric protein complex deving a mol.wt. of over 200 kDa, and preferably comprises all 9 proteins of the PrtR-PrtK complex (see also AAW2480-85). It can be used in a claimed composition to elicit an immune response directed against 66, and in a claimed method of reducing the prospect of PG infection and/or severity of disease. Antibodies directed against the complex are claimed for use in treating PG infection. Unlike whole PG cells or other previously prepared antigens based on fimbriae or the capsule, the PrtR-PrtK complex or component parts are safe and effective antigens. (Updated on 17-0CT-2003 to standardise OS field)

Sequence 1732 AA;

1100.0%; Score 9179; DB 2; Length 17  1106.0%; Pred. No. 0;  1111Asilidal Mismatches  1111Asilidal Mismatches  1111Asilidal Mismatches  1111Asilidal Mismatches  1111Asilidal Mismatches  111Asilidal Mismatches  11Asilidal Mismatches  11Asilidal Mismatches  11Asilidal Mis																																_	
Duetry Match  Best Local Similarity 100.0%; Score 9179; DB 2; Length:  Best Local Similarity 100.0%; Pred. No. 0;  Matches 1732; Conservative 0; Mismatches 0; Indels Matches 1732; Conservative 0; Mismatches 0; Indels National State of Conservative 0; Mismatches 0; Indels National State of Conservative 0; Mismatches 0; Indels National State of Conservative 0; Mismatches 0; Indels National State of Conservative 0; Mismatches 0; Indels National State of Conservative 0; Mismatches 0; Indels National State of Conservative 0; Mismatches 0; Indels National State of Conservative 0; Mismatches 0; Indels National State of Conservative 0; Mismatches 0; Indels National State of Conservative 0; Mismatches 0; Indels National State of Conservative 0; Mismatches 0; Indels National State of Conservative 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0; Mismatches 0;	0	9	9	12	18	18	4, 4	4 6	30	φ	9	42	42	48	48	4	4	09	09	99	99	Ö	N	00	8	4.	4	0	ō	Ÿ.	Ō	02	
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                                                                                                                                                                                            This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the prtP haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
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Matches 1732; Conservative
 UNIV FLORIDA.
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88US-00241640. 91US-00647119. 94US-00353485.

25-JAN-1991; 09-DEC-1994; 08-SEP-1988;

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Haemagglutinin; hagD; periodontal disease; vaccine; antibody

P. gingivalis hagD haemagglutinin

(first entry)

16-OCT-2003 04-SEP-1996

AAR96032

Porphyromonas gingivalis; strain FDC381

WO9617936-A2 13-JUN-1996. 95WO-US016108

11-DEC-1995;

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Porphyromonas gingivalis genes and proteins - used in the detection and vaccination against periodontal disease.

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Patti

Han N, Lantz M,

Lepine G,

Progulske-Fox A, Tumwasorn S,

WPI; 1996-287181/29. N-PSDB; AAT30655.

(UYFL ) UNIV FLORIDA. (UABR-) UAB RES FOUND

P. gingivalis 381 haemagglutinin hagD (AAR96032) was identified as the

Claim 5; Page 125-129; 153pp; English.

product of the second open reading frame of the hagb gene (AAT30655) derived from P. gingivalis 318 genomic DNA. A first open reading frame coded for hagb protease (see also AAR96031). The protease and haemagglutinin can be obtd. from transformed host cells and used in vaccines to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of live vaccines. The haemagglutinin and protease can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)

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AAR96032 standard; protein; 1358 AA

AAR96032 ID AAR9 RESULT

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Page

(first entry)

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This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagD haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
                                                                                      Jaemagglutinin protein; periodontal disease; vaccine; hagb
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88US-00241640. 91US-00647119. 94US-00353485.

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85.0%; Pred. No. 0;
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RESULT 5 AAW69494 ID AAW69494 standard; protein; 1358

Porphyromonas gingivalis lysine-gingipain protein complex

19-DEC-1995 (first entry)

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LFVTIEPANDVRANEAKVVLAADNVWGDNTGYQFLLDADHNTFGSVIPATGPLFTGTASS
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AAQ88141 encodes AAR72458 the Porphyromonas gingivalis lysine-gingipain protein complex (LGPC). The LGPC has amidolytic and proteolytic specificity for an amide bond, where lysine contributes the carboxyl gp., i.e. a lysine specific protease. LGPC can be used to identify agents that modulate the effect of LGPC on animals, and also for monitoring the exposure of an animal to LGPC. Such a method can be used to monitor the progress of a therapy designed to lessen the symptoms of periodontitis
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                                                         Lysine-gingipain protein complex; amidolytic; proteolytic;
lysine specific proteinase; modulator identification; periodontitis;
therapy monitoring.
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/label= sig_peptide
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                                                                                                                       Porphyromonas gingivalis
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N-PSDB; AAQ88141.
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                                                                                                                                      P. gingivalis 381 haemagglutinin hagD (AAR96028) was identified as the product of a gene (AAR3662) isolated from a P. gingivalis 318 genomic library. The haemagglutinin (see also AAR96032) can be obtd. from transformed host cells and used as a vaccine to protect humans or animals against periodontal disease. Expression in Salmonella cells allows produce of a live vaccine. The haemagglutinin can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise
                                                           Porphyromonas gingivalis genes and proteins - used in the detection and vaccination against periodontal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 VIPGGVYDYCITNPEPASGKMATAGDGDNQPARYDDFTFEAGKKYTFTMRRAGMGDGTDM
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                                                                                                                                                                                                                                                                                                                                   50.9%; Score 4673.5; DB 2; Length 1087; 81.4%; Pred. No. 3.7e-301; ive 56; Mismatches 120; Indels 29;
                                                                                                            Claim 5; Page 65-68; 153pp; English
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                WPI; 1996-287181/29
                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                QFDYVQPCFGEVITRVKEKGAYAYIGSSPNSYWGEDYYWSVGANAVFGVQPTFEGTSMGS
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                  IDKVLMYEKATMPDKSYLEKVLLIAGADYSWNSQVGQPTIKYGMQYYYNQEHGYTDVYNY
                                  LKAPYTGCYSHLNTGVSFANYTAHGSETAWADPLLTTSQLKALTNKDKYFLAIGNCCITA
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                                                                                                                                            62 GEEVALKWDTPSAKKAEASREVKRIGDGLFVTIEPANDVRANEAKVVLAADNVWGDNTGY
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                                                                                                                   GTGVANASGVATVSMTKQITENGNYDVVITRSNYLPVIKQIQVGEPSPYQPVSNLTATTO
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                                 50.9%; Score 4673.5; DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding haemagglutinin and/or
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                    FITFEEDGVATGNHEYCVEVKYTAGVSFKVCVNVTINPTQFNPVKNLKAQ--PDGGDVVL
                                                                                                                                                                                 839 VAISYSSLLQGQEYLPLIPNNFLITPKVE--GAKKITYKVGSPGLPQWSHDHYALCISKS
                                                                                                                                                                                                                                                                   943 VLGIMIDDVVITGEGEGPSYTYTVYRDGTKIQEGITETTYRDAGMSAQSHEYCVEVKYAA
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                                                                                                                                                            SAI CVSSASHINFEGPONPDNYLVTPELSLPGGGTLTFWVCAQD-ANYASEHYAVYASST
                                                                                                                                                                                                                                          GNDASNFANALLEEVLTAKTVVTAPEAIRGTRAQGTWYQKTVQLPAGTKYVAFRHFGCTD
                                                                             KWNAPASKRAEVINEDFE-NGIPASWKTIDADGDGNNW--TTTPPPGG-----SSFAGHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemagglutinin protein; periodontal disease; vaccine; hagD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumwasorn S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated Porphyromonas gingivalis genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1063 TAQGGYYAVMVVVDGKSYVEKLAIK 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Col 57-64; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW69486 standard; protein; 1087
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(UABR-) UAB RES FOUND
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N-PSDB; AAV58873.
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09-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-SEP-1988;
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RESULT 8 AAW69486

d  $\overset{\circ}{\alpha}$  1177

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943 VLGIMIDDVVITGEGEGBSYTYTVYRDGTKIQEGLETTYRDAGMSAQSHEYCVEVKYAA 1002

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               1003 GVSPKVCVDYIPDGVADVIAQKPYILIVVGKIIIVTCQGEAMIYDMNGRRLAAGRNIVVY 1062
       GESAIETATLNITSLADVTAQKPYTLTVVGKTITVTCQGEAMIYDMNGRRLAAGRNTVVY 1707
                                                                                                                                                              Periodontal disease; cell surface protein; thiol protease; endopeptidase; PrtR; PrtR45; PrtR44; PrtR15; PrtR17; PrtR27; haemagglutinin; adhesin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antigenic protein complex from Porphyromonas gingivalis - comprising Arg- and Lys- specific thiol endo-peptidase(8), used in the detection, prevention and treatment of periodontal disease.
                                                                                                                                                                                                                                                  /label= PrtR45
/note= "45 kDa Arg-specific thiol protease"
                                              . .227
||abel=_Pro-pro_peptide
                                     TAQGGHYAVMVVVDGKSYVEKLAVK 1732
                                                                                                                                                                                                                                                                                        note= "44 kDa adhesin"
                                                                                                                                                                                                                                                                                                                       note= "15 kDa adhesin"
273. .1274
                                                                                                                                                                                                                                                                                                                                              /label= PrtR17
/note= "17 kDa adhesin"
                                                                                                                                                                                                                                                                                                                                                                                    /note= "27 kDa adhesin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VICTORIAN DAIRY IND AUTHORITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Slakeski N;
                                                                                                                                                                              therapy; diagnosis; vaccine; antigen
                                                                                                                                                                                             Porphyromonas gingivalis; strain W50
                                                                                          AAW24786 standard; protein; 1706 AA
                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                PrtR antigenic protein complex.
                                                                                                                                                                                                                                                                          20. .1138
label= PrtR44
                                                                                                                                                                                                                                                                                                          139. .1273
label= PrtR15
                                                                                                                                                                                                                                                                                                                                                                             PrtR27
                                                                                                                                                                                                                                                                                                                                   /label= Pre-
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                                                                                                                                                                                                                                   227. .228
                                                                                                                                (first entry)
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                                                                                                                          (revised)
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Protein
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                                                                                                                       17-OCT-2003
25-NOV-1997
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                                                                                                         AAW24786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AICI-)
                                                                                                                                                                                                                    Peptide
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Example 1; Fig 8b; 68pp; English.

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comprises a 300 kDa complex composed a 45 kDa arginivalis (PG)
comprises a 300 kDa complex composed a 45 kDa arginine-specific thiol
comprises a 300 kDa complex composed a 45 kDa arginine-specific thiol
corresponding to the triangle of the triangle of the triangle of the triangle of the triangle of the triangle of the triangle of the triangle of the triangle of the triangle of the prick complex comprises at least one multimeric protein complex that and prick containing at least one adhesin domain, the complex having a mol.wt. of over 200 kDa, and preferably comprises all 9 proteins of the PrtR-PrtK complex (see also AAW24780-85). It can be used to a claimed composition to alicit an immune response directed against C PG, and in a claimed method of reducing the prospect of PG infection and/or severity of disease. Antibodies directed against the complex are claimed for use in treating PG infection. Unlike whole PG cells or other previously prepared antigens based on fimbriae or the capsule, the PttR-PttK complex or component parts are safe and effective antigens. (Updated on 17-0CT-2003 to standardise OS field)
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46.5%; Score 4272; DB 2;
Best Local Similarity 50.9%; Pred. No. 3.6e-274;
Matches 932; Conservative 204; Mismatches 456;
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KETVIKTINTNGEPNPYQPVSNLTATTQGQKVTLKWDAPSTKTNATTNTARSVDGIRELV
                                                                                                  G---PIKEDDYVFEAGKKYHFLMKKMGSGDGTELTISEGGGSDYTYTVYRDGTKIKEGLT
                                                                                                                                                                                                                            ATTFEEDGVATGNHEY CVEVKY TAGVS PKV CKDVTVEGSNEFA PVONL TGSAVGOKVTLK
                                                                                                                                                                                                                                                         WDAPNGTPNPNPNPNPNPNPG----TTLSESFBNG1PASWKT1DADGDGHGWKPGNAPG1AGY
                                                                                                                                                                                                                                                                        WDAPNGTPNPNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPGIAGY
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                             FVTIEPAND-VRANEAKVVLAADNVWGDNTGYQFLLDADHNTFGSVIPA-TGPLFTG-TA
                                             LLSVSDAPELLRSGQAEIVLEAHDVWNDGSGYQILLDADHDQYGQVIPSDTHTLWPNCSV
                                                                                    SSNLYSANFEYLVPANADPVVTTQNIIVTGQGEVVIPGGVYDYCITNPEPASGKMWIAGD
                                                                                                                                          GGNQPARYDDFTFEAGKKYTFTMRRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLT
                                                                                                                                                                                                  ATTFEEDGVAAGNHEYCVEVKYTAGVSPKVCKDVTVEGSNEFAPVQNLTGSSVGQKVTLK
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47;
                                                                                                                                                                                                                                   Arginine specific proteinase; Arg-gingipain; gingipain-2; haemagglutinin; immunogenic component; vaccine; inflammatory response; tissue damage; periodontal disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a Porphyromonas gingivalis arginine-specific proteinase known as Arg-gingipain/gingipain-2 amino acid sequence. Gingipain-2 consists or a 50kD protease component non-covalently associated with a 44kD haemagqlutinin component. The proteinase is stimulated by glycine containing peptides and glycine analogues. It is inhibited by cysteine protease group specific inhibitors. The protease propaganic compositions and vaccines against inflammatory response and tissue damage caused by P. gingivalis in periodontal disease. It can also be used to screen for agents that modulate Arg-gingipain proteinase activity inhibitors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Amino acids 720-1185 are specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 SVSIPGAFPT-----GEVGSPEVPAVRKLIAVPVGATPVVRVKS--FTEQVYSLNQYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          229. .719
/note= "Amino acids 229-719 are specifically claimed"
720. .1185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Porphyromonas gingivalis arginine-specific protease preparation useful for preparing vaccines against periodontal disease and for screening for Arg-gingipain inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 238;
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   standard; protein; 1704 AA
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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94US-00265441.
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                                                                                                                                                                                                                                                                                                                                                                     Porphyromonas gingivalis.
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Best Local Similarity
Matches 932; Conserv
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                                                                                                                                                                                    Arg-gingipain-2
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24-JUN-1994;
                                                                                                                        25-APR-2000
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/label= Proteolytic_component
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/label= Prepro_peptide
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                                    VQYDVVANQLKVRNNIEI---EVSFQGADEVATQRLYDASFSPYFETAYKQLFNRDVYTD
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/label= HGP_27kDa /note= "Haemagglutinin protein component"

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(UYGE-) UNIV GEORGIA RES FOUND INC
                                     93US-00119361.
94US-00265441.
94WO-US010283.
                            25-JAN-2000; 2000US-00490931
                                                                    Travis J, Potempa JS,
                                                                            WPI; 2001-588904/66.
                                                                                 N-PSDB; AAS15242.
                                                  08-NOV-1994;
            US6274718-B1
                                     10-SEP-1993;
                                          24-JUN-1994;
                                              09-SEP-1994;
                    14-AUG-2001
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Barr PJ, Pavloff N;

94US-00336308

The invention relates to a recombinant DNA molecule encoding high molecular weight (mature) Arg-gingipain (AG) protein, which has an enzymatically active protease component (AG-2) and a haemagglutinin component, from P. gingivalis. The nucleic acid is useful for producing mature Arg-gingipain protein. Immunogenic compositions comprising Argingipain are useful for immunising animals including humans against inflammatory response and tissue damage caused by an archaebacterium Porphyromonas gingivalis, which causes progressive periodontitis. Argingipain is also useful for identifying agents that modulate Argingipain proteinase activity, whether by acting on the protein in the gingipain protein as a such as complement factors C3 or C5. The present sequence New recombinant DNA molecule which encodes high molecular weight (mature) Arg-gingipain protein, useful for immunization against inflammation and tissue damage, comprises enzymatically active protease component and Claim 1; Col 29-41; 56pp; English. hemaglutinin component is Arg-gingipain-2 Sequence 1704 AA;

47; 282 116 ----GQVPTYTEGVNLSEKGMPTLPILSRSLAVSDTREMKVEVVSSKFIEKKNVL---- 116 117 SEKLIMPHQPSMSKSDDPEKVPFVYNAAAYARKGFVGQELTQVEMLGTMRGVRIAALTINP 176 233 222 287 288 KAFIHKKY----NDGLAASAAPVFLALVGDTDVISGE--KGKKTKKVTDLYYSAVDGDYF 341 332 342 PEMYTFRMSASSPEELTNIIDKVLMYEKATMPDKSYLEKVLLIAGADYSWNSQVGQPTIK 401 65 65 6 LLIAASLLGVGLYAQSAKIKLDAPITRTICINNSFKQFDASFSFNEVELTKVETKGGTFA 66 SVSIPGAFPT-----GEVGSPEVPAVRKLIAVPVGATPVVRVKS--FTEQVYSLNQYG 177 VQYDVVANQLKVRNNIEI---EVSFQGADEVATQRLYDASFSPYFETAYKQLFNRDVYTD NW----234 HGDLYNTPV-----RMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYTDEAEVGTTNASI Indels 238; Length 1704; tch 46.5%; Score 4270; DB 4; al Similarity 50.9%; Pred. No. 4.9e-274; 932; Conservative 204; Mismatches 456; Query Match Best Local Similarity 99 Best Loca Matches qq à В ŏ à 임  $^{\circ}$ 셤 à В à

qq	333	
	402	YLKAPYTG
Db	393	HENVIANLLTQYGYTKIIKCYDPGVIPKNIIDAFNGGISLVNYTGHGSETAW 444
۲۵.		PLITTSOLKALTNKDKYFLAIGNCCITAQFDYVQPCFGGVITRVKEKGAYAYIG 50
Пр	445	50
\$ 18	507	VGANAVFGVQPTFEGTSMGSYDATFI
αn	505	ASFMRG
& £		AGNIGNITHIGAHYYWEAYHVLGDGSVWFYRAMPKINIYTLPASL 611
ga	200	ו כ
λō	612	
DP DP	590	64
οy	671	YLPVIKQIQV-GEPSPYQPVSNLTATIQGQKVTLKWEAPSAKKAEGSREVKRIGDGL 726
Dp	648	KETVIKTINTNGEPNPYQPVSNLTATTQGQKVTLKMDAPSTKTNATTNTARSVDGIRELV 707
ά	727	FVIIEPAND-VRANEAKVVLAADNVMGDNTGYQFLLDADHNTFGGVIPA-TGPLFTG-TA 783
Db	708	LLSVSDAPELLRSGGAEIVLEAHDVMNDGSGYQILLDADHDQYGQVIPSDTHTLMPNCSV 767
ογ	784	SSNLYSANFEYLVPANADPVVTTQNIIVTGQGEVVIPGGVYDYCITNPEPASGKMMIAGD 843
Db	768	PANLF-APPEYTVPENADPSCSPTNMIMDGTASVNIPAGTYDFAIAAPQ-ANAKIWIAGQ 825
٥٧	844	GGNQPARYDDFTFEAGKKYTFTMRRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLT 903
Db	826	GPTKEDDYVFEAGKKYHFLMKKMGSGDGTELTISEGGGSDYTYTVYKDGTKIKEGLT 882
ò	904	ATTFEEDGVAAGNHEYCVEVKYTAGVSPKVCKDVTVEGSNEFAPVQNLTGSSVGQKVTLK 963
ΩÞ	883	ATTFEEDGVATGNHEYCVEVKYTAGVSPKVCKDVTVEGSNEFAPVQNLTGSAVGQKVTLK 942
ò	964	WDAPNGTPNPNPNPNPNPG-TILSESFENGIPASWKIIDADGDGHGWKPGNAPGIAGYNS 1022
DP	943	WDAPNGTPNPNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPGIAGYNS 1002
λ	1023	NGCVYSESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTG 1082
QQ	1003	NGCVYSESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTG 1062
ờ	1083	NDASNFTNALLEETTTAKGVRSPKAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFY 1142
Db	1063	NDASNFTNALLEETITAKGVRSPEAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFY 1122
ζζ	1143	IDLDEVEIKANGKRADFTETFESSTHGEAPAEMTTIDADGDGGWLCLSSGQLDWLFAHG 1202
Dp	1123	IDLDEVEIKANGKRADFTETFESSTHGBAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHG 1182
δŅ	1203	GSNVVSSFSWNGMALNPDNYLISKDVTGATKVKYYAVNDGFPGDHYAVMISKTGTNAGD 1262
Db	1183	GINVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGD 1242
δ	1263	FTVVFEETPNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNY 1322
Db	1243	FTVVFBETFNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNY 1302
λŏ	1323	ILLDDIQFTWGGSPTPTDYTYTVYRDGTKIKEGLTETTFBEDGVATGNHEYCVEVKYTAG 1382
QQ	1303	ILLDDIQFIMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAG 1362
È	1383	VSPKKCVDVTVNSTQFNPVQNLTABQAPNSMDAILKWNAPASKRAE 1428

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                                        A low mol.wt. arginine-specific gingipain (AG-1) and high mol.wt. AG (AG-2) were isolated from P. gingivalis strains H66 (ATCC 33277) and W50 (AG-KTCC 59373). The sequences of the proteins were used to design PCR primers and probes to isolate AG DNA. Lambda DASH and lambda ZAP libraries were screened with a probe based on amino acids 11-22 of the AG protein to obtain DNA encoding AG-1 (AAQ08484) and AG-2 (AAQ08489). AG-2 correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQFVKQEYBKBGND------LTYVLLVGDHXDIPAKITPGIKSDQV---YGQIVGNDHY 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393 HENVIANLLTOYGYTKIIK-----CYDPGVTPKNIIDAFNGGISLVNYTGHGSETAW 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    648 KETVIKTINTNGEPNPYQPVSNLTATTQGQKVTLKWDAPSTKTNATTNTARSVDGIRELV 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 VQYDVVANQLKVRNNIEI---EVSFQGADBVATQRLYDASFSPYFETAYKQLFNRDVYTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 GTSHFGTTHVKQLTNSNQLPFIFDVACVNGDFLFSMPCFAEALMRAQKDGKPTGTVAIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSPNSYWGEDYYWSVGANAVFGVQPTFEGTSMGSYDATFLEDSYNTVNSIMWAGNLAATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVSIPGAFPT-----GEVGSPEVPAVRKLIAVPVGATPVVRVKS--FTEQVYSLNQYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 LOYNPVTKTLRIYTEITVAVSETSEQGKNILNKKGTFAG-----FEDTYKRMF-----MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 HGDLYNTPV-----RMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYTDEAEVGTTNASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 YEPGRYTPVEEKQNGRMIVIVAKKYEGDIKDFVDWKNQRGLRTEVKVAEDIASPVTANAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADPLITTSQLKALTNKDKYFLAIGNCCITAQFDYVQPCFGBVITRV----KEKGAYAYIG
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                                                                                                                                                                                                                                                                                       Indels 238;
                                                                                                                                                                                                                                                   Length 1704;
                                                                                                                                                                                                                                                   46.5%; Score 4264; DB 2; llarity 50.9%; Pred. No. 1.2e-273; Conservative 204; Mismatches 457;
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             Disclosure, Page 70-77; 89pp; English.
                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                  Sequence 1704 AA;
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931;
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                                                       TIEPANDVRANEAKVVLAADNVWGDNTGYQFL-LDADHNTFGSVIPATGPLFTGTASSNL 1479
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VSPKECVNVTINPTQFNPVKNLKAQ--PDGGDVVLKWEAPSAKKTEGSREVKRIGDGLFV 1420
                                  -VLNEDFENGIPASWKTIDADGDGNNWTTTPPPGGSSFAGHNSAIC 1473
                                                                                                                                                                                                                                                       1583 HFGCTDFFWINLDDVVITSGNAPSYTYTIYRNNTQIASGVTETTYRDPDLATGFYTYGVK 1642
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                                                                                                         VSSASHINFEG--PONPD-----NYLVT--PELSLPGGGTLTFWVCAQDANYASEHYAV
                                                                                                                              -----AGKKYTFTMR
                                                                                                                                                                                                                                                                                         1560 RACMGDG----TDMEVEDDSPASYTYTVYRDGTKIKEGLTETTYRDAGMSAQSHEYCVE
                                                                                                                                                                                                                                                                                                                                                   1524 YASSTGNDASNFANALLEEVLTAKTVVTAPEAIRGTRAQGTWYQKTVQLPAGTKYV-AFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "corresponds to Arg-gingipain-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gingivalis; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                       NTVVYTAQGGHYAVMVVVDGKSYVEKLAVK 1732
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/label= Hemagglutinin
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/label= Hemagglutinin
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/label= Hemagglutinin
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/label= Protease
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93US-00141324.
94US-00265441.
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                                                                                                                                                                                                                  1533 -AGDGGNQPARYDDFTFE-
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arginine-specific protease.
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(first entry)
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24-JUN-1994;
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21-SEP-1995
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Protein
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                                                                                 G---PTKEDDYVFEAGKKYHFLMKKMGSGDGTELTISEGGGSDYTYTVYRDGTKIKEGLT
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SSNLYSANFEYLVPANADPVVTTQNIIVTGQGEVVIPGGVYDYCITNPEPASGKMWIAGD
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AAW34843 ID AAW34843 standard; protein; 1704

RESULT 13

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The present sequence represents an arginine-specific protease of Porphyromonas gingivalis. The following peptides, derived from Argand Psys-specific high molecular weight proteases, offer protection against infection: YTTYTYRDGK IKEGITATE DOGWATGHIB YCVEKTRAGS VBFWCK (I); YTPVEEKQNG RMIVIVAKKY (II); QLPFIFDVAC VNGDFLFSMP CFAEAMRAQ (III); YTPVEEKQNG RMIVIVAKKY (II); GNBEYCVERK YTAGVSPKVC KDVTV (V); RAEBPRYGORY TITAGORY TITAGORY TITAGORY THAGAFDTY RNEMNYEDGR (VII); DYTYTYTNG TKIKEGITAT TEREDGVATG NMEYCVCVKY TAGVSPKVC (VIII); NTYTVYRDGT KIKEGITATFE EDGG (IX); RAGGATLAGT FEBEDGVATG NMEYCVCVKY TAGVSPKVC (VIII); NTYTVYRDGT KIKEGITATFF EDGG (IX); RIGGATATF FEBEDGVATGH HEY (XII); CANDANGTPN NPNN PORTITISE (XII); and YTPVEEKENG RMIVIVAKKY (XIII). They are used in vaccines to protect animals, including humans, from gingivitis and/or periodontal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47;
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                                                                                                          Arg-specific gingipain protease; gingivalis; periodontal disease; vaccine; infection.
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                                                                         Arg-gingipain high molecular weight prepolyprotein sequence
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                                                                                                                                                                                                                             /note= "precursor protein"
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                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             (UYGE-) UNIV GEORGIA RES FOUND INC. (MORE-) MOREHOUSE SCHOOL MEDICINE.
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                                                   PEMYTFRMSASSPEELTNIIDKVLMYEKATMPDKSYLEKVLLIAGADYSWNSQVGQPTIK
                                                                                                                      Y-GMQYYYNQEHGYTDVYNYLKAPYTGCY-----SHLNTGVSFANYTAHGSETAW
                                                                                                                                   SSPNSYWGEDYYWSVGANAVFGVQPTFEGTSMGSYDATFLEDSYNTVNSIMWAGNLAATH
HGDLYNTPV-----RMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYTDEAEVGTTNASI
            ---NDGLAASAAPVFLALVGDTDVISGE--KGKKTKKVTDLYYSAVDGDYF
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This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagE haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
                                                                                                                                                                                   89
                                                                                                                                                                                                           FTEQVYSLNQYGSEKLMPHQPSMSKSDDPEKVPFVYNAAAYARKGFVGQELTQVEMLGTM
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                                                                                                                                                                                                                                                                                                         YKQLFNRDVYTDHGDLYNTPV-----RMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYT
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                                                                                                             Length 1687;
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                                                                                                                                      197; Mismatches 443;
                                                                                                             46.2%; Score 4245; DB 2;
51.6%; Pred. No. 2.2e-272;
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                            YRDGTKIKEGLIATTFEEDGVATGNHEYCVEVKYTAGVSPKVCKDVTVEGSNEFAPVQNL
                                                                              TGSSVGQXVTLXWDAPNGTPNPNPNPNPG----TTLSESFENGIPASWXTIDADGDGHG
                                                                                                        TGSAVGQKYTLKWDAPNGTPNPNPNPNPNPGTTTLSESFENG1PASWKT1DADGDGHG
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  YRDGTKIKEGLTATTFEEDGVAAGNHEYCVEVKYTAGVSPKVCKDVTVEGSNEFAPVQNL
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RDVRGQVVNFAPLQYNPVTKTLRIYTEITVAVSETSEQGKNILNKKGTFAG----FEDT 196
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                                                                                                                                                                                                                               P. gingivalis 381 haemagglutinin hagE (AAR96033) was identified as the product of a gene (AAT30656) identified in P. gingivalis 318 genomic DNA. The haemagglutinin can be obtd. from transformed host cells and used as a vaccine to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of a live vaccine. The haemagglutinin can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)
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        Porphyromonas gingivalis; strain
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UAB RES FOUND
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Best Local Similarity
Matches 918; Conserv
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                                                                                                                                                              NGNYDVVITRSNYLPVIKQIQV-GEPSPYQPVSNLTATTQGQKVTLKWEAPSAK---KAE
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OY 1570 VOLPAGTKYV-AFRHFGCTDFFWINLDDVVITSGNAPSYTYITKNNTQIASGVTETTYR 1628

Db 1533 ----AGKKKYTFTWRRACMGDG----TDMEVEDDSPASYTYTVYRDGTKIKEGLIFTTYR 1583

QY 1629 DPDLATGFYTYGVKVYPNGESALETATIANTTSLADVTAQKPYTLTVVGKTITVTCQGRA 1688

Db 1584 DAGMSAQSHEYCVEVKYAAGVSFKVCVDYIPDGVADVTAQNPYTLTVVGKTITVTCQGEA 1643

QY 1689 MIYDMRGRELAAGRATVVYTAQGGHYAVMVVVDGKKSYVEKLAVK 1732
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g

Search completed: May 18, 2004, 11:32:46 Job time: 93.0274 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model - protein search, OM protein

Run on:

May 18, 2004, 11:29:09 ; Search time 31.8582 Seconds (without alignments) 5229.534 Million cell updates/sec

US-08-353-485-10 9179 1 MRKLLLITAASLLGVGLYAQ......HYAYMVVVDGKSYVEKLAVK 1732

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB ség length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR 78:*
1: Pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	lysine-specific cy	gingipain R (EC 3.	hemagglutinin A -	gingipain R (EC 3.	arginyl endopeptid	cal	probable RTX famil	probable peptidogl	hypothetical prote	hypothetical prote	hypothetical prote	probable peptidogl	m	hypothetical Serin	w.	tical	hyalin - sea urchi	Ξ.	ര		hypothetical prote	cell wall-associat	tail-host specific	large repetitive p	hypothetical prote	٠,	hypothetical prote	cellulo	surface protein pr
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## ALIGNMENTS

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1980-30-30-30-30-30-30-30-30-30-30-30-30-30
C;Species: Porphyromonas gingivalis C;Date: 22-Oct-1999 #sequence_revision_22-Oct-1999 #text_change 17-Nov-2000
C;Accession: T30836; T30837; T30526; A53113 R;Barkocy-Gallagher, G.A.; Han, N.; Patti, J.M.; Whitlock, J.; Progulske-Fox, A.; Lantz,
J. Bacteriol. 178, 2734-2741, 1996 A.Title: Analysis of the prtP gene encoding porphypain, a cysteine proteinase of Porphyr A.Title: Analysis of the mith.ec.12011. PMID: 8641659
A; Kelefelice number: 22005); North-Valler   A; Accession T30836 A; Accession T30836
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A; Keslaues: 1-1/32 < DAK) A; Cross-references: EMBL: U42210; NID: 91314325; PID: 91314326; PIDN: AAB06565.1
R;Slakeski, N.; Cleal, S.M.; Keynolus, B.C. submitted to the EMBL Data Library, October 1996
A;Reference number: Z20896
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA A;Residues: 1-795,'I',797-1389,'N',1391-1478,'Y',1480-1732 <sla></sla>
A) Cross references: RMB1.U75366; NID:92182811; PID:92182812; PLUN:AABOUGO:1.
Infect. Immun. 66, 3035-3042, 1998
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A;Accession: T30526
A; Molecule type: DNA
A; Residues: 1-1350,'N',1352-1363,'Y',1365-1447,'H',1449-1732 <lew></lew>
A;Cross-reletances; Embly Mr. 1 (1) Travis, J. Travis, J. R. Potempa, J.; Travis, J.
J. Biol. Chem. 269, 406-411, 1994 B.Title. Inside- and arginine-specific proteinases from Porphyromonas gingivalis. Isolat
A; Reference number: A53113; MUID: 94103245; PMID: 8276827
A;Accession: A53113 A;Status: preliminary
A, Molecule type: protein
A; KeBlaues: 229-249 <firs A; Experimental source: H66</firs 
A;Note: sequence extracted from NCBI backbone (NCBIP:141690)
C, Venieller); prtK A, Gene: prtP; prtK C, Keywords: cysteine proteinase; hydrolase
100.0%;
Best Local Similarity 100.0%; Pred. No. 0; Matches 1732; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

	Oy 1381 AGUS Db 1381 AGUS OY 1441 SWKT Db 1441 SWKT OY 1501 GGGT OY 1501 GGGT OY 1561 AQGT OY 1561 AQGT	Db 1561 AGH Qy 1621 GVF Db 1621 GVF Qy 1681 TVF Db 1681 TVF	RESULT 2 A55426 gingipain R (BC 3. N.Alternate names: C.Species: Porphyr C.Date: 10-Peb-19 C.Accession: A5545 R.Pavloff, N., Pot J. Biol Chem. 27 A,Title: Molecular A,Reference number A,Reference number A,Accession: A5544 A,Scession: A5544	A;Molecule type: I A;Residues: 1-1708 A;Cross-reference R;Pike, R.; McGrav U, Biol. Chem. 26 A;Title: Lysinne- A;Reference number A;Accession: D5311 A;Colecule type: I A;Molecule type:
	ASAAPVELALVODTDVISGEKGKKTKKVTDLYYSAVDGDYFPEMYTFRMSASSPEELTNI 36 ASAAPVELALVGDTDVISGEKGKKTKKVTDLYYSAVDGDYFPEMYTFRMSASSPEELTNI 36 ASAAPVELALVGDTDVISGEKGKKTKKVTDLYYSAVDGDYFPEMYTFRMSASSPEELTNI 36 IDKVLMYEKATMPDKSYLEKVLJAGADYSWNSQVQPTIKYGMQYYYNQEHGYTDVYNY 42 IDKVLMYEKATMPDKSYLEKVLJAGADYSWNSQVQPTIKYGMQYYYNQEHGYTDVYNY 42 ILKAPYTGCYSHLNTGVSFANYTAHGSETAWADPLLTTSQLKALTNKDKYFLAIGNCCITA 48 ILKAPYTGCYSHLNTGVSFANYTAHGSETAWADPLLTTSQLKALTNKDKYFLAIGNCCITA 48 ILKAPYTGCYSHLNTGVSFANYTAHGSETAWADPLLTTSQLKALTNKDKYFLAIGNCCITA 48	481 QPDYQQPGGEUTTRVKEKGAYAYIGSSPNSYWEDDYWASQAAAVGOPTEGISMS 540 481 QPDYQQPGGEUTTRVKEKGAYAYIGSSPNSYWEDYYWSGAAAAVGOPTEGISMS 540 481 QPDYQQPGGEUTTRVKEKGAYAYIGSSPNSYWGEDYYWSGANAVGQYPTPEGISMGS 540 541 YDATFLEDSYNTVNSIMWAGNLAATHAGNIGNITHIGAHYYWEAYHVLGDGSVMPYRAMP 600 [	661 NYDVVITRSNYLPVIKQIQVGEBSPYQPVSNLTATTGGQKVTLKWEAPSAKKAEGSREVK 720 661 NYDVVITRSNYLPVIKQIQVGEPSPYQPVSNLTATTGGQKVTLKWEAPSAKKAEGSREVK 720 661 NYDVVITRSNYLPVIKQIQVGEPSPYQPVSNLTATTGGQKVTLKWEAPSAKKAEGSREVK 720 721 HIGDGLFYTIEPANDVANEAKVVLAADNVWGDNTGYQFLLDADHNTFGSVIPATGPLFT 780 721 RIGDGLFVTIEPANDVRANEAKVVLAADNVWGDNTGYQFLLDADHNTFGSVIPATGPLFT 780 781 GTASSNLYSANFEYLVPANADPVVTTQNIIVTGGGEVVIPGGVYDYCITNPEPASGKAMI 840 781 GTASSNLYSANFEYLVPANADPVVTTQNIIVTGGGEVVIPGGVYDYCITNPEPASGKAMI 840 841 AGDGGNQPARYDDFTFEAGKKYTFTWRRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKE 900	AGDGGNQPARYDDFTFEAGKKYTFTMRRAGMGDGTDMEVEDDSFASYTYTVYRDGTKIKE GLTATTFEEDGWAAGNHEYCVEVKYTAGWSPKVCKDVTVEGSNEFAPVQNLTGSSWGGKV CLTATTFEEDGWAAGNHEYCVEVKYTAGWSPKVCKDVTVEGSNEFAPVQNLTGSSWGGKV TLKWDAFNGTPNPNPNPNPNPNFTLSSFFBNGIPASWKTIDADGDGHGWKPGNAPGIAGY TLKWDAFNGTPNPNPNPNPNPNFTLSSFFBNGIPASWKTIDADGDGHGWKPGNAPGIAGY TLKWDAFNGTPNPNPNPNPNPTLTLSSFFBNGIPASWKTIDADGDGHGWKPGNAPGIAGY NSNGCVXSESFGLGGIGWLTPDNYLITPALDLPNGGKLTFWVCAQDANYASSHYAVYASS NSNGCVXSESFGLGGIGWLTPDNYLITPALDLPNGGKLTFWVCAQDANYASSHYAVYASS TGNDASNPTNALLEBTITAKGWRSPKAIRGRIQGTWRQKTVDLPAGTKVVAFRHFQSTDM
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3.4.22.37) precursor - Porphyromonas gingivalis
ss: 50K high molecular mass arginine-specific cysteine proteinase; HGP; F
yromonas gingivalis
395 #sequence_revision 10-Feb-1995 #text_change 08-Oct-1999
426; D53113
Octempa, J.; Pike, R.N.; Prochazka, V.; Kiefer, M.C.; Travis, J.; Barr, F
y70, 1007-1010, 1995
ar cloning and structural characterization of the Arg-gingipain protein
er. A55426; MUID:95138080; PMID:7836351

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ew, NIS282, NID:q557067; PIDN:AAA69539.1; PID:q557068
ew, W.; Potempa, J.; Travis, J.
69, 406-411, 1994
and arginine-specific proteinases from Porphyromonas gingivalis. Isolater A53113; MUID:94103245; PMID:8276827

inary protein 249 - PIKS-ource: H66 extracted from NCBI backbone (NCBIP:141694) eine proteinase; hydrolase

Length 1704; Score 4270; DB 2; Pred. No. 1.2e-228; 46.5%; ilarity

LLIAASLLGVGLYAQSAKIKLDAPTTRTTCINNSFKQFDASFSFNEVELTKVETKGGTFA 65 :::     :	SEKLMPHQPSMSKSDDPEKVPFVYNAAAYARKGFVGQELTQVEMLGTWRGVRIAALTINP 176	HGDLYNTPVRMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYTDBAEVGTTNASI 287	PEMYTPRMSASSPEELTNIIDKVLMYEKATMPDKSYLEKVLLIAGADYSMNSQVGQPTIK 401  ::         :       :       :	ADPLLITSQLKALTNKDKYFLAIGNCCITAQFDYVQPCFGEVITRVKEKGAYAYIG 506   : :        : :         :	AGNIGNITHIGAHYYWEAYH		
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hemagglutinin A - Porphyromonas gingivalis
C;Species: Porphyromonas gingivalis
C;Species: Porphyromonas gingivalis
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Aug-2001
C;Accession: 728651
R;Han, N.; Whitlock, J.; Progulske-Fox, A.
Infect. Immun. 64, 4000-4007, 1996
A;Title: The hemagglutinin gene A (hagA) of Porphyromonas gingivalis 381 contains four 1
A;Reference number: Z20494; WUID:9704762; PMID:8926061
A;Reference number: Z20494; WUID:9704762; PMID:8926061
A;Reference number: Date in the contains four language in the limitary; translated from GB/EMBL/DDBJ
A;Residues: 1-2628 cHAN>
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96 A9 A9

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Query Match

A; Gene: hagA

92 Pb

45.9%; Score 4217; DB 2; Length 2628;

A; Cross-references: EMBL: U41807; NID: g1552410; PID: g1469916; PIDN: AAB17128.1 C; Genetics:

cherichia coli of prpRl of re 31-Mar-1997 s (fragment) rtis, M.A.

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68 VPTYTEGVNLSEKGMPTLPLLSRSLAVSDTREMKVEVVSSKFIEKKKNVL-----IAPS 120
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                                                                                                                                                                              68 VPIYTEGVNLSEKGMPTLPILSRSLAVSDTREMKVEVVSSKFIEKKNVL-----1APS 120
                                                                                                                                                                                                                               NQLKVRNNIEI---EVSFQGADEVATQRLYDASFSPYFETAYKQLFNRDVYTDHGDLYNT 240
                                                                                                                                                                                                                                                                                             229
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                                                                                                                                                                                                                                                                                                                                                                    295 Y----NDGLAASAAPVFLALVGDTDVISGE--KGKKTKKVTDLYYSAVDGDYFPEMYTFR 348
                                                                                                                                                                                                                                                                                                                                                                                                                                        340 FSCESKEDLKTQIDRTIHYERNITTEDKWLGQALCIASAEGGPSADNGESDIQHENVIAN 399
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                                                                                                                                                                 66 SVSIPGAFFTGEVGSPEVPAVRKLIAVPVGATPVVRVKS--FTEQVYSLNQYGSEKLMPH 123
                                                                                                                                                                                                                  QPSMSKSDDPEKVPFVYNAAAYARKGFVGQELTQVEMLGTMRGVRIAALTINPVQYDVVA 183
                                                                                                                                                                                                                                                                                                                      241 PV-----RMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYTDEAEVGTTNASIKAFIHKK 294
                                                                                                                                                                                                                                                                                                                                                                                                                       349 MSASSPEELTNIIDKVLMYEKATMPDKSYLEKVLLIAGADYSWNSQVGQPTIKY-GMQYY 407
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                                                                                                                               10 IALCSSLLGGMAFAQQTELGRNPVYRLLESTQQSVTK--VQFRMDNLKFTEVQTPKGMAQ
                                                                                                                                                                                                                                                                                          180 KILRIYTEITVAVSETSEOGKNILNKKGTFAG-----FEDTYKRMF-----MNYEPGRYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           514 GEDYYWSVGANAVFGVQPTFEGTSMGSYDATFLEDSYNTVNSIMWAGNLAATHAGNI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    512 -----ASPMRG------CEKHPNNIKRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             678 IQV-GEPSPYOPVSNLTATTQGQKVTLKWEAPSAK---KAEGSREVKRIGDGLFVTIEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   734 ND-VRANEAKVVLAADNVWGDNTGYQFLLDADHNTFGSVIPA-TGPLFTG-TASSNLYSA
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                                                                                                              6 LLIAASLIGVGLYAQSAKIKLDAPTTRITCINNSFKQFDASFSFNEVELTKVETKGGTFA
                                                                                                                                                                                                                                                                                                                                                                                      290 YEKEGND-----LTYVLLIGDHXDIPAKIIPGIKSDQV---YGQIVGNDHYNEVFIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQLKALTNKDKYFLAIGNCCITAQFDYVQPCFGEVITRV----KEKGAYAYIGSSPNSYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408 YNQEHGYTDVYNYLKAPYTGCY-----SHLNTGVSFANYTAHGSETAWADPLLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 LLTQYGYTKIIK-----CYDPGVTPKNIIDAFNGGISLANYTGHGSETAWGTSHFGT
                                                                                       176; Gaps
                                                               Length 1526;
                                                                                      Indels
                                                           Query Match 41.5%; Score 3808; DB 2; Best Local Similarity 51.7%; Pred. No. 4.7e-203; Matches 817; Conservative 183; Mismatches 403;
A;Cross-references: EMBL:X82680
C;Genetics:
A;Gene: prpRl
C;Keywords: cysteine proteinase; hydrolase
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arginyl endopeptidase - Porphyromonas gingivalis
c;Species: Porphyromonas gingivalis
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c;Species: Porphyromonas gingivalis
c;Species: Porphyromonas gingivalis
c;Accession: 140229
R;Okamoto, K.; Misumi, Y.; Kadowaki, T.; Yoneda, M.; Yamamoto, K.; Ikehara, Y.
Arch. Biochem. Biophys. 316, 917-925, 1995
Artitle: Structural characterization of argingipain, a novel arginine-specific cysteine
A;Reference number: 140229; MUID:9516884; PMID:7864651
A;Accession: 140229
A;Accession: I40229
A;Accession: 1309 1387 1369 1129 1148 VEIKANGKRADFTETFESSTHGEAPAEWTIDADGDGQGWLCLSSGQLDWLTAHGGSNVV 1207 32; 949 66 SVSIPGAFPIGEVGSPEVPAVRKLIAVPVGAIPVVRVKS--FIEQVYSLNQYGSEKLMPH 123 67 950 PNPNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPGIAGYNSNGCVY 1250 EETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDD 1428 NDVRANEAKVVLAADNVMGDNTGYQFL-LDADHNTFGSVIPATGPLFTGTASSDLYSA--1070 FTWALLEETITAKGVRSPEAIRGRIQSTWRQKTVDLPAGTKXVAFRHFQSTDMFYIDLDE 1130 VEIKANGKRADFTETFESSTHGEATAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVV 1190 SSFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVF IOFTMGGSPTPIDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKK 1370 CVNVTVNSTQENPVKNIKAQ--PDGGDVVLKWEAPSAKKTEGSREVKRIGDGLFVTIEPA ------VINEDFENGIPASWKTIDADGDGNNWTTTPPPGGSSFAGHNSAICVSSAS 890 GVAAGNHEYCVEVKYTAGVSPKVCKDVTVEGSNEFAPVONLTGSAVGQKVTLKWDAPNGT FINALLEETITAKGVRSPKAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDE 1310 IQFIMGGSPIPIDYTYTVYRDGTKIKEGLIEITFEEDGVAIGNHEYCVEVKYTAGVSPKK 10 IALCSSLLGGMAFAQQTELGRNPNVRLLESTQQSVTK--VQFRMDNLKFTEVQTPKGMAQ SESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASN **EETPNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDD** 1388 CVDVTVNSTOFNPVQNLTAEQAPNSMDAILKWNAPASKRAE------LLIAASILIGVGLYAQSAKIKLDAPTTRTTCTNNSFKQFDASFSFNEVELTKVETKGGTFA GVAAGNHEYCVEVKYTAGVSPKVCKDVTVEGSNEFAPVQNLTGSSVGQKVTLKWDAPNGT PNPNPNPNPNPG---TTLSESFENGIPASWKT1DADGDGHGWKPGNAPGIAGYNSNGCVY SSFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVF Query Match 13.3%; Score 1222.5; DB 2; Length 991; Best Local Similarity 31.8%; Pred. No. 8.7e-60; Matches 322; Conservative 174; Mismatches 381; Indels 135; 1479 HINFEG--PONPONYLVTP 1495 1485 --NFEYLIPANADRNVRPP 1501

A,Status: p A,Molecule A,Residues: A,Experimen C,Genetics: A,Gene: ECS	Query Mat Best Loca Matches	Qy 16	Oy 2						Oy 5. Db 20:				Db 214 Qy 73	Db 220
		•												<u> </u>
QPSMSK : : : KGMIMR NQLKVR: KTLRIY	241 PVRMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYTDEAEVGTTNASIKAFIHKK 294	295 YNDGLAASAAPVFLALVGDTDVISGEKGKKTKKVTDLYYSAVDGDYFPEMYTFR 348	349 MSASSPEELTNIIDKVLMYEKAIMPDKSYLEKVLLIAGADYSWNSQVGQPTIKY-GMQYY 407 	408 YNOEHGYTDVXNYLKAPYTGCYSHLNTGVSFANYTAHGSETAWADPLLTT 457 ::    :				619 SIQAS-AGSYVAISKDGVLXGTGVANASGVATVSMTKQITENGNYDVVITRSNYLPVIKQ 677 	678 IQV-GEPSPYQPVSNLTATTQGQKVTLKWEAPSAKKAEGSREVKRIGDGLFVTIEPA 733	734 ND-VRANEAKVVLAADNVWGDNTGYQFLLDADHNTFGSVIPA-TGPLFTG-TASSNLYSA 790 : : :: ::				oso smaranatuvevaranaskavavavavavavavavavavavavavavavavavava
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d gend RI C. G. hypothetical protein ECs0542 [imported] - Bacherichia coli (strain 0157:H7, substrain 16./Species: Bacherichia coli (5/Date: 18-Uul-2001 #sequence_revision 18-Uul-2001 #text_change 18-Uul-2001 (5/Date: 18-Uul-2001 #sequence_revision 18-Uul-2001 #text_change 18-Uul-2001 (5/Date: 18-Uul-2001 (5/Date: 18-Uul-2001 (7/Date: 18-

754 ---EAGVEQTISGOVTGAAAGDIVI-----VILGGATYTAIVQANLSWS-----VDVPA 1799 86; 917 STSAGNPVSVTHPV--TVDLSA-----VAVSINALTA------DDVINAAEKG 1956 163 TMRGVRIAAL----TINPVQYDVVANQLKVRNNIEIEVSFQGA--DEVATQRLYDASFS 215 216 PYFETAYKQLFNRDVY-TDHGDLYNTPVRMLVVAGAKFKEALKPWLTWKAQKGFYLDVHY 274 TDBAEVGTINASIKAFIHKKYNDGLAASAAPVFLALVGDTDVISGEKGKKTKKVTDLYYS 334 335 AVDGDYFPEMYTFRMSASSPEELTNIID--KVLMYEKA------TMPDKSYLEK 380 143 VAGDDVINATEHAQAQIISGSATGAATGSTVTVTIGTNTFTTVLDASGNWSVGVPASVVS 2202 2415 e type: DNA_ s: 1-5291 <HAY> eferences: GB:BA000007; PIDN:BAB33965.1; PID:g13360000; GSPDB:GN00154 ental Bource: strain O157:H7, substrain RIMD 0509952 501 AYAYIGSSPN-----SYWGEDYYWSYGANAVFGVQPTFEGTSMGSYDATFLED-- 548 604 TYTLPASLPQNQASYSIQASAGSYVAISKDG----VLYGTGVANASGVATVSM----TK 654 655 QITENGNYDV-----VITRSNY-LPVIKQIQVGEPSPYQPVSNLTATTQGGKVTLKW 705 ----SYNTVNSIMWAGNLAATHAGNIGNITHIGAHYYWEAYHVLGDGSVMPYRAMPKTN 603 381 VLLIAGADYSWNSQVGQPTIKYGMQYYYNQEHGYTDVYNYLKAPYTGCYSHLNTGVSFAN 441 YTAHGSETAWADPLLTTSQLKALTNKDKYFLAIGNCCITAQFDYVQPCFGEVITRVKEKG Gaps ----NDVRANEAKVVLAADNVWGDNTGYQFLLDADHN---203 ALANGTVTINASVTDAGGNSGSATHQVTVNTGLPTITFNAISGDN-----ILNADEKGQP ----TGQGBVVIPGGVYDYCITNPEPASGKMMIAGDGGNQPARYDDFTFEAGKKYTFT 866 --MRRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEEDGVAAGNHEYCVEV 924 KYTAGVSPKVCKDVTVEGSNEFAPVQNLTGSSV-----GQKVTLKWDAPNGTPNPNPNP ---TEGSVIPATGPLFTGTASSNLYSA-----NFEYLVPANADPVVTTQNIIV--ch 3.5%; Score 322; DB 2; Length 5291; l. Similarity 19.6%; Pred. No. 1.3e-08; 365; Conservative 228; Mismatches 697; Indels 572; -----PSAKKAEGSREVKRIGDGLFVTIEPA---------DVSAWPAGSVT--010 ASAQASVSNVN----GNSATT-----706 EA---preliminary B0542 549 134 167

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qa	:  : :: :	C; Access:	;
oy Oy	978 NPNPGTTLSESFENGIPASWKTIDADGDGHGWKPG-NAPGIAGYNSNGCVYSESFGL 1033 2466 GLNAGAVLTVTI-NSVAXS-ATVQADGSWSVGIPAANVSAWPAGPLITVEVDGOSSAN 2520	iller, L Nature 40 A;Title:	iller, L.; Grotbeck, B. 2.; Davis, N.W.; Lim, A.; Dimalanta, E.; Fotamousis, K.; Apodaca, A;Ttle: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
Qy Db	1034 GGIGVLTPDNYLITPALDLPNGGKLIFWVCAODANYASEHYAVYASSTGNDASNFTN 1090 1	A; Access: A; Access: A; Molecul	A;Accession: B8547 A;Accession: B5547 A;Status: preliminary A;Molecule type: DNA
Qy Db	1091 ALLEETITAKGVRSPKAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDBYEI 1150 	A, Kestum A, Eross-1 A, Experin C, Genetic A, Genetic	A. SEZIGUES: 1-3150 C.SUC. A) CTOSS-Teferences: GB:AE005174; NID:G12513368; PIDN:AAG54838.1; GSPDB:GN00145; UWGP:Z06 A) Experimental source: strain 0157:H7, substrain EDL933 C;Gentics: 20615
oy Oy	1151 KANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSG 1193 	Query Match Best Local S Matches 363	
<b>상</b> 名	1194 QLDWLTAHGGSNVVSSFSWNGMALNPDNYLLISKDVTGATKVKYYYA 1239 2670 QTVTVTLNGATYTGTVQADGSWSVSVPTSALGALNASNYTVSATVNDXAGNPGSASHNLA 2729	\dot \( \frac{1}{2} \)	163 TMRGVRIAALTINPVQYDVVANQLKVRNNIEIEVSFQADEVATQRLYDASFS 215
ζς Db	1240 VNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARF 1281 	8 7	1 Д
Qy 25	CSD	gg & ;	
ço Qo	1320INYILLDDIQFTMGGSPTPTDYTYTYYRDGTKIKEGLTETT 1360   2834 APVISINTIAGDDVINATEKGSDLALSGTSDQAGTAIIII		SALQEI AVDGDY
QV	1361 FEEDGV-ATGNHEYCVEVKYIAGVSPKKCVDVTVNSTQENPONLTAEQAPNSM 1413 2894 VPASAVSALGEATYSVTASVTINAQGNSSTASHNVQVNTALPGITINDV	g & 6	DANLPGLKVDTVAGDDVVNIIBHGQAL LIAGADYSWNSQVGQPTIKYGWQYYXNQEHG
ro qa	1414 DAILKWNAPASKRAEVLNEDFENGIPASWKTIDADGDGNNWTTTPPPGGSSF 1465 2944 DDIINASEAGSAQTISGQVTGAAAGSTVTVELGGKTYTATVQADLSMNVSPAADWQA 3001		YTAHGSETAMADPLLTTSQLKALTNKDKYFLAIGNCCITAQFDYQPC
Qy	1466 AGHNSAICVSSASHINFEGPQNPDNYLVTPELSLPGGGTLTFWVCAQDANYASEHYA 1522 3002 LG-NGELTV-NASVTNAVGNTGSGTRDITIDASLPGLRVDTVAGDDVVNIIEHAQAQV 3057		SISAGNEVSVIHEVTVDLSADDVINAAEKG AYAXIGSSPNSYWGEDYYMSVGANAVEGVQPTFEGTSWGSYDATFLEDSALTH COGNIT TO THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSACTION OF THE TRANSA
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Sy q	1563 GTWYQXTVQLPAGTKYVAFRHFGCTDFFWINLDDVVITSGN 1603 		TYTLPASLPON
yo da	1604 ARSYTYTIYRNNTOIASGVIETTYRDPDLATGRYTYGVKVVYRNGESAIETATLNIT 1660 3178 KTYTTTVAANGSWSTTVPAADLAALRDGDASAQVRVTNVNGNSAIATHEYSVD 3230		
Qy Dp	1661 SLADVTAQKPYTLTVVGKTITVTCQGBAMIYDMNGRRLAAGBNTVVYTAQGGHYAVMVVV 1720 		
δ	1721 DG 1722	2 2 2 2	
qa	3286 bg 3287		7.34
RESULT	7	λŏ	

1754 ---EAGVEQTISGOVTGAAAGDTVT-----VTLGGATYTATVQANLSWS------VDVPA 1799 335 AVDGDYFPEMYTFRMSASSPEELTNIID--KVLMYEKA------TMPDKSYLEK 380 275 IDBAEVGTINASIKAFIHKKYNDGLAASAAPVFLALVGDTDVISGEKGKKTKKVTDLYYS 334 2143 VAGDDVINATEHAQAQIISGSATGATGSTVTVTIGTNTFTTVLDASGNWSVGVPASVVS 2202 2203 ALANGTVIINASVIDAGGNSGSATHQVIVNTGLPTITFNAISGDN-----ILNADEKGQP 2257 654 ----TGOGEVVIPGGVYDYCITNPEPASGKWWIAGDGGNQPARYDDFTFEAGKKYTFT 865 163 TWRGVRIAAL----TINPVQYDVVANQLKVRNNIEIEVSFQGA--DEVATQRLYDASFS 216 PYFETAYKQLFNRDVY-TDHGDLYNTPVRMLVVAGAKFKEALKPWLTWKAQKGFYLDVHY 381 VILIAGADYSWNSQVGQPTIKYGWQYYYNQEHGYTDVYNYLKAPYTGCYSHLNTGVSFAN 441 YTAHGSETAWADPLLTTSQLKALTNKDKYFLAIGNCCITAQFDYVQPCFGEVITRVKEKG 1800 SALQELGNGELTISASVTNS---------GNGTREIT----1957 AALTLSGSTSGVEAGGTVTVTFGGKTYSATVAANGSW-----STSVPAADMAALRDGD Gaps 501 AYAYIGSSPN-----SYWGEDYYWSYGANAVFGYQPTFEGTSWGSYDATFLED--549 ----SYNTVNSIMWAGNLAATHAGNIGNITHIGAHYYWEAYHVLGDGSVMPYRAMPKTN 604 TYTLPASLPQNQASYSIQASAGSYVAISKDG----VLYGTGVANASGVATVSM----TK 655 QITENGNYDV------VITRSNY-LPVIKQIQVGEPSPYQPVSNLTATTQGQKVTLKW 2258 LTISGGŚTGLATGAQVTVTLNGHNYSATTDASGNWTLTVPVSDLAALGQANYTVSASATS ---TFGSVIPATGPLFTGTASSNLYSA-----NFEYLVPANADPVVTTQNIIV---------CNDVRANEAKVVLAADNVWGDNTGYQFLLDADHN------PSAKKAEGSREVKRIGDGLFVTIEPA------Y Match 3.4%; Score 315; DB 2; Length 5188; Local Similarity 19.5%; Pred. No. 3e-08; Conservative 228; Mismatches 700; Indels 570; 2010 ASAQASVSNVN----GNSATT-----706 EA----ò 셤 ò

RESULT 7 B85547 Probable RTX family exoprotein [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

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-VAGDDIINAAEAGADQTIS 2361  KIKEGLTATTEEDGVAAGNHEYCVEV 923  III	LITEWYCAQDANYASEHYAVYASSIGNDASNETN 1090	YEDRAGNSDDASRIVIVSISA 2834   YRDGTKIKEGLITETTF 1361
AAGNTASSQANLLVDSGLPDVTINTVAGMRRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKE	GGIGULTPDNYLITPALDLPNGGKLTFWVC	TILDASSINTILIDII
2318 866 2362 924 2416 978	1034 2521 1091 2574 1151 2670 1244 2723	1320 2835 1362 2895 1415 2945 1467 3003 3003 1524 3119 1605 3232 1722 1722

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AFP450

probable peptidoglycan bound protein (LPXTG motif) lin0141 [imported] - Listeria innocue (c)Species: Listeria innocue (c)Species: Listeria innocue (c)Date: 27-Nov-2001 #text_change 27-Nov-2001 (c)Date: 27-Nov-2001 #text_change 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-Nov-2001 (c)Date: 27-No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 MPHQPSMSKSDDPEKVPFVYNAAAYARKGFVGQELTQVEMLGTMRGVRIAALTINPVQYD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 IT---SVTVPNKETG------YNKATYGTLSYELDPATEKLTLNFSVQVDAAKYYGPTD 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 VVANQLKVRNNIEIEVSFQGADEVATQRLYDASFSPYFETAYKQLFNRDVYTDHGDLYNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atch 3.4%; Score 313; DB 2; Length 1993; cal Similarity 20.3%; Pred. No. 8.5e-09; 434; Conservative 208; Mismatches 702; Indels 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 YTFRMSASSPEELTNIIDKVLMYEKATMPDKSY----LEKVLL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 GNESVSYEI-----QNELSSDKKKAKLKITTPKNE----EVKILFIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|: |||: |:||: |
7 LRRPLLLVMAALLIIG-----QLNL-----SSFRVF----
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Matches 434;
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1444 1418 1474 1513 1569	OY 1580 AFRHEGCIDERWINLDDVVITSGNAPSYTYTIYRNNTQI-ASGVTETTYRDPDL 1632  DD 1628 AVNAHNSTVYGETWEAKDNFDSARNKDGETVAFADVEVGRVVDTVAGTYSITYK 1683  OY 1633 ATGFYTYGVKVVYDNGESAIETATLNITSLADVTAGKPYTLTVVGKTI 1680  DD 1684 YDGF-SKTIKVTVKNPQTAITAHDSVVYTGDNWSAKDNFDSAID-KAGKPVAYRDI 1737  OY 1681 TVTCQGEAMIXDNNGRRLAAGRNTVVYTAQGGHYAVMVVV 1720  DD 1738 TVEEDPTVDLNTPGTYSVTYKYQGISKVVQITV 1770	RESULT 9 A33412 hypotherical protein PA1874 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Accession: A83412 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hiokey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Nature 406, 999-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunist A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Recession: A33412 A;Recession: A33412 A;Realduse: 1-2468 (STO) A;Coss-references: GB:AE004613; GB:AE004091; NID:g9947856; PIDN:AAG05263.1; GSE A;Experimental source: strain PAO1	A/Gene: PA1874
OY 549 SY-NTVNSIMMAGNLAATHAGNIGNITHIGAHYYWEAYHVLGDGSSV 593	OY 708 PSAKKAEGSREVKRIGDGLFVTIEFANDVRANEAKVVLAADNVWGDNTGYQFLLDA 763  DD 732 GTTVKPSSIKLTDQDGKEVDFTVEAKTAKNGDKVXVIKTKDITVGEFVGYFSKKQYLNIS 791  OY 764 DHNTFGSVIPATGP-LFTGTASSNLYSANFE 793  DD 792 XNTTFDMTLSKSIHTDIQELLAWGGSNVISALGANVFLDNGLDVNQNGRDAERLLSTNTS 851  OY 794 XLVPANADPVVTTQNIIVTGQGEVVIPGGVXDXCITN 830  DD 852 ILSVPRQDTVAVETFLNVAGEGIKAGXVEGDDSTVGYFTPGTDADYMVKITNTSSGSASS 911	QY   B31PEPASGKOWIAGDGGNOPARYDDFTFEAGKKYTFTWRRAGWGDGTD   B76	1062 VCAQDANYASEHYAYYASSTGNDASNFTNALLEETITAKGVRSFKAIRGRIGGTW 1166 VKDIDPAQPDAQHINAGYISYVPETD

im, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
'; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
' M.V.
1, 2000 enome sequence of Paeudomonas aeruginosa PA01, an opportunistic patho A82950; MUID:20437337; PMID:10984043 GB:AE004613; GB:AE004091; NID:g9947856; PIDN:AAG05263.1; GSPDB:GN001 ce: strain PA01 HINFEGPONPDNYLVTPELSLPGGG---TLTFWVCAQDANYASEHYAVYASSTGN 1530 |: |: : -----NAHDSTI 1488 WNAPASKRAEVINEDFENGIPASWKTIDADGDGNNWTTTPPPGGSSFAGHNSAIC 1473 TINTANTAQAGTYPIT----YTYGGVSKTITVTVKENKKGINAHNATIYVGDSWT 1568 -----VA 1512 ANALLEE----VLTAKTVVTAPEAIRGTRAQGTWY------QKTVQLPAGTKYV 1579 | | : :: | | | | | : : | | | | DNAVDKDGNPVBFSKVTVTETPNVNTNKA-GTYQLKYTFDGASKTVTLTVKNIQT 1627 GCTDFF---W---INLDDVVITSGNAPSYTYTIYRNNTQI-ASGVTETTYRDPDL 1632 SKIIKVIVKNPQTAITAHDSVVYTGDNWSAKDNFDSAID-KAGKP----VAYRDI 1737 ----TATLNITSLADVTAOKPYTLTVVGKTI 1680 74; SSYDATFLEDSYNTVNSIMMAGNLAATHAGN-------IGNITHIGAH 579 XHVLGDGSVMPYRAMPKTNTYTLPASLPQNQASYSIQASAGSYVAI--SKDGVLY 637 695 .n PA1874 [imported] - Pseudomonas aeruginosa (strain PAO1) onas aeruginosa #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 VASGVATVSMTKQITENGNYDVVIT--RSNYLPVIKQIQVGEPSPYQPVSNLTAT Indels 535; Gaps 3.3%; Score 300.5; DB 2; Length 2468; rity 20.5%; Pred. No. 5.9e-08; nservative 140; Mismatches 505; Indels 535; GEAMIYDMNGRRLAAGRNTVVYTAQGGHXAVMVVV 1720 -EDPTVDLM----TPGTYSVTYKYQGISKVVQITV 1770 WSA-----ADNFDSA-----ADRDGNE-TYGVXVVYPNGESAIE-----<STO>

----- NGIPASWKTIDADGDGHGW-- 1009 -----KPGNAPGIAGYNSNGCVYS 1028 1084 ASNFTNALLEETI -----OKTVDLPA 1125 1184 1221 NYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGAR 1280 1281 FGLSTEANG-----AKPQSVWIERTVDLPAGTKXVAFRHYNCSDLNYILLDDIQFTMG 1333 1334 GSPTPTDYTYTVY-----RDGTKI----KEGLTETTFEEDG------VATGNHEYCVE 1376 : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 1377 VKYTAGVSPKKCVDVTVNSTQFNPVQNLTAEQAPNSMDAILKWNAPASKRAEVLNEDFEN 1436 1458 ---SSFSW-----NGMALNPD 1220 1047 TPLADG-----TVVNATATDPAGN-TGGGGSTTVDAI----APATPTVNLSNGSSLS 1093 1213 PGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALLEEVLTAKTVVTAPEAI--- 1556 1611 895 733 363 TV-GVDTDGDGQPDTTVVVGRGGSFEVPL-NPPLTNGETVTVIVTDPAGNSSTPVTABAP 420 896 TKIKEGLTATTFEEDGVAAGNHEYCVEVKYTAGVSPKVCKDVTVEGSNEFAPV----- 949 ----SP--ATSITVDGVAPNAPVVEPSNGS 516 517 ELSGTAEPĠSSŸTLTDGNGNPIGQTTADANGNWSFTPSTPLPDGTVVNVVARDAAGNSSP 576 693 734 ASGNTSAGSSVTVDSVAPATPVINPSNGTTLSGTAEPGSSVTLTDGNGNPIGQVTAD--- 790 937 938 VTL-TDGNGNPIGOVTADGSGNW----SFTPGTPLA----NGTVVNATASDPTGNTSA 986 1499 TTQNIIVTGQGE-----VVIPGGVYDYCITNPEPASGK---MWIAGDGGNQ----PARYD ---TFEAGKKYTFTMRRAGMGDGTDM-EVEDDSPASYTYTVYRDG 421 DFPDAPQVNASNGSVLSGTAEAGVIIVIT-----DGNGNPIGQTSADANGNWSFT---PG 634 TPSTPLPNGTVVNATATDPSGNASSPASVTVDAVAPATPVVNPSNGTTLSGTAEPGATVT BSFGLGG-IGVLTPD---NYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGND 1126 GTKYVAFRHFQSTDMFYIDLDBVEIKANGKRADFTETFBS-STHGBAPABWTTIDADGDG | : ; | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 835 TPTVNLSNGSSLSGTAEPGSTVILTDGNGNPIAEVTADGSGNWTYTPSTPIANGTVNN----VVAQDAAGNSSPGASVTVDSQAPA--APVVNPSNGT------TLSGTAEPGAT ----TVVNATATD GTAEPGSTVILTDGNGNPIAEVTADGSGNWTYTPSTPIANGTVNNVAQDASGNSSPPAT 1154 VIVDSSAPPAPVINPSNGVVISGTAEAGATVTLTDAGGNPIGQVTADGSGNWSFTPGTPL 214 ANGTVIV-----TYDDPJGNTGPQAA-----TTVDAVAPPAAVIDP ----PP-----GGSSFAGHNSAICVSSASHINFEGPQNPDNYLVTPELSL 1557 -RGTRAQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVVJTSGNAPSYTYTI------VILTDGNGNPIGETTADGS ----KWDAPNGTPNPN---LTDGNGNPIGQVTADGSGNWSFTPTTPLPNG----GIPASWKT-IDADGDGN-------NWTTTP--- PNPNPNPGTTLSESFE-OGWLCLSSGOLDWLTAHGGSNVV-----

984 NGGQFQVTVNGNSTSPITVTSVTVADTSITLVLNQIIGQGQLVTIT-----YTPNSNGEN 1038

DVYNYLKAPYTGCYSHLNTGVSFANYTAHGSETAW------

----KVLLIAGADYS----WNSQVGQ---PTIKYGMQYYYNQEHGYT

ISNLYLADATNTSFWVPDFTNSVQSAGSTSTAPTSLLGSVIS-NLITIPFNQTLNVNQIP 983

----TFRMSASSPEELTNIIDKVLMYEKATMPDKSYLE---

341 FPEMY-----

380

867

DSANPPSNSQFIIKTSDG--NTTTPTNVSLAQNTIILTLTNSVNASQIVEVSYSLSGTNL

281 GTTNASIKAFIHKKYNDGLAASAAPVFLALVGDTDVISGEKGKKTKKVTDLYYSAVDGDY

826 ALTSQGDILLAWSSDTPPITPISVLA-----

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769

KVRNNIEIEV-----SPQGADEVATQRLYDASFSPYFETAYKQLFNRD 229

---VYNAAAYARKGFVGQELTQVEMLGTMRGVRIAALT-INP-----VQYDVVAN---QL

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230 VYTDHGDLY-----NTPVRMLVVAGAKFKEALKFWLTWKAQKGFYLDVHYTDEAEV 280

770 KAANQKTITAFTVSNGTAPTAWGLINRTFAGVINVQTQPVLSNLTSDFAQDTSPAL-

340 924

----EGDYLYLVFADNLKN

1039

Dypothetical protein slr0408 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Species: CCC 6803
C;Date: 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S76412
E;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Matanabe, A.; Yamada, M.; Yasudā DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis A. Reference number: S74322; MUID:97061201; PMID:8905231
A. Accession: S76412
A. Status: preliminary
A. Molecule type: DNA
A. Molecule: 1-4199 < KAN>
A. Residues: 1-4199 < KAN>
A. Molecule: BRHEL:D90915; GB:AB001339; NID:g1653604; PIDN:BAA18541.1; PID:g16536; A. Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Superfamily: Synechocystis hypothetical protein slr0408 ---PQGSTTVDAVAPNTPVVNPSN 1334 533 İLGİLGARIAĞFPTWTQTFAASSSQNNQTGLEANNTASVDGFLLTINLAQFLEPNLSLNP 592 VELT-KVETKGGTFASVSIPGAFPTGEVGSPEVPAVRKL-IAVPVGATPVVRVKSFTEQV 109 VKYSGNOLGNFTSSPVALQSPDTLIYTYNPTSGTGNDYTQNNQQITIAFNGPLDPDILPT 709 Gaps LLLLIAASLLGVGLY-----AQSAKIKLDAPTTRTT----CTNNSFKQFDASFSFNE 955; DB 2; Length 4199; 1362 1661 -SLADVIAQKPYTLTVVGKIITVTCQGEAMIYDMNGRRLAAGRNT 1704 Indels ---DGNGNPI---GOTT Query Match
3.2%; Score 295.5; DB 2;
Best Local Similarity 18.1%; Pred. No. 2.6e-07;
Matches 438; Conservative 281; Mismatches 752; --XSTNQYGSEKLMP------HQPSMSKSD-1285 GNWSFTPGTPLANGTVVNAVAQDPAGNTG--1335 GNLLNGTAEP-----GSTVTLT-22 110 10 유 ò g 셤 à à ద ò g

us-08-353-485-10.rpr

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hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Species: Synechocystis sp.
C;Acraety: PCC 6803
C;Accession: S76109
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A;Accession: S76109
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3029 «KRN»
A;Residues: 1-3029 «KRN»
A;Cross-references: EMBL:D63999; GB:AB001339; NID:g1001396; PIDN:BAA10087.1; PID:d101073
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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                                                                                                                                                                                                                                                                                                                                                          ---DGTKIKEGLTETTFEEDG--
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                                                                                          1238 YAVNDGFPGDHYAVMISKTGTNAG----DFTVVFEETPNGINKGGARFG---LSTE-
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2079 -DLDGDGHQDLAISA----LGVNGSAGAV--YALSGSKFTPSSSLQALNBAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VATGNHEYCV------EVKYTAGVSPKKCVDVTVNSTQ-
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2701 NGDGYDDVLLWGDNGNQVAWGNSTGV 2726
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3.1%; Score 280.5; DB 2; Length 3029;

Query Match

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Gaps 85;	TGEVG 79 -DLAG 1182	KVPF 138   -VDD 1210	IEIE 195   : IPVA 1261	VVAG 249 	GLAASA 303     :   STAEAD 1332	INII 361 : SATA 1385	YNYL 421   :   1812	KYFL 471 : : -FNI 1455	-NSY 512  :  INAI 1502	AGNI 570   IANF 1562	612 ANDF 1612		LFVT 729    VT 1695	GTAS 784   : ATVT 1743	GGVY 824 : NAIA 1799	GD 873 : ANFE 1859		DDIL 1915 PNPN 976
Indels 613;	TKGGTFASVSIPGAFPT  -  - ATEEVVATVS	EKLMPHQPSMSKSDDPE	FVGQELTQVEMLGTMRGVRIAALTINPVQYDVVANQLKVRNNIEIE  EAGSPVAVSGTTTGVEDGOVVTVTIDGNTYTATVTGNAMTFNIPVA	DHGDLYNTPVRMLVVAG	TLVFN	FPEMYTFRMSASSPEEL   ::   ::     .xELSVTATNPTGN	.KYGMQYYYNQEHGYTDVYNYL  :   : 7TINAIAVDDIINAV	NYTAHGSETAWADPLLTTSQLKALTNKDKYFL      :    GNTYTATVTGNAWTPNI	TPATRNITVDTTAPTVT	n-tvnsimmagnlaath 	HVLGDGSVMPYRAMPKTNTYTLPASLP	ATVSMTKQITENGNYDVV  :  : : : :: YTLDYTGTLLADGDYELS	SAKKAEGSREVKRIGDG  : ?T	INTFGSVIPATGPLFTGTAS     :     :   :   :  DGQVVTVTIDGNTYTATVT	VPANADPVVTTQNIIVTGQGBVVIPGGYY	SAGKKYTFTMRRAGMGD- 	ATTFEEDGVAAGNH	-DIVARAVIIDSISDDIGAQANDRIINDDIL LTGSSVQQKVTLKWDAPNGTDNPNPN : : :
Pred. No. 1.1e-06; ; Mismatches 705;	QFDASFSFNEVELTKVETKGGTFASVS	RVKSFTEQVYSLNQYGS ; ; TINAIA	LGTMRGVRIAALTI       :: :    SGTTTGVEDGOVVTVTI	PYFETAYKQLFNRDVYT	KGFYLDVHYTDEAEVGTTNASIKAFIH	CKTKKVIDLYYSAVDGDY	IAGADYSWNSQVGQPTIKY	NYTAHGSETAK 	GEVITRVKEKGAYAYIGSSP-   : ::  -EVVATVSDLAGNPA	SGTSMGSYDATFLE-DSY 	SVMPYRAMPKTNTYTLP? :	SKDGVLYGTGVANASGVA	QPVSNLTATTQGQKVTLKWEAPS. 	NVWGDNTGYQFLLDADF 	ANFEYLVPANADPVVT	DGGNQPARYDDFTFEA 	GTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEEDGVAAGN-	1 Z
18.9%; vative 219	OSAKIKLDAPITRITCINNSFKQPDASFSFNEVELTKVETKGGTFASVSIPGAFPTGEVG 	SPEVPAVKKLIAVPVGAT-PVVRVKSFTEQVYSLNQYGSEKLMPHQPSMSKSDDPEKVPF 	ARKG	ADEV       TEEV	AKFKEALKPWLTWKACKGFYLDVHYTDEAEVGTTNASIKAFIHKKYND-	APVELALVGDT DVISGEKGKKTKKVTDLYYSAVDGDYFPEMYTFRMSASSPEELTNII	DKVIMYEKATMPDKSYLEKVLLIAGADYSWNSQVGQPTIKYGMQYYYNQEHGYTDVYNYL   : : :     :     :   TQTIVVDTTANAIAVDIINAV	KAPYIGCYSHLNIGVSFANYTAHGSETAWA 	CCITAQEDYVQPCF    ::: IANFEATE	WGEDYYWSVGANAVFGVQPTFEGTSMGSYDATFLE-DSYN-TVNSIMMAGNLAATHAGNI 	GNITHIGAHYYWEAYHVLGDGSVMPYRAMPKTNTYTLPASLP :	ONQASYSIQASAGSYVAISKDGVLYGTGVANASGVATVSMTKQITENGNYDVVITRS	NYLPVIKQIQVGEPSPYQPVSNLTATTQGQKVTLKWBAPSAKKABGSRBVKRIGDGLPVT 	IEPANDVRANEAKVVLAADNVWGDNTGYQFLLDADHNTFGSVIPA- 	ANFEYL      NIPVADIANFE	DYCITNPEPASGKWMIAGDGGNQPARYDDFTFEAGKKYTFTMRRAGMGD	GTDMEVEDDSPAS	ATEEVVATVSDLAGNFATFATKNITVDTVAFAVILD EVKYTAGVSPKVCKDVTVEGSNEFAPVQNLTGSSVGQKV- 
Simi 59;	20 OSAKI   1135 QVVTV	80 SPEVE       1183 NPATI	139 VYNAAAY.       1211 IINAV			304 APVFI :   : 1333 STVV	362 DKVLA : : : 1386 TQTIV	422 KAPY7 :  1413 EAGS1	472 AIGN( : : 1456 PVAD	513 WGED	571 GNITHIGA:	: =	670 NYLP	730 IEPA. 1696 INAL	785 SNLXS-   :: 1744 GNAWTF	825 DYCI		1860 ATEE 922 EVKY
Best Local Matches 3	35 ₹ 1	2y ob 1	2y Ob			2y 3b	2y Ob	Qy Db	Qy Db	Qy Db				Qy Db	 QZ QI	Oy Db		g XX

1969	1033	2018	1084	20.12	1128	2132	1173	2187	1233	2228	1293	2269	1350	2319	1409	2370	1455	2430	1515	2454	1574	2496	1627	2543	1670	2603		
VFNGTAEADSTVVVSLDGIEIGTVTANGAGEWTLDYTGTLLADGDYELSVTATN	PNPNPGTTLSESFENGIPASWKTIDADGDGHGWKPGNAPGIAGYNSNGCVYSESFGL	PIGN-SATATQTIVVDTTAPTVTINALAVDDIINAVEAGSPVAVSGTTTG	GGIGVLFPDNYLITPALDLFNGGKLTFWVCAQD-ANYASEHYAVYASSTGND	VEDGQVVTVTIDGNTYTATVTGNAWTFNIPVADIANFEATEEVVATVSDLAGNP	ASNFTNAL-LEETITAKGVRSPKAIRGRIQGTWRQKTVDLPA-GTK	ATPATRNITVDTTAPTVTINAIAVDDIINAVEAGSPVAVSGTTTGVEDGQVVTVTIDGNT	YVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETFESSTHGBAPA	YTATVTGNAWTFNIPVADIANFEATEEVVATVSDLAGNPATPATRNITVDTVAPA	EWITIDADGDGQGWLCLSSGQLDWLTAHGGSNVVSSFSWNGMALNPDNYLISKDVTGATK	vridsisddigàqandfitndDīlvfngtaeadstvvvsld	4 VKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLSTBANGAKPQ	:     :   :   :   :   :   :   :   :   :	SVWIERT VDLPAGIKYVAFRHYNCSDLNYILLDD-IQFTWGGSPTPTDYTYTVYRDGT	SATATOTIVVDTTAPTVTINAIAVDDIINAVBAGSPVAVSGTTTGVEDGO	KIKEGLTETTFEEDGVATGN-HEYCVEVKYTAGVSPKKCVDVTVNSTQFNPVQNLTAEQA			PATRNITVDITAPIVTINAIAVDDIINAVEAGSPVAVSGTTIGVEDGQVVTVTIDGNIYT	6 TIPPPGGSSFAGHNSALCVSSASHINFEGPQNPDNYLVTPELSLPGGGTLTFWVCAQDAN	ATVTGNAWTFNI PVADIANFEATE	YASEHYAVYASSTGNDASNFA-NALLEEVLTAKTVVTAPEAIRGTRAGGTWYQKTVQLPA	SEVVATVSDLAGNPATPATRNITVDTVAPAVTIDSISDDTGAQ	S GTKYVAFRHFGCTDFFWINLDDVVITSGNAPSYTYTIYRNNTQIASGVTETTY	7ANDFITNDDTLVFNGTAEADSTVVVSLDGIRIGTVTANGAGEWTLDY	8 RDPDLATGEYTYGVKVVYPNGESAIETATLNITSLADVTAQKP	TGTLLADGDYBLSVTATNYTGNSATATQTIVVDTTAPTVTINAIAVDDIINAVEAGSFVA	1YILIVUGKITIVICQGBAMIXDM 1693	4 VSGTTTGVEDGQVVĮVIIDGNIYTATVTGNAWTFNI 2639
1916	977	1970	1034	2019	1085	2073	1129	2133	1174	2188	1234	2229	1294	2270	1351	2320	1.410	2371	1456	2431	1516	2455	1575	2497	1628	2544	1671	2604
Db	οχ	qq	δλ :	DP DP	δy	Db	δy	ΩÞ	δ	qq	λŏ	QC	0y	Db	δλ	Db	ζζ	QQ	δ	Dip	δy	QQ	δλ	qq	Qy	qq	ζ	qq

RESULT 12

ADB180

probable peptidoglycan bound protein (LPXTG motif) lmo0842 [imported] - Listeria monocyt

C;Species: Listeria monocytogenes

C;Date: 27-Nov-2001

C;Accession: AB1180

C;Accession: AB1180

C;Accession: AB1180

C;Accession: AB1180

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C;Accession: A; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,

C;Accession: A;Acstruction and A;Acstruction and A;Action ``
SYATTATGDNYDSTDIYSNTVADYEKVNMVRIKVKTQINAGETQTFKVPLKVDETF--DS 1028
          Astatus: preliminary
Astatus: preliminary
Astatus: DNA
Astatus: DNA
Astatus: 1-2044 (GLA>
Astatus: 1-2044 (GLA>
Astatus: 1-2044 (GLA>
Astatus: GB:NC_003210; PIDN:CAC98920.1; PID:gl6410230; GSPDB:GN00177
C;Genetics: strain EGD-e
A;Genetics: lmo0842
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                                                                                                                                                                                                                                                                                                                                                                                                                               460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLTDOGGKDVNFTVEQETANNGDKVYALKTTDVSVGYVYGYPTKHKYLNISYDTTFDVTL 815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                865 TWRRAGMGDGTD-MEVEDDSPASY---TYTVYRDGTKIKEGLTAT-----TFEEDG 911
                                                                                                                                                                                                                        314
                                                                                                                                                                                                                                                         242
                                                                                                                                                                                                                                                                                           D----VISGEKGKKTKKVTDLYYSAVDGDYFP--EMYTFRMSAS-----SPEELTNI 360
                                                                                                                                                                                                                                                                                                                             302
                                                                                                                                                                                                                                                                                                                                                               412
                                                                                                                                                                                                                                                                                                                                                                                             ----VASADQAIRAEGNKVVGYADQNHVKTMFRTWYNDQRL 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N----EAKVVLAADNVWGDNTGYQFLLDADHNTFGSVIPATGP-LFT-----GTA 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     578 EVQYKTNINDAFRIFDGALIKNNNQMYRLDAKAVGLEEGEYFTEVKANVGDFAPGYQSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---FLALVGDT
                                                                                                                                                                                                                                                     ---KKVNFTLPDGMRFVSLPVPSNYQAGTNEDTGVLSYLGAS
                                                                                                                                                                                                                                                                                                                           243 DPLGIAITSVEVPNKETAYSQAFFGTVSYELSPGTEKASFKFSVRVDAAKYYGPTDLADP
                                                                                                                                                                                                                                                                                                                                                               IDKVLMYEKATMPDKSYLEKVLLIAGADYS----WNSQVG---QPTIKYGMQYYYNQEH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 SEVLASTDITDSYNYTKS-----YSVVNGSNSLDSRGAAVYIAKNIEVTLYYP-EGMEFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    461 KALTNKDKYFLAIGNCCITAQFDYVQPCFGEVITRVKEKGAYAYIGSSPNSYWGEDYYWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407 NVVNNAGTVLKENSNVTIT---NY--PSENKVVINNKHLNNSA----TSNSIYGVKYKVP
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                                                                                                                                                                                      Gaps
                                                                                                                                                                                      591;
                                                                                                                                                    Length 2044;
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                                                                                                                                                                                     Indels
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                                                                                                                                                   3.0%; Score 276.5; DB 2;
larity 19.8%; Pred. No. 9.4e-07;
Conservative 211; Mismatches 688;
                                                                                                                                                                                                                       272 VHYTDEAEVGTINASIKAFIHKKYN----DGLAASAAPV-
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es 368; Conserv
Accession: AB1180
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| 966<br>ML 1074                                        | XN 1021<br>:<br>TD 1125                                                             |                               | IFQ 1136<br>:<br>:XN 1201                                      | CL 1190<br>VA 1260                                                                             | PG 1246<br>VA 1320                                   | 1279<br>DQ 1373                                       | IGG 1334<br> -<br>IGD 1433                                                                                | KCV 1389<br>:<br>I 1485                             | FEN 1436<br> <br>                                   | IYL 1492<br>HA 1598                                          | : 1658<br>: 1658                           | )FF 1590<br>CTI 1706                                             | 3FY 1637<br>Jee 1763                                                | 1674<br>GD 1820                               | , 1731<br>, 1858                                              |
|-------------------------------------------------------|-------------------------------------------------------------------------------------|-------------------------------|----------------------------------------------------------------|------------------------------------------------------------------------------------------------|------------------------------------------------------|-------------------------------------------------------|-----------------------------------------------------------------------------------------------------------|-----------------------------------------------------|-----------------------------------------------------|--------------------------------------------------------------|--------------------------------------------|------------------------------------------------------------------|---------------------------------------------------------------------|-----------------------------------------------|---------------------------------------------------------------|
| GQKVTLKWDA-<br>  ::: <br>GAELVIGEVAC                  | ADGDGHGWKPGNAPGIAGYN :                                                              | DANYASEHYAV<br>  ;<br>AGYQYTL | GTKYVAFRHFQ<br> -:- <br> -SQYTNAGYYAYN                         | -PAEWTTIDADGDGQGWLCL<br> ::  : <br>EPSFFKNIKATTNGYKWTVA                                        | -ATKVKYYYAVNDGFPG<br>::     <br>KSSKAPVYVTGTDGTVA    | TVVFEETPNGINKGGA<br>      : :<br> TAAFEEVKDGVNSSAEDRI | YILLDDIQFT<br>:<br>:<br>:<br>:<br>:<br>:<br>:<br>:<br>:<br>:<br>:<br>:<br>:<br>:<br>:<br>:<br>:<br>:<br>: | -BVKYT-AGVSPKKCV<br>            :<br>YPVTYTYNGVSKKI | ASKRAEVLNED:<br>:   ::<br>;VAFADITVTG               | HINFEGPONPD:                                                 | ASEHYAVYASS: :  :  !AHDSAIYIGD             | LPAGTKYVAFRHFGCTDFF<br>     : :   :<br>-KVGTYPVTYTYDGVSKTI       | PDLATGFY<br> :  <br>CDINVSENPAVDLE                                  | NEDNFDNATDKO                                  | /DGKSYVEKLA<br>                                               |
| EYCUEVKYTAGUSPKUCKDVTVEGSNEFAPUQNLIGSSUGQKVTLKWDA<br> | KTID                                                                                | GGKL                          | SSTGNDASNPTNALLEETITAKGVRSPKAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQ<br> | EDTI                                                                                           | 1 [6]                                                | TNAGDFTVVPEETPNGINKGGA<br>                            | registeangakposvw-iertvdlpagtkyvafrhyncsdinyillddigftmgg<br>                                              | AGS                                                 | VONLTAEGAPNSMDAILKWNAPASKRAEVLNEDFEN<br>            | GIPASWKIIDADGDGNNWTTTPPEGGSSFAGHNSALCVSSASHINFEGPQNPDNYL<br> | VTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGN<br> | DASNFANALLEBVLTAKTVVTAPBAIRGTRAQGTWYQKTVQLPAGTKYVAFRHFGCTDFF<br> | WINLDDVVITSGNAPSYTYTIYRNNTQIASGVTETTYRDPDLATGFY   :                 | AIETATLNITSLADVTAQKPYTLT                      | -VVGKTITVTCQGEAMIYDMNGRRLAAGRNTVVYTAQGGHYAVWVVDGKSYVEKLAV<br> |
| CKDVTVEGSNE.                                          | PNGTPNPNPNPNPNPGTTLSESFENGIPASW<br>  : : :  <br>FNDKDVNGSYEKXKGDEPLANETV-ELYKMYSTS- | NYLITPALDLP                   | RSPKAIRGRIQ<br>  :<br>NSDVPYSGADR                              | STDMFYIDLDEVEIKANGKRADFTETFESSTHGEA-<br>  ::   ::   : <br>PTQDLKVNLDEKQVQM-GRSLEITLFKVASTTGQAA | SSGQLDWLTAHGGSNVVSSFSWNGMALNPDNYLIS-KDVTG-<br>:<br>: | EATDLTKAQAL                                           | RTVDLPAGTKY<br> : :  <br>:YTITKDSKTVS                                                                     | SPTPTDYTYTVYRDGTKIKEGLIETTFEEDGVALGNHEYCV<br>:      |                                                     | PPGGSSFAGHN:  :  :<br>7LENKEGISAHD                           | <br>:<br>VTYKYGKVSKKI                      | TAKTVVTAPEAIRGTRAQGTW :    ::     -GNSVAFADIEVKGTVDTD            | RNNTQI<br>:: <br>GDNWNAKDNFDS                                       | TYGV-KVVYPNGESAIETATLMITSLADVTAQKPYTLT<br>    | RLAAGRNTVVYT<br>  :<br> VDS                                   |
| VKYTAGVSPKV<br>  :<br>NPYYRVI                         | PNPNPNPGTTL<br> <br>                                                                | GLGGIGVLTPD<br>               | LLEETITAKGV<br>:                                               | IIKANGKRADFT<br>::  :  <br>VQM-GRSLEIT                                                         | SSNVVSSFSWNG                                         | GTNAGDF<br>    <br>GATDFSLEYK                         | NGAKPQSVW-IE<br> :  : :<br>NGSNQGGVYPLI                                                                   | NDGTKIKEGLTE<br>                                    | NLTAEQAPNS-<br>      : <br> XLTAVNAHDST             | ADGDGNNWTTT<br>                                              | TPELSLPGGGT<br>  :  <br>KPTVDTTKAGAYEN     | /LTAKTVVTAPE<br> - GNSVAFADI                                     | MAPSYTYTIY<br>   :   <br>MAHDSEIYIC                                 | SSAIETATLNI1<br> - : : : <br>3VSKTINL1        | BEAMIYDMNGRE                                                  |
| VAAGNHEYCVEVKYTAGV<br>                                | PNGTPNPN<br>  :<br> VDKDVNGSYEKD                                                    | SNGCVYSESFGLGGIGVLTPDNY<br>   | SSTGNDASNFTNA<br>:      <br>KNIGKDTS                           | rdmfyidldeve<br>  ::   :<br>rqdlkvnldekq                                                       | SGQLDWLTAHGG<br>:<br> <br> <br>  KVATVQTLADG         | DHYAVMISKT<br>                                        | RFGLSTEAN<br>:  <br>QVNQTQLDAIK                                                                           | SPTPTDYTYTVYF<br>:<br>TWDAEDNF                      | DVTVNSTQENPVQNLTAEQAPNS<br>    <br> VTVKDKLTAVNAHDS | IPASWKTIDA<br> <br> <br> <br>  NQAGTNTITYS                   | VTPI<br> <br> <br>VDLEDVTVTEKP             | DASNFANALLEEV<br>   :   ::<br>AEDNFDSALDKD-                      | WINLDDVVITSGNAPSYTYTIY-<br>  :   :   :    <br>NIQVKD-ILTAVNAHDSEIYI | TYGV-KVVYPNGES<br>     :   <br>TVGVXQVTYSYGG- | -VVGKTITVTCQC<br>:   :        <br>OIPFKDVTVTGO-               |
| 912 VZ                                                | 967                                                                                 | 7 9                           | 1079 SE                                                        | 1137 ST                                                                                        | 1191 St                                              | 1247                                                  | 1280<br>1374 V                                                                                            | 1335 S<br>:<br>1434 T                               | 1390 D                                              | 1437 G<br>1539 T                                             | 1493 V<br> <br> <br> <br>  1599 V          | 1531 D                                                           | 1591 W<br>1707 N                                                    | 1638 T<br> <br> <br>  1764 T                  | 1675 -                                                        |
| oy<br>Ob                                              | \(\delta \)                                                                         | Sy du                         | % qa                                                           | \$ 6<br>6                                                                                      | දුරු ප්                                              | yo da                                                 | QX<br>Dp                                                                                                  | DP GA                                               | S G                                                 | රු අ                                                         | & q                                        | 8 S                                                              | oy<br>Db                                                            | 중 원                                           | රු සි                                                         |

RESULT 13
AF1489
cell wall-associated protein precursor wapA (B. subtilis) homolog lin0454 [imported] - I
C;Speiss: Listeria innocua
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001
C;Accession: AF1489
B;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
B;Glaser, P.; Frangeul, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

| 751 VRGGEVNATRGNFLFHETDFNLEGRGPSINVNRTFNSQDDATGIFGKGWTSTLEEKLVEE 810 660 GNYDDVJTRSNYLPVIKQIQVGEPSPYQPVSNLTATTQGQKVTLKWAAPSAKKA 713                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 952<br>866<br>990<br>917<br>1045 | 1105 TLATESQVSSVTQYD  1010KPGNAPGIAGYNS  1165 FDNTQSAPG  1068 NYASEHYA  1193 GXSVTQRVDVEPET  1110 GRIQGTWRQKTVD  1253 IKKNGDWVRQLTFK |                                                                                          | 1352 IKEGLIGARMEDDYRVEGGEVILLANGIGESCHALTSTEIN (17.1)  1509 TETDERGUNGTLYPDADNALITTLANGISVAKKUDUNUTTAFINONULTA  1407 EQAPNSMDAILKWNAPASKRABVINEDFROIPPASWKTIDADGDGNNWTTTPPP  1558 SGKTQKNIYEYDVDNKITAFTDALNRTIKYEYDAAGNETKAIMPN  1461 GGSSFAGHNSAICVSSASHINFGEPQNPDNYLVTPELSLEGGGTLTFWVCAQDAN  1603 GRVTESTYDSADRMDGIKWNDKLAFKFQYDPNGNQTKVTDBINSIVTDKT  1516 YASEHYAVYASSTGNDASNPANALLEEVLTAKTUTAFBAIRG  1553 YDDANRITKVAERGGDVSYTYKDKPTKDNKGKTDKVGEVAINHGDYTAKTSYTYNDLDRN |
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| 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 4 6 6 6 6                        | 4 8 8 8 8 8 8                                                                                                                        | 5 6 6 6 6 6 6                                                                            | 8 6 8 6 8 6 8                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 Science 294, 849-852, 2001 Science 294, 849-852, 2001 Science 294, 849-852, 2001 Science 294, 849-852, 2001 Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative genomics of Listeria species. A; Reference number: AB1077; MUID:21537279; PMID:11679669 A; Recession: AF1489 A; Status: preliminary A; Status: preliminary A; Status: J-2167 GLA> A; Residues: 1-2167 GLA> A; Residues: 1-2167 GLA> A; Residues: Statin Clip11262 C; Genetics: A; Genetics: Strain Clip11262 C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; | Query Match                      | VGQELTQVEMLGTWRGVRIAALTINPVQYDVVANQLKVRNNIEIEVSF                                                                                     | 309 IGSKLWDSGQNAYTLKLGKWDNSTGNNAAFLKMDTSTLNKATISKATLKVYNIWHM 364 329TDLYYSAVDGDYFPEMYTER | DD 535 GEFEFHDGKGTDFRADFRAQYENAFGAGSTFGLRNLTRYLFRVQAVFPGGESP 588  QY 510 NAYWGEDYYWSVGANAVFGVQP                                                                                                                                                                                                                                                                                                                                                                            |

| 524 NAVEGVOPTEEGTSMGSYDATELEDSYNTVNSIM- 557                                                                                                                                                                                                                                                                                                                                                            | 673 PVIKQIQVGEPSPXQPVSNLTATTQGQKVTLKWEAPSAKKAEGSREVKRIGDGLFVTIEB 732  285 ETIVSGSVGYTSTFPANGTISGTVEVVEPTAGTITETIVSGSVGYTSTFP 334 733 ANDVRANEAKVVLAADNVWGDNTGYQFLLDADHNTFGSVIPATGPLFGTASS 785 | ANGTISCIVEVVEPTACTVIETIVSGSVGYISTFPASGITSGTVEVVEPTACTITETIVS  NLYSANFEYLVPANADPVVITQNIIVTGQGEVVIPGGVYDYCIINPEPASGKMMIAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 903 TATTFEEDGVAAGNHEYCVEVKYTAGVSFKVCKDVTVEGSNERAPVONLTGSSVGQKVTL 962    : | 562TITETIVSGSVĞYTSTFPASGTTSGTVEVVEPTAĞTVTETIVSGSVĞYTŠTFPASGT 618 1079 SSTGNDASNFTNALLEETITAKĞVRSPKAIRGRIQGTWRQKTVÜLPAGTKYVAFRHFQ 1136 1137 STGTVEVVEPTAGTVTETIVSGSVĞYTSTFPASGTTSĞTVEVVEPTAĞT                                                                                                                                                                                                                                                                                                                                                     | OLDWLTAHGGSNVVSSFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMI  :                                                                                                                                                                                                                                                                                                                                                                                                             | 1357 TETTEEDGVATGNHEYCVEVKYTAGVSPKKCVDVTVNSTQFNPVQNLTAEQA 1409                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
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| 8 8 8 8 8                                                                                                                                                                                                                                                                                                                                                                                              | o a o                                                                                                                                                                                         | 868686                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | \$ 6 \$ 6 \$                                                              | 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 3 6 6 6 6 6 7 1                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 8 6 8 6 8 6 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| OY 1559 TRAQGTWYOKTVOLPAGTKYVAFRHFGCTDFFWINLDDVVITSGNAPSYTYTIYRNNT 1616  Db 1713 TRVNDGSKNAYFEFDEFGNINYTAGNGTANYTYDSTÇKYT 1754  QY 1617 QIA-SGVTETTYRDPDLATGFYTYGVKVVYPNGESALETATLN-ITSLADYT 1666  Db 1755 NAAISSASGTQILDENYIYDAASNTTSIDNKQDGRYTYSTDANVQLTKETLPDGT 1809  QY 1667 AOKPYTLTVVGTYTTCGGBANTYDMNGRRIAAGRNIV 1705  DD 1810 V-KAXTYDGFGNRTQVALSGSETKTIDASYNDGNQLVSWNGBALTYDANGRRIAAGRNIV 1705 | Qy 1706 VYTAQGGHYAVMVVVDGKS 1724  Db 1868 -YTWDTGDRLSSITKKGES 1885                                                                                                                            | RESULT 14 T39174 T39174 T39174 hypochetical Serine/threonine repeat containing protein [imported] - fission yeast (Schi hypochetical Serine/threonine repeat containing protein [imported] - fission yeast (Schi C; Species: Schizosaccharomyces pombe C; Date: 03-Dec-1999 #sequence revision 09-Jun-2000 C; Accession: T50375; T39172; T39174; T39366 C; Accession: T50375; T39172; T39173; T39174; T39366 R; Connor, R; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A. Submitted to the EMBL Data Library, February 1998 A; Reference number: Z21832 A; Reference number: Assance T50375 A; Reference number: Assance T50375 A; Reference number: Assance T50375 | N00067; SPDB:SPBC8E4.70c                                                  | A; Accession: 13.0.7<br>A; Residues: 'ME', 179, 'PLV', 183, 'W', 'KL', 556-761, 'HRGSS' <co3><br/>A; Residues: 'ME', 179, 'PLV', 183, 'W', 'KL', 556-761, 'HRGSS' <co3><br/>A; Cross-references: EMBL: AL021815; PIDN: CAA17001.1<br/>A; Note: this is an interim translation for a sequence replaced by GenBank/EMBL<br/>A; Molecule type: DNA<br/>A; Residues: 1-555.'S' <co4><br/>A; Cross-references: EMBL: AL021815; PIDN: CAA17002.1<br/>A; Note: this is an interim translation for a sequence replaced by GenBank/EMBL</co4></co3></co3> | R; Wood, V; Rajandream, M.A.; Barrell, B.G.; Oliver, K.; Harris, D. submitted to the EMBL Data Library, March 1999 A; Reference number: 221848 A; Accession: T39366 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-896, 'G', 988-904, 'I', 906-1283 «WOO> A; Cross-references: EMBL:AL035675; PIDN:CAB38695.1; GSPDB:GN0067; SPDB:SPBC1289.15 A; Genetics: C; Genetics: SPDB:SPBC1289.15; SPDB:SPAC8E4.07C | A; Map position: 2 C; Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase C; Superfamily: yeast glucan 1,4-alpha-glucosidase best Local Similarity 20.5%; Pred. No. 1.9e-06; Best Local Similarity 20.5%; Pred. No. 1.9e-06; Matches 298; Conservative 174; Mismatches 535; Indels 448; Gaps 71;  Qy 414 YTDVXNYLKAPYTGCYSHUNTGVSFANYTAHGSETAWADPLITTSQLKAL 463 Db 70 YTTLITINSQCTGNYSTLITSSQPLHTINTSISKDSQTATPQNTNTTQV-SL 121  Qy 464 TNKDKXFLAIGNCCITAQFDXVQPCFGEVITRVKEKGAYAYIGSSPNSYWGEDYYWSVGA 523 Db 122 TN |

| 260 TLAAVSIGDUSSTRIKTROLIGGLAAGTSKTDAVWAQLKUVDEIASRGMILTASGAN 316 583 EAYHULGDGSVMPYRAMPKTRITYLPASLPONGASTSIOASAGSTVALSKD 584 GULYGTGVANAGSV      | INKGGARFGLSTEA-NGAKPQSVWIERTVDL                        |
|---------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------|
| 8 4 8 4 8 4 8 4 8 8 4 8 8 8 8 8 8 8 8 8                                                                                                           | 8 6 8 6 8 6 8 6                                        |
| VYASEHYAV-YASSTGNDAG<br>INTELFAQCTTETVEVU<br>INTELAGGT-WYOKTYOLP<br>TYSTTGSGTSWFTTTVPY<br>NNTOIASGTVETTYRDPDLJ<br>TYSTTGSGTSWFTTTVPY<br>INTELSE I | CONSCIVATIVE 197; Mismat GMQYYYNOEHGYTDVYNYLKAPYTGCYSH |

Search completed: May 18, 2004, 11:36:13 Job time: 48.8582 secs

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922 --DPVQFNPVQNLTGSAVGQKVTLK----WDAPNG---TPNPNPNPNPGTTTLS----- 966
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P59915 porphyromon
P28734 porphyromon
P58784 porphyromon
Q67836 strongyloce
Q07833 bacillus
P15293 methanococc
P42782 haemophilus
P15293 lactococcus
P25927 salmonella
Q058791 methanococc
P25927 salmonella
Q08879 celulomona
Q88897 escherichia
Q9889 celulomona
Q88897 escherichia
P5089 celulomona
Q88897 escherichia
Q98897 escherichia
P1592 lactococcus
P38058 clostridium
Q53047 router mem
P38058 clostridium
Q5305 t amylopull
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P1592 lactococcus
P1593 t amylopull
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P1591 staphylococ
Q02470 lactobacill
Q0213 gallus gallu
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4145.156 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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HYAL_STRPU
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P2P_LACLC
B1GA_HABIN
P2P_LACLC
B1GA_BALTY
SPB_CEBEI
APU THETU
VEEJ_ECOST
P1P_LACLC
B1GA_BALCH
GUNB_RICCN
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| ህፋፋ                     | 204                                                                                            | بنبن                                                                                                                                                             | ი ი ი                                              | 1341<br>1829<br>4303                                                                | ннн                                                                |                                                                                                                                 | BPT2<br>NEIMB<br>HUMAN                                            |                                                         | P07067<br>Q9jyv5<br>P98161                                                                                            | bacte<br>neiss<br>homo                                                                              | rlopha<br>eria m<br>sapien               |
| <b>ਚਿੱਚਾ ਚਾ</b>         | 175<br>174.5<br>174.5<br>174.5                                                                 | ન <u>ં</u> નં નં                                                                                                                                                 | თთთთ                                               | 6632<br>872<br>1419<br>1045                                                         | нннн                                                               | UN89 CAEEI<br>GUXA CELF.<br>ALA1 CANAI<br>GUNB CELF.                                                                            | CAEEL<br>CELFI<br>CANAL<br>CELFI                                  |                                                         | 001761<br>P50401<br>013368<br>P26225                                                                                  | caen<br>cell<br>cand                                                                                | orhabdi<br>ulomona<br>ida alb<br>ulomona |
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| RESULT<br>HGA2_P        | T 1<br>PORGI<br>HGA2 PORGI                                                                     |                                                                                                                                                                  | CTANTAR                                            | . נואמנ                                                                             |                                                                    | E<br>Q<br>Q                                                                                                                     | 4 8 C 9 C                                                         |                                                         |                                                                                                                       |                                                                                                     |                                          |
|                         | 44401                                                                                          | Re Re                                                                                                                                                            | 1. 35                                              | 39, Creat<br>39, Last<br>42, Last                                                   | 1.3                                                                | rai,<br>nence<br>lotati                                                                                                         | updat<br>on upd                                                   |                                                         |                                                                                                                       |                                                                                                     |                                          |
|                         | HAGA.<br>HAGA.<br>Porphyromonas ging<br>Bacteria; Bacteroi<br>Porphyromonadaceae               | က်တိုင်းကာ ႏ                                                                                                                                                     | A precursugingly gingivalisteroidetes; aceae; Porp | · - 73                                                                              | (Bē<br>Bac<br>Bac                                                  | ursor.<br>alis (Bacteroides<br>tes; Bacteroides<br>Porphyromonas.                                                               | s gingiv<br>(class)                                               | lis).<br>Bacteroi                                       | dales;                                                                                                                |                                                                                                     |                                          |
|                         | [1] SEQUENCE FROM N.A STRAIN=381; MEDLINE=97047672; Han N., Whitlock, "The homeron", whitlock, | FROM N. 31; 37047672                                                                                                                                             | .A.<br>2, Pul<br>k J.,                             | PubMed=8926061<br>[., Progulske-F                                                   | =892<br>yule                                                       | ×                                                                                                                               | A.;<br>Downbywonen                                                |                                                         | יין.<br>מיינים איינים יינים | ā                                                                                                   |                                          |
|                         | contains four large<br>Infect. Immun. 64:9<br>-!- FUNCTION: Agglu-<br>-!- SIMILARITY: Bel      | ains four large, contiguous, ct. Immun. 64:4000-4007(1996) FUNCTION: Agglutinates erythr. SIMILARITY: Belongs to peptid                                          | arge,<br>64:4(<br>gglut<br>Belc                    | cont<br>000-4(<br>cinate                                                            | 100<br>100<br>100<br>100<br>100<br>100<br>100<br>100<br>100<br>100 | nous, di<br>(1996).<br>erythrocy                                                                                                | nues, direct repeats. (1996). erythrocytes. peptidase family C25. | **                                                      | 4                                                                                                                     | )                                                                                                   |                                          |
| 8888888                 | T G 0 0 G 5 T                                                                                  | SWISS-PROT entry is copy<br>en the Swiss Institute<br>uropean Bioinformatics I<br>by non-profit institut<br>ied and this statement i<br>ies requires a license a | entriss I<br>oinfo<br>ofit<br>is st                | entry is copy as Institute in informatics fit institute is statement is a license a | cor<br>cor<br>lcs<br>lcs<br>citt                                   | Y is copyright. It<br>nstitute of Bioinfor<br>rmatics Institute.<br>institutions as lo<br>atement is not<br>license agreement ( | is<br>rma<br>rma<br>nd<br>roc<br>vec                              | duced thr<br>s and th<br>are no<br>its cont<br>Usage by | h a<br>EMB<br>EMB<br>Trip<br>nd<br>'s                                                                                 | collaboration<br>L outstation -<br>ctions on its<br>s in no way<br>for commercial<br>b.ch/announce/ | ration<br>ion its<br>way<br>ercial       |
|                         | or send a                                                                                      | an email                                                                                                                                                         | 1 to<br><br>AB171                                  | 11Cer<br><br>128.1                                                                  | nse@                                                               | 0187-810                                                                                                                        | .ch) .                                                            | 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1                 | !<br>!<br>!<br>!                                                                                                      |                                                                                                     | <br>                                     |
|                         | PIR; T28651; T2<br>Hemagglutinin;<br>SIGNAL<br>CHAIN                                           | 51; T2<br>inin; 1<br>25                                                                                                                                          | 8651.<br>Virul<br>26                               | e)                                                                                  | , H,                                                               | drolase<br>POTENT<br>HEMAGGI                                                                                                    | , Thiol print.<br>LAL.<br>LUTININ A.                              | ase, S                                                  | ignal;                                                                                                                | Repeat.                                                                                             |                                          |
|                         | DOMAIN<br>DOMAIN<br>DOMAIN<br>DOMAIN<br>DOMAIN                                                 | 25<br>540<br>996<br>1452<br>2074                                                                                                                                 | 44.0                                               | 539<br>995<br>451<br>907<br>628                                                     |                                                                    | PEPTID<br>PEPTID:<br>PEPTID:<br>PEPTID:                                                                                         |                                                                   | KE 1.<br>KE 3.<br>KE 4.                                 |                                                                                                                       |                                                                                                     |                                          |
| SQ<br>Que<br>Bes<br>Mat | SEQUENCE<br>Query Match<br>Best Local S<br>Matches 958                                         | E 2628 AA<br>h<br>Similarity<br>58; Conser                                                                                                                       | AA;<br>ity<br>serva                                | 833<br>7.<br>7.                                                                     | 324<br>9%;<br>0%;<br>11                                            | Score Pred. 14; Miss                                                                                                            | S win                                                             | 99DA CRC64;<br>1; Length<br>23; Indels                  | 4;<br>h 2628;<br>ls 442                                                                                               | Gaps                                                                                                | 53;                                      |
| ð 6                     | 179                                                                                            | YDVVANQLKVRNNIEIEVSFQ-<br>    :   :   :   :<br>vrvxpncrkikbciremmee                                                                                              | OLKVE<br> ::                                       | RINITED  FEBRUARY                                                                   | EVE                                                                | 3FQ                                                                                                                             | EIBVSFOGADEVATGRLYDASPSPYFETAYKOLFNRDVYT                          | LYDASFSPY                                               | FETAYK(                                                                                                               | KQL FNRDVYT<br>  :    <br>KECVNVTV                                                                  | 232                                      |
| }                       | 233                                                                                            | DHGDLY                                                                                                                                                           | NTPVF                                              | GDLYNTPVRMLVVAGAKFR                                                                 | GAF                                                                | CPKEALKPI                                                                                                                       | DHGDLYNTPVRMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYTDEAEVGTTNASIKAFIH      | YLDVHYTDEAEV<br>:                                       | AEVGTT                                                                                                                | ASIKAFIH                                                                                            |                                          |

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| 847 OPARY                                                                                                                                          | DD 1196 ALNPDNYLLSKDVTGATKVKYYAVNDGFFGDHYAVMISKTGTNAGDFTVVFEETPNGIN 1255  QY 858                                                                                                                                                                                                                                | :                                                                                                  | 1001 DADGDGHGWKPGNAPGIAGYNSNGCVY                                                                                                                        | OY 1058 LTFWVCAQDANYASHYAYYASSTGNDASNFTNALLEETITAKG-VRSPKAIRG-RIQGT 1115 | 1548   WYQKTVQLPAGTIKYVAFRHFGCTDFFWINLDDVEIKANGKRADFTEFFESSTHGBAPAEW 1607   QY                                                 | 1236 YYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLSTEANGAKPQSV                                            | OY 1296 WIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIOFTWGGSPTPTDYTYTVYRDGTKIKEG 1355<br> | 1356            | 1416 ILKWNAPASKRAEVLAEDFENGIPASWKTIDADGDGNNWTTTPPPGGSSFAGHNSAICVS 147 1848 ILKWNAPASKRAEVLAEDFENGIPASWKTIDADGDGNNWTTTPPPGGSSFAGHNSAICVS 190 | 1476<br>1908                                                                  |                                                                                                                            | QY 1596 DVVITSGNAPSYTYTIYRNNTQIASGVTETTYRDPDLATGFYTYGVKVVYPNGESAIETA 1655  DD 2028 DVVITSGNAPSYTYTIYRNNTQIASGVTETTYRDPDLATGFYTYGVKVVYPNGESAIETA 2087 |     | Oy 1716 VMVVVDGKSYVEKLAVK 1732<br> | RESULT 3<br>PRTH_PORGI<br>ID PRTH_PORGI STANDARD; PRT; 989 AA. |
|----------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------|-----------------|---------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------|-----|------------------------------------|----------------------------------------------------------------|
| TION: Agglutinates erythrocytes (By similarity).  LARITY: Belongs to peptidase family C25.  SS-PROT entry is converight It is needland themselves. | is Institute of Bioinformatics and the EMBL outstation - informatics Institute. There are no restrictions on its fit institutions as long as its content is in no way statement is not removed. Usage by and for commercial ss a license agreement (See http://www.isb-sib.ch/announce/ to license@isb-sib.ch). | 6831.1; ALT_INIT. ence; Hydrolase; Thiol protease; Signal; Repeat;  25 POTENTIAL 64 HEMACALITHIALA | N 26 539 PEPTIDASE C25-LIKE 1.<br>N 540 991 PEPTIDASE C25-LIKE 2.<br>N 992 1443 PEPTIDASE C25-LIKE 3.<br>NCE 2164 AA; 233387 MW; 6DFAB2283288CG3 CRC64; | 45;                                                                      | HNSAICVSSAS-YINFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAV-YA 604 ASSPELINIIDKVLMYEKAIMPDKSYLEKVLLIAGADYSWNSQVGQPTIKYGMQYYY 408 | BEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVA 659NYLKAPYTGCYSHLNTGVSFANYTAHGSETAWADPL 454                       1 | 506                                                                           | 554<br>STEA 815 | 555SIMWAGNLAATHAGNIGNITHIGAHYYWEAYHVLGDGSVMPYRAMPKINTYTL 607  816 NGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTWGGSPTPTDXT- 870              | 608 PASLPQNQASYSIQASAGSYVAISKDGVLYGTGVANASGVATVSMTKQITENGNYD 663  871GNHE 900 | 664 VVITRSNYLPVIKQIQVGEPSPYQPVSNLTATTQQQKVTLKWBAPS 709 901 YCVEVKYTAGVSPKECVNVTVDPVQPNPVQNLTGSAVGQKVTLKWDAPNGTPNPDFTTT 960 | 710 -AKKAEGSREVKRIGDGLFVTIEPANDVRANBAKVVLAADNVWGDNTGY 757 C                                                                                          | 798 | 799 NADPUVITQNIIVIGEVUIPGG         | 823VYDXCITNDEPASGKM-WIAGDGGN 846 ::                            |

DP Có DP Có

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1659 ITSLADVIAQKPYTLTVVGKTITVTCQGEAMIYDMNGRRLAAGRNTVVYTAQGGHYAVMV 1718
                                                                                                                                                                                                                                                                   1599 ITSGNAPSYTYTIYRNNTQIASGVTETTYRDPDLATGFYTYGVKVVYPNGESAIETATLN 1658
                                                                                                                                                                                           1540 LEEVLTAKTVVTAPEAIRGTRAQGTWYQKTVQLPAGTKYV-AFRHFGCTDFFWINLDDVV 1598
                                                                                                                                               445 ADPVVITQNIIVIGQGBVVIBGG---VYDYCITNPEPASGKMWI-AGDGGNQPARYDDFT 500
         332 NPVKNLKAQ--PDGGDVVLKWEAPSAKKTEGSREVKRIGDGLFVTIEPANDVRANEAKVV 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     residues in P2 and P3.

ENZYME REGULATION: Requires cysteine for activation and Ca(2+) and/Or Mg(2+) for stabilization. It is stimulated by glycine-containing dipeptides. It is resistant to inhibition by proteinase inhuman plasma.

SIMILARITY: Belongs to peptidase family C25.
                                                                                                                                                                                                                                                                                                                                                               584 PDGVEDVIVQKPHILIVVGKIIIVSWQGEAMIYDMNGRRLAAGRNIVVYTAQGGYYAVWV
                                            LNEDFENGIPASWKTIDADGDGNNWTTTPPPGGSSFAGHNSAICVSSASHINFEG--PQN
                                                                               390 LAADNVWGDNTGYQFL-LDADHNTFGSVIPATGPLFTGTASSDLYSA----NFEYLIPAN
                                                                                                                    PD-----NYLVT--PELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANAL
                                                                                                                                                                                                                                  ----AGKKYTFTMRRAGMGDG-----TDME
                                                                                                                                                                                                                                                                                            524 VEDDSPASYTYTVYRDGTKIKEGLTETTYRDAGLSAQSHEYCVEVKYTAGVSPKVCVDYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen Z., Potempa J., Polanowski A., Wiketrom M., Travis J.;
Chen Z., Potempa J., Polanowski A.,
"Purification and characterization of a 50-kDa cysteine proteinase
(gingipain) from Porphyromonas gingivalis.";
J. Biol. Chem. 267:18896-18901 (1992).

-I-FUNCTION: Thiol protease which is believed to participate in
intracellular degradation and turnover of proteins. Its
proteolyptic activity is a major factor in both periodoncal tissue
destruction and in bacterial host defense mechanisms. Activates
complement C3 and C5.

-I-CATALYTIC ACTIVITY: Cleavage of proteins, including collagens and
imminoglobulins, with a preference for Arg in P1, and hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPGI_PORGI STANDARD; PRT; 991 AA.
P28764; Q45168;
01-DEC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Gingipain R1 precursor (EC 3.4.22.37) (Gingipain) (Arg-gingipain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arginine-specific cysteine proteinase as a major periodontal pathogenic factor from Porphyromonas gingivalis."; Arch. Biochem. Biophys. 316:917-925(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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MEDLINE=95168884; PubMed=7864651;
Okamoto K., Misumi Y., Kadowaki T., Yoneda M., Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 228-290 AND 517-541.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural characterization of argingipain,
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                                                                                                                                                                                                                                                                                                                                                                                                                  1719 VVDGKSYVEK 1728
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                                                                                                                                                                                                                                                                                                                                                                 Fletcher H.M., Schenkein H.A., Macrina F.L.;
Infect. Immun. 62:5707-5707(1994).
-!- FUNCTION: CLEAVES HUMAN COMPLEMENT COMPONENT C3. MAY ENABLE
P.GINGIVALIS TO EVADE COMPLEMENT-MEDIATED KILLING DURING THE
IMMUNE RESPONSE. PLAYS AN IMPORTANT ROLE IN SOFT TISSUE INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1100 KGVRSPKAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYID-LDEVEIKANGKRAD
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                                                                                                        Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: In membrane vesicles. SIMILARITY: Belongs to peptidase family C25.
                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00551; formyl transf; 1.
Hydrolase; Thiol protease; Repeat; Virulence.
                                                                                                                                                                                                                                                           Fletcher H.M., Schenkein H.A., Macrina F.L., "Cloning and characterization of a new prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1399 NPVQNLTAEQAPNSMDAILKWNAPASKRAE
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Infect. Immun. 62:4279-4286(1994)
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               01-NOV-1995 (Rel. 32, Created Ol-NOV-1995 (Rel. 32, Last se 16-OCT-2001 (Rel. 40, Last ar Protease prtH (EC 3.4.22.-).
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SEQUENCE FRO
STRAIN=W83;
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SEQUENCE
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STANDARD;
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P95493;
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15-MAR-2004
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                cch 13.3%; Score 1222.5; DB 1; Length 991; al Similarity 31.8%; Pred. No. 2.2e-59; 322; Conservative 174; Mismatches 381; Indels 135; Gaps
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                                                                                                                                                         InterPro; IPR07110; Ig-like.
InterPro; IPR007109; Peptidase_C25.
InterPro; IPR005536; Peptidase_C25_C.
Pfam; PF01364; Peptidase_C25_C.
Pfam; PF03785; Peptidase_C25_C; I.
Virulence; Hydrolase; Thiol protease; Calcium; Signal; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 VPTYTEGVNLSEKGMPTLPILSRSLAVSDTREMKVEVVSSKFIEKKNVL-
                                                                                                                                                                                                                                                                    GINGIPAIN R1.
PROTON DONOR (BY SIMILARITY)
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RT -> TK (IN REF.
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SIQAS-AGSYVAISKDGVLYGTGVANASGVATVSMTKQITENGNYDVVITRSNYLPVIKQ 677
                                                                                                                                                                                                                                   655 INTNGEPNPYOPVSNLTATTOGOKVTLKWDAPSTKTNATTNTARSVDGIRELVLLSVSDA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 774 PFEYIVPENADPSCSPTNMIMDGTASVNIPAGTYDFALAAPQ-ANAKIMIAGGG---PTK
                                                                                                                                                                    --KAEGSREVKRIGDGLFVTIEPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   791 NFEYLVPANADPVVTTQNIIVTGQGEVVIPGGVYDYCITNPEPASGKMWIAGDGGNQPAR
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-!- FUNCTION: Thiol protease which is believed to participate in intracellular degradation and turnover of proteins. Its proteolytic activity is a major factor in both periodontal tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potempa J., Mikolajczyk-Pawlinska J., Brassell D., Nelson D., thoegarean I.B., Enghild J.J., Travis J., travis J., trongarative properties of two cysteine proteinases (gingipains R) the products of two related but individual genes of Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               911 GVAAGNHEYCVEVKYTAGVSPKVCKDVTVEGSNEFAPVQNLTGSSVGQKVTL 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGPB OR RGP2 OR PRIRII OR PG0506.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83."; J. Bacteriol. 185:5591-5601(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-2004 (Rel. 43, Last annotation update)
Gingipain R2 precursor (EC 3.4.22.37) (Gingipain 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     736 AA
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     complement C3 and C5 (By similarity).
CATALYTIC ACTIVITY: Cleavage of proteins, including collagens and immunoglobulins, with a preference for Arg in P1, and hydrophobic residues in P2 and P3.
SIMILARITY: Belongs to peptidase family C25.
destruction and in bacterial host defense mechanisms. Activates
                                                                                                                            TIGR; PG0506; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Pptidase C25.
InterPro; IPR005536; Peptidase C25.
Pfam; PF01364; Peptidase C25, I.
Pfam; PF03785; Peptidase C25, I.
Virulence; Hydrolase; Thiol protease; Calcium; Signal; Zymogen; 3D-structure; Complete proteome.
SIGNAL
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EMBL; AE017173; AAQ65700.1; -.
PDB; ICVR; 01-MAR-00.
                                                                                                                      MEROPS; C25.003; -.
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GTFASVSIPGAFPTGEVGSPEVPAVRKLIAVPVGATPVVRVKS--FTEQVYSLNQYGSEK 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 IMPHQPSMSKSDDPEKVPFVYNAAAYARKGFVGQELTQVEMLGTMRGVRIAALTINPVQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.9%; Score 541; DB 1; Length 736;
Best Local Similarity 25.1%; Pred. No. 3.5e-22;
Matches 200; Conservative 130; Mismatches 328; Indels 140; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 NPVTKTLRIYTEİVVAVSETAEAGONTISLVKNSTFTGFEDIYKSVFMNYEATRY----
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                                                                                                                     WGEDYYWSVGANAVFGVQPTFEGTSMGSYDATFLEDSYNTVNSIMWAGNLAATHAGNI-- 570
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           -SHLNTGVSFANYTAHGSETAWADPLLT 456
                                  101 NLLTQYGYTKIIK------CYDPGVTPKNIIDAFNGGISLANYTCHGSETAWGTSHFG 452
                                                                                                                                                                                                       TFGGVIMNGMFAMVEKYKKDGEKMLDTWTVFGDPSLLVRTLVPTKMQVTAPANISASAQT 597
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                                                                                          TTHVKQLINSNQLPF1FDVACVNGDFLYNVPCFAEALMRAQKDGKPTGTVAIIASTINQS
                                                                                                                                                                             ----VLGDGSVMPYRAMPKTNTYTLPASLPQNQAS
                                                              TSQLKALTNKDKYFLAIGNCCITAQFDYVQPCFGEVITRV----KEKGAYAYIGSSPNSY
                                                                                                                                                    ------ODEMNEI-----LCEKHPNNIKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strongylocentrotus purpuratus (Purple sea urchin).
Bukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida, Strongylocentrotidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98142007; PubMed=9473317; Wessel G.M., Berg L., Adelson D.L., Cannon G., McClay D.R.; "A molecular analysis of hyalin -- a substrate for cell adhesion in the hyaline layer of the sea urchin embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Major constituent of the hyaline layer. The hyaline layer of echinoderm embryos is an extraembryonic matrix that functions as a substrate for cell adhesion through early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Homooligomer in presence of calcium.
SUBCELLULAR LOCATION: Secreted. Extracellular matrix.
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SIMILARITY: Contains at least 15 HYR domains.
                                                                                                                                                                                                                                                                                                            (Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                             571 --GNITHIGAHYYWEAYH-----
        YYNQEHGYTDVYNYLKAPYTGCY-
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10-OCT-2003 (Rel. 42, Last Beg
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NCBI_TaxID=7668;
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SEQUENCE FROM N.A.
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InterPro; IPR003410; Hyalin. Pfam; PF02494; HYR; 15. PROSITE; PS50825; HYR; 15. Cell adhesion; Extracellular matrix; Glycoprotein; Repeat.

EMBL; AF076472; AAC31909.1; -. PIR; T17404; T17404.

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                                                                                                                                                                   1236 YYYAVNDGFPGD--HYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLSTEANGAKPQ 1293
                                                                                                                                                                                                                                 1294 SVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSPTPTDYTYTVYRDGTKIK 1353
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VEEMVDTTPPTVTVSGGNIVRTVELGQSRLSVIYTEPTATDNSGEANLVSRTAQPGDLFP 601
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"Molecular analysis of three major wall-associated proteins of Bacillus subtilis 168: evidence for processing of the product of a gene encoding a 258 kDa precursor two-domain ligand-binding
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                                                                                                                                                                                                                                                                                                                          Wall-associated protein precursor. WAPA OR N17G OR BSU39230. Bacillus subtilis.
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STRAIN=168 / BGSC1A1;
MEDLINE=95219098; PubMed=7704263;
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01-0CT-1994 (Rel. 30, Last seq
10-0CT-2003 (Rel. 42; Last anno
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Accorded V. Bertero M.G. Bessieres P., Bolotin A.M., Alloni G.,

Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V.,

Carter N.M.,

Brouillet S., Bruschi C.V., Cannerton I.F., Cummings N.J., Daniel R.A.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Berian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

Ramerson P.T.,

RA Entian K.D., Errington J., Funa S., Galizzi A., Galleron N.,

Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandin G.,

A Ghim S.Y., Calser P., Goffeau A., Golightly E.J., Grandin G.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Joris B., Karamata D., Kasahara Y., Klaert-Banchard M., Klein C.,

RA Joris B., Karamata D., Kasahara Y., Klaert-Banchard M., Melin C.,

RA Joris B., Koetter P., Golightly E.J., Grander C.,

RA Miller K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

Ramer O', Pohl T.M., Portetelle D., Porwollik S., Prescort A.M.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescort A.M.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

Scholdth J., Sekowska A., Seror S.J., Serror P., Shin B.S.,

Sorokin A., Tanakoshi A., Tanaka T., Terspira P., Tognoni A.,

Takeuchi M., Tamakoshi A., Tanaka T., Terspira P., Tognon A.,

Yoshida K., Yoshikawa H.P., Zamamoto H., Wannier F., Vassarotti A.,

Winters P., Wipat A., Zamamoto H., Wannier F., Vassarotti A.,

Winters P., Wipat A., Yamamoto H., Wannier F., Vassarotti M.,

Rah H. Chen C., Rocha E., Roche E., Rochila K., Yashin H.P.,

Rah H. Chen C., Rocha E., Roche E., Roche E., Roche E., Roche E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller E., Waller Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y., Cloning and sequencing of a 29 kb region of the Bacillus subtilis genome containing the hut and wapA loci."; Microbiology 141:337-343(1998). ż MEDLINE=97124196; PubMed=8969509; Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N. Miwa Y., Fujita Y.; Shindo K. Sano H., Seki S., Fujimura M., Yanai N. Sequencing of a 65 kb region of the Bacillus subtilis genome containing the lic and cel loci, and creation of a 177 kb contiguencing the gnt-sacXY region."; Microbiology 142:3113-3123 (1996). MEDLINE=98044033; PubMed=9384377; FROM N.A. 58 / BGSC1A1; SEQUENCE FROM N.A. STRAIN=168 / SEQUENCE subtilis. 

Nature 390:249-256(1997).
-1- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM, MOTILITY, SECRETION OR DIFFERENTIATION.
-1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED INTO THE MEDIUM.

DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED MOTIF REPEATED 31 TIMES.

SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).

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EMBL; L05634; AAA22883.1; -.
EMBL; D31856; BAA06656.1; -.
EMBL; D29985; BAA062560.1; -.
EMBL; D3026; BAA11683.1; -.
EMBL; Z99124; CAB15959.1; -.

| 238 -YMT - PURMLVVAGAKEKBALKPMLTWRAQKGFYLDVHYTDDARV-GTTNASI- 365 KRNILKPIQNATVTKATLKTYVHASYTGTRATGIALDTVNNY DINKVTWANTREASKNI 286 - KAPTHKKYNDGLAASAA-VFLALVODTDVIGGEKGKKTKKYDLYYSAVDGDKFPENTT 424 GRADVHKGOWASWDVTAAVKSWNSGGANYGFKLHT 347 FEMSASSPEELTNIIDKVLMYEKATNPORSYLEKVLLJAGADDSWNSGVGQPIIKYGWQY 659NGNGKEYMKULISSANSANKPYIEVTIPKGN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | B54 FTEACKKYTT              |
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| ETRY, 332920; 332920.  Subtities FRO03035; CMB.  InterPro; IRRO03035; CMB.  Ffam; PFOC531 ND.  Ffam; PFOC531 ND.  Ffam; PFOC531 ND.  Ffam; PFOC531 ND.  Ffam; PFOC531 ND.  Ffam; PFOC531 ND.  Ffam; PFOC531 ND.  Ffam; PFOC531 ND.  Ffam; PFOC531 ND.  Ffam; PFOC531 ND.  Ffam; PFOC531 ND.  Ffam; PFOC531 ND.  Ffam; PFOC531 ND.  Ffam; PFOC531 ND.  Ffam; PFOC531 ND.  Ffam; PFOC531 ND.  FFAM; PFOC531 ND.  FFAM; PFOC531 ND.  FFAM; PFOC531 ND.  FFAM; PFOC531 ND.  FFAM; PFOC531 ND.  FFAM; PFOC531 ND.  FFAM; PFOC531 ND.  FFAM; PFAM; PFOC531 ND.  FFAM; PFAM; PFOC531 ND.  FFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; PFAM; P | 14 GVGLYAQSAKI              |
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1484 NDDVSLKAARTSASQAGSVTKQTVVLGQSANDKPVYLTLTGMSKASSVKFTDEKDYSLQA 1543
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1424 VYMEVDHKOKOKKAWFDEVQLEKGEVSSSYNPVQNSSFTSATENWNVSGASVDSEEGF 1483
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                                                                         1365 GKIK-TDLAKSRAYFNIDLRDKDQKRIQWIHNEYSALAGKNDWTKRQITFTTPANAGKAV
                                                                                                         EWITI---DADGDGQGW---LCLSSGQL--DWLTAHGGSNVVSSFSWNGMALNPDN----
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(Rel. 43, Last sequence update)
(Rel. 43, Last annotation update)
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Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.

15-MAR-2004 (Rel. 43, Last av Hypothetical protein MJ1396.

Methanococcus jannaschii.

MJ1396.

NCBI\_TaxID=2190;

SEQUENCE FROM N.A. STRAIN=JAL-1 / DSM 2661 / ATCC 43067; MEDLINE=96337999; PubMed=8688087;

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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nauyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 FSPYFETAYKQLFNRDVYTDHGDLYNTPVRMLVVAG---AKFKEALKPWLTWKAQKGFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          839 GYNYTDMMNEINWGLSQLYDTGVKSIDYPNNGDSFNPNIGPIIYINSTIALYGLVDAYNL
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InterPro; IPR001220; Lectin_legB.
InterPro; IPR001220; Debli.
InterPro; IPR00139; lectin_legB; l.
SMART; SM00710; PbH1; 20.
Hypothetical protein; Transmembrane; Repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.4%; Score 224; DB 1; Length 2894;
18.2%; Pred. No. 0.0007;
ive 213; Mismatches 562; Indels 626;
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PIR; C64474; C64474.
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2589 261
2612 263
2638 266
2894 AA;
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| Db 1851 WVEFYAXLGDNPDGADGITFTLQSLGT | MESUIT 9  10a1 Harin  10b                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
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| 420YUKAPYT                          | KEDSEDKGITGS    EPANDVRANEAKVULAADAVWGDNTGYGFILDADHNTEGSVIPATGPLFTGTASSNILYS   KEDSEDKGITGGVALLAADAHNTGYGFILDADHNTEGSVIPATGPLFTGTASSNILYS   KEDSEDKGITGGVANGILEDSNNDGIPDIGDTIVNSTTTDIFGHYSFLVYN   SKTYFVVNASTYGTRGLANPOYSKNDIWAEETYGTVYTPINSSGMIANGISFP   SKTYFVNASTYGTRGLANPOYSKNDIWAEETYGTVYTPINSSGMIANGISFP   SKTYFVNASTYGTRGLANPOYSKNDIWAEETYGTVYTPINSSGMIANGISFP   SKTYFVNASTYGTRGLANPOYSKNDIWAEETYGTVYTPINSSGMIANGISFP   SKTYFVNASTYGTRGLANPOYSKNDIWAEETYGTVYTDBPBASYTYTVYBGT   SKTYFVNASTYGTRGLANPOYSKNDIWAEETYGTVYTDBPBASYTYTVYBGT   SKTYFVNASTYGTRGGBOGY |

| 809 IIVTGQGEVVIPGGVYDYCITNPEPASGKMMIAGDGGNQPARYDDFTFEAGKKYTFT 865                                                                                                                                                                                                         | 866 MRRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEEDG 911       | 608GASTRSELPKNSGESNENWLYMGKTSDEAKRNVMNHINNERMNGFNGYFGEEEG 661 | VAAGNHEYCVEVKYTAGVSPKVCKDVTVEGSNEFAPVONLTGSSVGOKVTLKWDA | 662 KNNGN      | LSGRPTPHARDIAGISSTKKDPHFABNNEVVVEDDWINNNFKATTMNVTGNASITYSGRN-                              | 1015 PGIAGYNSNGCVYSESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHY 1074 |                                                                                                         | 10.7 TO THE STREET THE STREET THE STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STR | 1135 FQSTDMFYIDLDEVEIKANGKRADFTETESSTHGEAPAEWTTIDADGDGQGWLCLSSGQ 1194 | 1195 LDWLTAHGGSNVVSSFSWNGMALNPDNYLISKDVTGATKVKYYYAVN-DGFPG 1246 : : | 1247 DHYAVMISKTGTNAGDFTVVPEETPNGINKGGARPGLSTEANGAKPQSVWIERTVDLPAG 1306 |                                                                                                                          | WKYKLRNVNGRYDLYNPEVEKRNQTVDTTNITTPNNIQADVPSVPSNNEEIARVDEAPVP | 1337TPIDYTYTYVXBGTKIKEGLTETTFEBDGVATGNHEYC 1374<br>                                                                       | 1375VEVKXTAGVSPKKCVDVTVNSTQFNFVQNLTAEQAPNSMDAILKMNA 1421<br> | 1422 PASKRAEVLNEDFENGIPASWKTIDADGDGNNWTTTPPPGGSSFAGHNSAICVSSASHIN 1481 | 1482 FEGPONPDNYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGND 1531     | 1532 ASNPAGTWYQKTV 1570 1244 RSTVALCDLTSTNTNAVLSDA-RAKAQFVALNVGKAVSQHISQLEMNNEGQYNVWYSNT- 1301 | QLPAGTKYVAFRHFGCTDFFWINLDDVVITSGNAPSYTYTIYRNNTQIASGVTETT | 1502 SMNNNYSSSQYKKFSSKSTQTQLGWDQTISNNVQLGGVFTVVRNSNNFDKATSKNT 1357<br>1627 YEDDDIATGFVTYGVKVKYDNGSGATETATMITETADVTBANDERG 1677 | LAQVNFYSKYYADNHWYLGIDLGYGKFQSKLQTNHNAKFARHTAQFGLTAGKAFNLGNFG                                                              | 1678 XT 1679 | 1418 IT 1419              |
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| S S                                                                                                                                                                                                                                                                       | δλ                                                           | qa                                                            | 8                                                       | 8 8            | 7 d                                                                                        | λō                                                                     | අ<br>අ                                                                                                  | <u>2</u>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | yy dd                                                                 | <i>∂</i> 8                                                          | کم <del>ا</del>                                                        | 3 8                                                                                                                      | q <sub>Q</sub>                                               | λλ<br>QO                                                                                                                  | 75<br>DP                                                     | <i>₹</i> 6                                                             | <i>₹</i> ₹3                                                      | ර් යි                                                                                          | ે ક                                                      | g à                                                                                                                            | <i>7</i> 원                                                                                                                | δλ           | ପ୍ପ                       |
| CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/CC or send an email to license@isb-sib.ch). | DR EMBL; X64357; CAA45708.1;<br>DR EMBL; M87492; AAA24969.1; | PIR; 1                                                        | Inte                                                    | Inter<br>Pfam; | DR Pfam; PF02395; IGA1; 1. DR Pfam; PF03212; Pertactin; 1. DR PRINTS; PR0921; IGASERPTASE. | TIGRFAMS; TIGR01414; autotra<br>Hydrolase; Serine protease;            | SIGNAL 1 25 POTENTIAL. CHAIN 26 1008 IMMUOGLOBULIN AI PROTE PROPEP 1009 1541 HELDER PEPTIFIR LOTTENTIAL | PROBABLE.<br>S->T: LOSS OF A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 2.4%; Score 223; DB 1; Length 1541; LY 19.3%; Pred. No. 0.00031;      | 271 DVHXTDEAEVGTTNASIKAFIHKKYNDGLAASAAPVFLALVGDTDVISGEK             | 322                                                                    | Db 85 RIATLINPQYVVĠVKHVSNGVSELHFGNLNĠNMNNGNAKAHRDVSSEENRYF 136 QY 350 ŞASSPEELTNIIDKVLMYEKAŢMPDKSYLEKVLLIAGADYSWNSQV 395 |                                                              | Qy 396 GQPTIKYGMQYYYNQEHGYTDV7NYLKAPYTGCYSHIN 433  Db 197 KYPAFVRLGSGSQPIYKKGDNYSLILINNHEVGGNNLKLVGDAYTYGLAGTPYKVNHEN 254 | PCFGEV<br>   <br>                                            | 493 ITRVKEKGAYAYIGSSPNSYMGEDYYMSVGANAVFGVQPTFEGTSMGSYDATFIL            | 547 EDSYNTVNSIMWAGNIAATHAGNIGNITHIGAHYYWEAYHVLGDGSVMPYRAMPKTNTYT | 607 LPASLPQNQASYSIQASAGSYVAISKDGVLYGTGVANASGVATVSMTKQITEN                                      |                                                          | 409 GDYEVKGTSDNTT                                                                                                              | OY 716 SREVKRIGGGLFVIIEPANDVRANEAKVVLAADNVWGDNTG 756  DD 454 TLIVEGIGDDNKGSLKVGDGTVIIKQQNGSGGHAFASVGIVSGRSTLVLNDDRNSI 513 |              | :<br> <br> Sarlvnhnmtnasn |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMBL outstation. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C STRAIN=NCDO 763;

X MEDLINE=0931328B; PubMed=2501630;

X Kiwaki M., Ikemura H., Shimizu-Radota M., Hirashima A.;

Kiwaki M., Ikemura H., Shimizu-Radota M., Hirashima A.;

XI Molecular characterization of a cell wall-associated proteinase gene

XI Molecular characterization of a cell wall-associated proteinase gene

XI MOLECULAR STEPPLOCOCCUS 12611899;

XI MOLECULAR STORESE WHICH BREAKS DOWN MILK PROTEINS DURING THE

GROWTH OF THE BACTERIA ON MILK.

- I- FUNCTION: PROTEINSE WHICH BREAKS

C GROWTH OF THE BACTERIA ON MILK.

- I- CATALYTIC ACTIVITY: Endopeptidase activity with very broad

Specificity, although some subsite preference have been noted,

G Specificity, although some subsite preference have been noted,

G Specificity, although some subsite preference have been noted,

G Pro in the P2 position. Beet known for its action on caseins,

Although it has been shown to hydrolyze hemoglobin and oxidized
                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
PII-type proteinase precursor (EC 3.4.21.96) (Lactocepin) (Cell wall-associated serine proteinase) (LPISI).
                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLUIAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (Potential).
-!- SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease; Cell wall; Peptidoglycan-anchor; Zymogen;
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W; 4B8D8B844D88CDF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
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CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
LPXTG SORTING SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                           Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PII-TYPE PROTEINASE.
REMOVED BY SORTASE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR003137; PA.
InterPro; IPR003137; PA.
InterPro; IPR003137; PA.
Fam; PF07046; Gram pos_anchor; 1.
Pfam; PF07046; Peptidace S8; 1.
Pfam; PF00082; Peptidace S8; 1.
PRINTS; PR00723; SUBTILISIN.
TIGREAMS; IIGRAPANS; IGRAPANS; INTERPANS; INTE
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PROSITE; PS00138; SUBTILASE SER; 1.
Hydrolase; Serine protease; Cell wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200139 MW;
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                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33
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HSSP; P00782; 2SBT.
MEROPS; S08.019; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1359;
                                                                                                                                                                                                                                                                                                                                                                              Plasmid pLP763.
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                                                                         P2P_LACLC
P15293;
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SEQUENCE
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Score 220.5; DB 1; Length 1902;

2.48;

Query Match

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                                                                                                                                                                                                                                                                                                                       -- 321
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                                                                              160 MLGTWRGVRIAALTINPVQYDVVANQLKVRNNIEIEVSFQGADEVATQRLYDASFSPYFE
                                                                                                                                                                                             220 TAYKQLFNRDVYTDHGDLYNTPVRMLVVAGAKFKEALKPWLTWKAQKGFYLDV----HYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----NNGYTNMSGTSMASPFI----AGSQALLKQALNNKNNPFYAYYKQLKGT
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                                                                                                                                12 LAĞTVALGALAVLPVGEIQAKAAISQOTKGSSLANTVTAATAKQAATDTTAATT-
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19.5%; Pred. No. v.vvvv.,
tive 200; Mismatches 672; Indels
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                                                                                                                                                                                                                                                                                                                            J. Backeriol, 173:325-333(1991).
-!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts in positions 414 and 732.
                                 SEQUENCE FROM N.A.
STRAIN=LTZ / SGSC1412 / ATCC 700720;
STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spiech J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Miguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Materston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                  Wu J.Y., Siegel L.M., Kredich N.M.;
"High-level expression of Escherichia coli NADPH-sulfite reductase:
requirement for a cloned cysG plasmid to overcome limiting siroheme
      Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                       STRAIN=LT2;
MEDLINE=91100301; PubMed=1987123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF133696; AAD39458.1; -.
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                                                                                                                                                                                          Nature 413:852-856(2001).
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         ----NFTNALLEETITAKGVRS 1104
                                                                                                                                                                                  978 ISGVPEGGDKRQVFDV------PFKLDSKAPTVRHVALSAKTENG---KTQYYLT 1023
                                                                                                                                                                                                                                   ---NGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDI 1328
                                                                                                                                                                                                                                                                                                                                         QFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKKC 1388
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                                                                                                              923 -NKVTTLSSSTNRKKTYYNAHSQQYI-YYHAPAWDGTYYDQRDGNIKT---ADDGSYTYR 977
    ---NFGTVPLLTNKNTGTQYYGG 871
                                                 1105 PKAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETFE
                                                                                                                                                     SSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGSNVVSSFSWNGMALNPDNYLI
                                                                                                                                                                                                                SK----DVTG--ATK-VKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETP-----
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   ---STNGITYSPAGG-----
                              1063 CAQDAN------YASEHYAVYASSTGNDAS-
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                                                         Complete proteome.
POTENTIAL.
PUTATIVE SURFACE-EXPOSED VIRULENCE PROTEIN BIGA.
15 X 11 AA TANDEM REPEATS.
1 (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                / Match 2.4%; Score 219.5; DB 1; Length 1953; Local Similarity 20.2%; Pred. No. 0.00068; Los 266; Conservative 125; Mismatches 408; Indels 521;
                                                                                                                                                                                                                                                                                   D -> DRGDDDVTPPDD (IN REF. 1).
A -> R (IN REF. 3).
D -> N (IN REF. 1).
QYLE -> ITLQ (IN REF. 1).
SA -> T (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                        611B3F1C954D91AE CRC64;
                                                                                                                                                                                                                                                                          (INCOMPLETE)
                                                                                                                           2 (INCOMPLETE)
3 (INCOMPLETE)
EMBL; M64606; ÄAA27042.1; ÄLT_FRAME.
EMBL; M64606; AAA27043.1; ÄLT_FRAME.
PIR; C39200; D39200.
PIR; D39200; D39200.
                                                                                                                                                                                                                                                                                                                                           200150 MW;
                                    PIR; Distant, Strong, Strong, Strong, Strong, Strong, Strong, Strong, Strong, Strong, 28 1953
                                                                                                                                                                                                                                                                                                                                                                                                              663 DVVITRSNYLPVIK----
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1953 AA;
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Matches
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.

Salmonella typhimurium.

BIGA OR STM3478

STRAIN=ATCC 14028; Stojiljkovic I., Valentine P., Heffron F.; "Salmonella typhimurium rhs homolog.";

SEQUENCE FROM N.A.

NCBI\_TaxID=602;

|                                                                                                                                                                                                                                                                                                                                              | DD 1263                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | TITUTIALIZED OF INTERMODERATION CLEARMORN INTEGERS MAINTITUTATION OF THE COMPOSITE STRUCTURE OF THE ENZYME, and a common model for its RT attachment to the cell surface.";  RI ACTECION OF THE CASSE-3302(1994).  CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic CC - - CATALYTIC ACTIVITY: Endohydrolysis of (1,-6)-alpha-D-glucosidic CC - - CATALYTIC ACTIVITY: Hydrolysis of camylopectin and glycogen, and the CC - - COFACTOR: Binds 1 calcium ion per subunit (By similarity). |
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| TRANSMEM 2567 2589 POTENTIAL. TRANSMEM 2567 2589 POTENTIAL. TRANSMEM 2836 2868 POTENTIAL. TRANSMEM 2936 2961 POTENTIAL. TRANSMEM 2936 2961 POTENTIAL. TRANSMEM 2938 2961 POTENTIAL. TRANSMEM 2938 2961 POTENTIAL. DOMAIN 266 1196 SER/THR-RICH. DOMAIN 2107 2120 DOMAIN 2182 2305 PLAT. SEQUENCE 3178 AA; 344726 MW; F8239436D03666CD CRC64; | ### SOCRE ALM SIMILARITY 15.4%; SOCRE ALM STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND STATES AND ST |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |

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1002 ELGNESGISNDAVAYPAYPIGWVGNLT--OVSDNHIIGVDKPTEDIYAEVWADGLTN-ST 1058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1059 GQGPNMIAQLGYKYVSGTVYDSVYGSVYNSVGVDDSGFTWVNAQYVGDIGNNDQ---YK 1115
                                                                                                     EMYTFRMSASSPEELTNIIDKVLMYEKATMPDKSYLEKVLLIAGADYSWNSQVGQPTIKY 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1116 ASF-----TPDRIGQWEYLMRFSDNQGQDWITTSTLSFYVVPSDDLIKPTAPYLNQP 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1168 GTESSRVSLTWNPSTDNVGIYDYEIYRSDGGTFNKIATVSNFYNYIDTSVINGV---- 1222
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            FIHKK-----XNDGLAASAAPVFLALVGDTDVISGEKGKKTKKVTDLYYSAVDGDYFP 342
                                                              ----- DTVNKDF-- 371
                                                                                                                                                                                                                                              ------GDLWSNDFF--GDLK 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    696 NGOHNPIDAAKLDQRLMSIYERYPLP-----AFYSTMNLLGSHDTMR---ILTVFGYN 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       643 NASGVATVSMTKQITENGNYDVVITRSNYLPVIKQIQVGEPSPY----QPVSNLTATTQG 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         805 EDITLODFFKNISSIRNNNQVLKTGD--LETLYAQNDVYAIGRRIINGKD---AFGTSYP 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    926 TAGVSPKVCKDVTVEGSNEFAPVQNLTGSSVGQKVTLKWDAP------NGTPNPNP 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     814 QGEVVIPGGVYDYCIINPEPA-SGKMMIAGDGGNQPARYDDFTFEAGKKYTFTMRRAGMG 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                904 NGQIVI------DVPAMSGVMLISDDG-----QDLTAPQAPSNVVVTSGNGKV 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              873 DGTDMEVEDDSPASYTYTVYRDGT-----KIKEGLTATTFEEDGVAAG-NHEYCVEVKY 925
                                                                                                                                                                                                                                                                                                                             456 GIDDKLDYLKGLGVSVIYLNPIFESPSNHKYDTADYTKIDEMFGTTQDFEKLMSDAHAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  576 GYDSLPVIKSLNGSEYNVTSWANFIINDENAISKYWLNPDGNLNDGADGWRLDVENEVAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    699 QKVTLKWEAPSAKKAEGSREVKRIGDGLFVTIEPANDVRANEAKVVLAADNVWGDNŢGYQ
                                                                                                                                                                                              103 GMOYYYNOEHGYTDVYNYLKAP-YTGCYSHLNTGVSFANYTAHGSETAWADPLLTTSQLK
                                                                                                                                                                                                                                                                                         -----TAQFDYVQPCFG----EVITRVKEKG
                                                                                                                                                                                                                                                                                                                                                                                     -----WSVGANAVFGVQPTFEGTSMGSYDATF
                                                                                                                                                                                                                                                                                                                                                                                                                              516 IKIILDGVFNHTSDDSIYFNRYGKYPGLGAYQAWKEGNQSLSPYGDWYTINSDGTYECWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GNLAATHAGNIGNITHIGAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         597 ------RAMPKINIYILPASLPQNQASYSIQASAGSYVAISKDGVLYGIGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  746 SADPNENSDAAKOLAEQKLKLATILQMGY-PGMADIYYGDEAGVSGGKDPDDRRTFPWGN
                                                                                                                                                372 ELTVYDKNFDTPDWMKGAV----MYQ--IFPDRFYNGD----TSNDHAKTLSRGNDPIE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----FLLDADHNTFGSVI PATGPLFTGTASSNLYSANFEYLVPANADPVVTTQNI IVTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSAAIVAINRSKSDKQIAIDTTKFLRDGVTFKDLINNNVSYSI------
                                                         FDHPTRIWYYFILKDGTKT-----AYYGDNDDQLGGVGKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VLGD--GSVMPY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              546 LEDSYNTVNSI ------MWA-----
                                                                                                                                                                                                                                            ----FHNNWNDLPDNPNNAGTPGYTG----
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                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 QGADEVATQRLYDA----SFSPYFETAYKQLFNRDVYTD-HGDLYNTPVRMLVVAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 VYNAAAYARKGFVGQELTQVEMLGTMRGVRIAALTINPVQYDVVANQLKVRNNIEIEVSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---NDADITFYYDANTHNIWTNYSPILTGLDNNIYYDDLKHDTHDSFFRNPFGAVKV---
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  SUBCELLULAR LOCATION: CELL-BOUND. IT C-TERMINUS MAY SERVE AS
                                                                                                                                                                                                                                                                                                                                                                                  R InterPro; IPR006698; Alp amyl cat sub.
R InterPro; IPR006698; Alpha amyl cat.
R InterPro; IPR0066048; Alpha amyl cat.
R InterPro; IPR006047; Alpha amyl cat.
R InterPro; IPR004185; Glycohydro 131G.
R InterPro; IPR004185; Glycohydro 131G.
R InterPro; IPR004185; Glycohydro 131G.
R InterPro; IPR004185; Glycohydro 13N.
R Pfam; PF020203; alpha-amylase; 1.
R Pfam; PF020203; alpha-amylase c; 1.
R Pfam; PF020203; alpha-amylase N; 1.
R Pfam; PF02025; isoamylase N; 1.
R Pfam; PF02025; Sloamylase N; 1.
R SMART; SM00642; Aamy; 1.
R SMART; SM00661; Aamy; 2.
R SMART; SM00661; Sluh DOWAIN; 3.
R PROSITE; PS01072; SLH DOWAIN; 3.
R PROSITE; PS01072; SLH DOWAIN; 3.
R SMART; SM0066; ENS; 2.
R PROSITE; PS01072; SLH DOWAIN; 3.
R SMART; SM0066; ENS; 2.
R SMART; SM0066; ENS; 2.
R SMART; SM0066; ENS; 2.
R PROSITE; PS01072; SLH DOWAIN; 3.
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R SMART; SM0066; ENS; 2.
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R SMART; SM0066; ENS; 2.
R PROSITE; PS01072; SLH DOWAIN; 3.
R SMART; SM0668; 2.
R SMART; SM0668; 2.
R PROSITE; PS01072; SLH DOWAIN; 3.
R SMART; SM0668; 2.
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R PROSITE; PS010772; SLH DOWAIN; 3.
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FIBRONECTIN TYPE-III 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CALCIUM (BY SIMILARITY).
CALCIUM (UIA CARBONYL OXYGEN) (I
                                        -!- FTM: Glycosylated.
-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
-!- SIMILARITY: Contains 2 fibronectin type III domains.
-!- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 2.3%; Score 214; DB 1; Length 1861;
Local Similarity 18.8%; Pred. No. 0.0013;
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CALCIUM (BY SIMILARITY).
CALCIUM (VIA CARBONYL OXYGEN)
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                                      --SNV----VSSFSWNG--MA 1216
                                                                                                         -----SVYGNDQGRITELT 1438
                                                                                                                              -----VVFEETPNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCS 1318
                                                                                                                                                                            DLNYILLDDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVK 1378
                                                                                                                                                                                                    ------TGSGSTGSTSITSNISN------TSNTSNTIGVITKNGN-VITLT 1508
                                                                                                                                                                                                                                             LDAG----KAKDLIVNSKDKKVVFDITTIGEGQQKVVQISKDILDTSAANGKDIVIKSDN 1564
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                                                                                                                                                                                                                                                                                        1217 INPDNY-----LISKDVT---GATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFT--- 1264
                                                                                                                                                                                                                                                                                                                      SHI--NFEGPONPDNYLV-----TPELSLPGG-----GTLTFWVCAQDANYASEHYAV 1523
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STRAID=KIZ / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NETALINE=9725158; PubMed=9097040; Itch T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Itch T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Itch T., Aiba H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motcomura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Santo N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T., "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map."; DNA Res. 3:379-392(1996).
                                                                                                                                                    1439 KDIBIDVIRQĖNNSGSGTGNN----NTSTSGSNSSS-------
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"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Hypothetical protein yeed.
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NCBI_TaxID=562;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
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2.3%; Score 211; DB 1; Length 2358;
Best Local Similarity 19.3%; Pred. No. 0.0026;
Matches 371; Conservative 212; Mismatches 700; Indels 642;
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232249750BF631BD CRC64;
SIMILARITY: Belongs to the intimin/invasin family.
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EMBL; D90836; BAA15800.1;
EMBL; D90836; BAA15799.1; ALT_INIT.
ECGGENE; EG13779; Veed.
InterPro; IPR003344; Big 1.
InterPro; IPR003535; Intimin.
InterPro; IPR003535; Intimin.
InterPro; IPR003535; Intimin.
InterPro; IPR004804; Invasin_intimin.
InterPro; IPR00601; PKD.
Pfam; PF0236; Big 1; 13.
PKNYRS; PR01369; INTIMIN.
SWART; SM00534; BID 1; 13.
SWART; SM00537; LySM; 1.
SWART; SM00537; LySM; 1.
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12449 155
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1763 1855
1952 205
2358 AA;
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TVTYLGNAFVGNIGDSDTPVASVRFTGSDG-----GAGLQGNIYSQVIDFGTYNLGIS 1119
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        TNPLABINFGSKGAANVDTVLN-----VGKGV-----NLYATNITTTDANVGSFIFNAG 746
                                                                                    GKMWIAGD-GGNQPARYDDFTFEAGKKYTFTMRRAGMGDGTDMEVEDDSPASYTYT---- 890
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                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-layer with hexagonal symmetry (By similarity).
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTS
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
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InterPro; IPR005546; Autotransporter.
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Pfam; PF03797; Autotransporter; 1.
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Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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|        |          | Q51818 porphyromon |        |        | Q92fg5 listeria in | m      | _      | ~      | _      | 8      |        | Q7wn54 bordetella | P74440 synechocyst | Q8gj03 enterococcu | Q8eka6 shewanella | Q8tjs8 methanosarc |        | Q89134 bradyrhizob | н      | 7      | Q55582 synechocyst | Q8tjs9 methanosarc |        |        | _      |        | Q8y8q4 listeria m | Q977v5 methanosarc |  |
|--------|----------|--------------------|--------|--------|--------------------|--------|--------|--------|--------|--------|--------|-------------------|--------------------|--------------------|-------------------|--------------------|--------|--------------------|--------|--------|--------------------|--------------------|--------|--------|--------|--------|-------------------|--------------------|--|
| 033441 | 608X6O   | 051818             | Q8X2T1 | Q8X4H5 | Q92FG5             | Q82YW8 | Q88WI9 | Q89J13 | Q912M3 | Q7UDU8 | Q8TI59 | Q7WN54            | P74440             | 086703             | QBEKA6            | QBTJS8             | QBTPZ1 | Q89L34             | Q9AE52 | Q8TSE7 | Q555B2             | Q8TJS9             | Q7U7J7 | Q88RG2 | 610010 | QBBPP2 | Q8Y8Q4            | Q977V5             |  |
| 2      | 7        | 7                  | 16     | 16     | 16                 | 16     | 16     | 16     | 16     | 16     | 17     | 16                | 16                 | Ŋ                  | 16                | 17                 | 17     | 16                 | ~      | 17     | 16                 | 17                 | 16     | 16     | 16     | 16     | 16                | П                  |  |
| 736    | 293      | 422                | 5291   | 5188   | 1993               | 1744   | 2219   | 4210   | 2468   | 8173   | 1817   | 3346              | 4199               | 1975               | 2522              | 2523               | 3988   | 1861               | 1752   | 2566   | 3029               | 2016               | 2230   | 8682   | 1541   | 6310   | 2044              | 1673               |  |
| 5.9    | 9.<br>6. | 3.7                | 3.5    | 3.4    | 3.4                | 3.4    | 3,3    | •      | 3.3    | •      |        | •                 | •                  | •                  | •                 | 3.5                | 3.1    | 3.1                | 3.1    | 3.1    | 3.1                | 3.1                | 3.1    | 3.0    | 3.0    | 3.0    | 3.0               | 3.0                |  |
| 541    | 354.5    | 4                  | 322    | 315    | 313                | 309    | 306.5  | 303    | 300.5  | 300    | 295.5  | 295.5             | 295.5              | 295                | 294               | 291                | 289    | 285                |        | æ      | 280.5              | 280                | 280    | •      | 278.5  |        | 276.5             | 274.5              |  |
| 17     | 18       | 13                 | 20     | 21     | 22                 | 23     | 24     | 25     | 56     | 27     | 28     | 29                | 30                 | 31                 | 32                | 33                 | 34     | 32                 | 36     | 37     | œ <sup>*</sup>     | 39                 | 40     | 41     | 42     | 43     | 44                | 45                 |  |

## ALIGNMENTS

Created) Last sequence update) Last annotation update)

(TrEMBLrel. 01, TrEMBLrel. 01, TremBLrel. 25,

PRT; 1732 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1441 SWKTIDADGDGNNWTTTPPPPGGSSFAGHNSAICVSSASHINFEGPQNPDNYLVTPELSLP 1500
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                                                                                                                                                                                                                                                                                                                                                         1201 HGGSNVVSSFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNA
NSNGCVYSESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASS
                                 1021 NSNGCVYSESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASS
                                                                                                                                 FYIDLDEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTA
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                                                                                                      TGNDASNFTNALLEETIITAKGVRSPKAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDM
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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EMBL, U75366; AAB60809.1; -.
MEROPS; C25.002; -.
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                                                      AGDGGNQPARYDDFTFEAGKKYTFTMRRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKE
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 25, Last annotation update)
Lysine specific cysteine protease.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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                                                                                                                                                                                                                                                                                                                Score 9167; DB 2; Length 1732;
Pred. No. 0;
3; Mismatches 0; Indels 0
GG; GG:0005524; F:ATP binding; IEA.
GG; GG:0008234; F:Gysteine-type peptidase activity; IEA.
GG; GG:0006310; P:DMA ligase (ATP) activity; IEA.
GG; GG:0006310; P:DMA ligase (ATP) activity; IEA.
GG; GG:0006281; P:DMA repair; IEA.
GG; GG:0006580; P:DMA replication; IEA.
GG; GG:0006580; P:DMA replication; IEA.
InterPro; IPR000977; DNA ligase.
InterPro; IPR001769; Peptidase.C25.
InterPro; IPR001769; Peptidase.C25.
Refam; PF01364; Peptidase.C25.
Refam; PF01386; Peptidase.C25.
Refam; PF01386; Peptidase.C25.
Refam; PF01786; Peptidase.C25.
Refam; PF01786; Peptidase.C25.
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Refam; PF01786; Peptidase.C25.
Refam; PF01786; PARGENERA; AM; 45D5B91377391703 CRC64;
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Best Local Similarity 99.8
Matches 1729; Conservative
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121 MPHQPSMSKSDDPEKVPFAYNAAAYARKGFVGQELTQVEMLGTMRGVRIAALTINPVQYD 180
                                                                                                                                                                                   241 PVRMLVVAGAKFKEALKPWLTWRAQKGFYLDVHYTDEAEVGTTNASIKAFIHKKYNDGLA
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                                                                                     PVRMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYTDEAEVGTTNASIKAFIHKKYNDGLA
                                                                                                                                                                                                                                                                                         301 ASAAPVFLALVGDTDVISGEKGKKTKKVTDLYYSAVDGDYFPEMYTFRMSASSPEELTNI
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                                                     VVANOLKVRNNIEIEVSFOGADEVATORLYDASFSPYFETAYKOLFNRDVYTDHGDLYNT
                                                                                                                                                                                                                                                            ASAAPVFLALVGDTDVISGEKGKKTKKVTDLYYSAVDGDYFPEMYTFRMSASSPEELTNI
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                                                                                                                                                                                                                                                                                                                                                               IDKVLMYEKATMPDKSYLEKVLLIAGADYSWNSQVGQPTIKYGMQYYYNQEHGYTDVYNY
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                                                        1550 TQGGANLTREK------DLPAGTKYVAFRHYNCTDVLGIMIDDVVITGEGEGPSYTYT
                                                                                                                                                                                                                                 IYRNNTQIASGVTETTYRDPDLATGFYTYGVKVVYPNGESAIETATLNITSLADVTAQKP
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                                                                                                                           1552 APEAIRGTRAQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVVIT-SGNAPSYTYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.7%; Score 7774.5; DB 2; Length 1723; 84.9%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria, Bacteroidetes, Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U54691; AAA99810.1;
R GO; GC:0005524; F:ATP binding; IEA.
GO; GO:0008234; F:ATP binding; IEA.
GO; GO:0008234; F:DNA ligase (ATP) activity; IEA.
GO; GO:0006310; P:DNA recombination; IEA.
GO; GO:0006281; P:DNA replication; IEA.
GO; GO:0006281; P:DNA replication; IEA.
GO; GO:0006289; P:DNA replication; IEA.
GO; GO:0006508; P:DNA replication; IEA.
GO; GO:0006508; P:DNA replication; IEA.
GO; GO:0006508; P:DNA replication; IEA.
GO; GO:0006508; P:DNA replication; IEA.
R DITERPO; IPRO0176; DNA ligase.
InterPro; IPRO0176; Peptidase C25.
R InterPro; IPRO016556; Peptidase C25.
R Pfam; PF03184; Peptidase C25.
R Pfam; PF03184; Peptidase C25.
R Pfam; PF03185; Peptidase C25.
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84.7%; Score (1.0.), ---,

Best Local Similarity 84.9%; Pred. No. 0;

Matches 1505; Conservative 60; Mismatches 118; Indels
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SEQUENCE 1723 AA; Î86831 WW; 4508A7E50197CEBD CRC64;
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Last sequence update)
Last annotation update)
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SEQUENCE FROM N.A.
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| FT NON TER 1<br>SQ SEQUENCE 1223 F<br>Query Match<br>Best Local Similarit<br>Matches 1211: Conse | 510 NSX | Db 1 NSYMGED) Qy 570 IGNITHIC                              | 61                                              | Oy 630 ISKDGVL) | Oy 690 SNLTATTO                                                                                                                       | 750                               | Db 241 VWGDNTGY                                                                                                                           | 301                                                               | Oy 870 GMGDGTDN<br>        <br>Db 361 GMGDGTDN                           | 930                                   | Db 421 SPKVCKDV | Oy 990 ENGIPASV<br>        <br>Db 481 ENGIPASV | 1050                                                                                                                                          | Db 541 LDLPNGG                                               | Oy 1110 GRIQGTWI<br>       <br>  Db 601 GRIQGTWI                                                                         | Qy 1170 EAPAEWT |                                                                         | Oy 1230 GATKVKY<br>                 <br>  Db 721 GATKVKY                                                                                                | Qy 1290 AKPQSVW                                                                                            | Db 781 AKPQSVWI                                                                                                                                             | Cy 1350 TXIKEGL                                                                         | 1410                                                                                    | 106                                                                                                          | Qy 1470 SAICVSS/                    |
|--------------------------------------------------------------------------------------------------|---------|------------------------------------------------------------|-------------------------------------------------|-----------------|---------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------|--------------------------------------------------------------------------|---------------------------------------|-----------------|------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------|-----------------|-------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------|-------------------------------------|
| 1261 GDFTVVFBETPNGINKGGARFGLSTBANGAKPOSVWIBRTVDLPAGTKYVAFRHYNCSDL 1320                           |         | 1381 AGVSPKKCVDVTVNSTQENPVQNLTAEQAPNSMDAILKWNAPASKRAE 1428 | 1429VLNEDFENGIPASWKTIDADGDGNNWTTTPPPGGSSFAGHNSA | 1438            | 1497 NLYSANFEYLIPANADPVVTTQNIVTGQGEVVIPGGVYDYCITNPEPASGKM 1549 1522 AVYASSTGNDASNFANALLEFVLTAKTVVTAPRATRGTBAOGTWYOKTVOLPAGTKYV-A 1580 | 1550 WI-AGDGGNQPARYDDFTEEAGKKYTFT | 1581 FRHFGCTDFFWINLDDVVITSGNAPSYTYTIYRNNTQIASGVTETTYRDPDLATGFYTYG 1640 1577 MRRAGMGDGTDMEVEDDSPASYTYTVYRBGTKIKKGLIFFTTYRDAGMSAGSHEYC 1631 | 1641 VKVVYPNGESALETATLNITSLADVTAQKPYTLTVVGKTITVTCQGEAMIYDMNGRELAA | 1632 VEVKYAAGVSPKVCVDYIPDGVADVTAQKPY 1701 GRNTVVYTAQGGHYAVMVVDGKSYVEKLAV | 1692 GRNTVVYTAQGGYYAVMVVVDGKSYVEKLAVK | RESULT 6        | 9ZNBS PRELIMINARY;<br>9ZNBS;                   | 01-MAY-1999 (TrEMBLrel. 10, Created) 10.1-MAY-1999 (TrEMBLrel. 10, Last sequence update) 10.1-MAY-1-990 (TrEMBLrel. 25, Last sequence update) | 30k-HMGD (Fragment).<br>orphyromonas gingivalis (Bacteroides | OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales; OC Porphyromonadaceae; Porphyromonas. OX NCBI_TaxID=837; | STRAINS 81:     | EDLINE=99143166; PubMed=9988746;<br>Libata Y., Hayakawa M., Takiguchi F | <pre>"Determination and characterization of the hemagglutinin-associated short motifs found in Porphyromonas gingivalis multiple gene products.";</pre> | J. Biol. Chem. 274:5012-5020(1999).  RMBL; AB019365; BAB344341.1;  CO. CO. CO. CO. CO. CO. CO. CO. CO. CO. | 3 GO; GO:0008234; F:ORT DINGLING; IEA.<br>3 GO; GO:0008234; F:Cysteine-type peptidase activity; IEA.<br>3 GO; GO:0003910; F:DNA ligase (ATP) activity: IEA. | R GO; GO:0006310; P:DNA recombination; IEA. R GO; GO:0006211; P:DNA recombination; IEA. | CO; CO:0005508; P:proception and peptidolysis; IEA.  A InterPro: IRR000977; DNA licase. | R InterPro; IPR001769; Peptidase C25. R InterPro; IPR00556; Peptidase C25 C. Dram. DF01364. Dartidase C25 C. | PEOSITE; PS00697; DNA_LIGASE_A1; 1. |
| 6 B 6                                                                                            | d<br>d  | \$ g                                                       | δ i                                             | 8 8             | 원<br>6                                                                                                                                | d<br>d                            | \$ A                                                                                                                                      | δ                                                                 | 음 ở                                                                      | d<br>d                                | pr              | (OHA                                           | AAA                                                                                                                                           | 00                                                           | 0001                                                                                                                     | 4,04,04         | A 12                                                                    | ጆጁጁ                                                                                                                                                     | K (1) (                                                                                                    | 100                                                                                                                                                         | ппп                                                                                     | 100                                                                                     | ппс                                                                                                          | 100                                 |

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                               NDASNFANALLEEVLTAKTVVTAPBAIRGTRAQGTWYQKTVQLPAGTKYVAFRHFGCTDF
                                                   FWINLDDVVITSGNAPSYTYTIYRNNTQIASGVTETTYRDPDLATGFYTYGVKVVYPNGE
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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Best Local Similarity
Matches 1171; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kirszbaum L., Sotiropoulos C., Jackson C., Cleal S., Slakeski N., Reynolds B.C.;
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Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
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                                                                                                --GEVGSPEVPAVRKLIAVPVGATPVVRVKS--FTEQVYSLNQYG
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Porphyromonas gingivalis (Bacteroides gingivalis).

Bacteria, Bacteroidetes, Bacteroides (class); Bacteroidales, Porphyromonadaceae, Porphyromonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 QQFVKQEYEKEGND-----LTYVLLVGDHKDIPAKITPGIKSDQV---YGQIVGNDHY 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEMYTFRMSASSPEELTNIIDKVLMYEKATMPDKSYLEKVLLIAGADYSWNSQVGQPTIK 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GQVPTYTEGVNLSEKGMPTLPILSRSLAVSDTREMKVEVVSSKFIEKKNVL----
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LQYNPVTKTLRIYTEITVAVSETSEQGKNILNKKGTFAG----FEDTYKRMF-----MN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEKLMPHQPSMSKSDDPEKVPFVYNAAAYARKGFVGQELTQVEMLGTMRGVRIAALTINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 VQYDVVANQLKVRNNIEI---EVSFQGADEVATQRLYDASFSPYFETAYKQLFNRDVYTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 HGDLYNTPV-----RMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYTDEAEVGTTNASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 HENVIANLLTQYGYTKIIK-----CYDPGVTPKNIIDAFNGGISLVNYTGHGSETÄW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 ADPLLTTSQLKALTNKDKYFLAIGNCCITAQFDYVQPCFGEVITRV----KEKGAYAYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 GTSHFGŤTHVKQÍTNSNQLPFIFDVAČVNGDFLFSMPČFABALMRAQKDGKPTGTVALÍA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    567 AGNI----GNITHIGAHYYWEAYH------VLGDGSVMPYRAMPKTNTYTLPASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 238;
                                                                                                                                                                                                                                                                                                                                                                                                  MATURE 50-KDA CYSTEINE PROTEINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1704;
GINGIPAIN.
1704 AA; 185436 MW; 6A34B40131C2A676 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 46.5%; Score 4270; DB 2; Local Similarity 50.9%; Pred. No. 1.8e-212; Les 932; Conservative 204; Mismatches 456;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 QPSMSKSDDPEKVPFVYNAAAYARKGFVGOELTQVEMLGTMRGVRIAALTINPVQYDVVA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 VPTYTEGVNLSEKGMPTLPILSRSLAVSDTREMKVEVVSSKFIEKKNVL-----IAPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LLIAASLIGVGLYAQSAKIKLDAPTTRTTCTNNSFKQFDASFSFNEVELTKVETKGTFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rangarajan M., Aduse-Opoku J., Slaney J.M., Young K.A., Curtis M.A.; "The prpR1 and the prR2 arginine-specific protease genes of Porphyromonas gingivalis W50 produce five biochemically distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE=96071894; PubMed=7591131;
Aduse-Opoku J., Muir J., Slaney J.M., Rangarajan M., Curtis M.A.;
Aduse-Tization, genetic analysis, and expression of a protease
antigen (PrpRI) of Porphyromonas gingivalis W50.";
Infect. Immun. 63:4744-4754(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1706;
                                                                                                                                                                                                                                                                                                                                                                                                                                Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 23 POTENTIAL.
228 ALPHA-PROTEASE.
720 1262 BETA-ADHESIN.
1706 AA; 185705 MW; 0E56DC087FDA8CDD CRC64;
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GO; GO:000524; F:ATP binding; IEA.

GO; GO:000524; F:ATP binding; IEA.

GO; GO:0008234; F:Styte binding; IEA.

GO; GO:0006310; F:DNA ligase (ATP) activity; IEA.

GO; GO:0006310; F:DNA recombination; IEA.

GO; GO:0006281; P:DNA replir; IEA.

GO; GO:0006280; P:DNA replir; IEA.

GO; GO:0006260; P:DNA replication; IEA.

GO; GO:0006260; P:DNA replication; IEA.

InterPro; IPR001077; DNA ligase.

InterPro; IPR001769; Peptidase C25.

InterPro; IPR001769; Peptidase C25.

InterPro; IPR001769; Peptidase C25.

Ffam; PF01364; Peptidase C25.

Ffam; PF01364; Peptidase C25.

Ffam; PF01364; Peptidase C25.

Ffam; PF01364; Peptidase C25.

Ffam; PF01364; Peptidase C25.

Ffam; PF01364; Peptidase C25.

Ffam; PF01364; Peptidase C25.
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Last annotation update)
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50.8%; Pred. No. 9.7e-212;
Live 206; Mismatches 465;
                                                           1675 NTVVXTAQGGYYAVMVVDGKSYVEKLAVK 1704
                                                                                                                                                                                                                                      Ş
                             1703 NTVVYTAQGGHYAVMVVVDGKSYVEKLAVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Microbiol. 23:0-0(1997).
EMBL; X82680; CAA57997.1; -.
HSSP; P95493; ICVR.
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                                                                                                                                                                                                                                                                                         01-NOV-1996
01-MAY-1997
01-OCT-2003
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es 928;
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Q51838;
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                                                                                         648 KETVIKTINTNGEPNPYQPVSNLTATTQGQKVTLKWDAPSTKTNATTNTARSVDGIRELV
                                                                                                                                                                                                        108 ILSVSDAPELLRSGQAEIVLEAHDVWNDGSGYQILLDADHDQYGQVIPSDTHTLWPNCSV
                                                                                                                                                                                                                                                                                         SSNLYSANFEYLVPANADPVVTTQNIIVTGQGEVVIPGGVXDYCITNPEPASGKMWIAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                         WDAPNGTPNPNPNPNPNPG-TTLSESFENGIPASWKTIDADGDGHGWKPGNAPGIAGYNS
                                                        671 YLPVIKQIQV-GEPSPYQPVSNLTATTQGQKVTLKWEAPSAK---KAEGSREVKRIGDGL
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        VVYPNGESAIETATLNITSLADVTAQKPYTLTVVGKTITVTCQGEAMIYDMNGRRLAAGR 1702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria, Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R GO; GO: 0005524; F:ATP binding; IEA.

R GO; GO: 0005234; F:ATP binding; IEA.

R GO; GO: 0005310; F:DNA ligase (ATP) activity; IEA.

R GO; GO: 0006310; P:DNA recombination; IEA.

R GO; GO: 0006510; P:DNA repair; IEA.

R GO; GO: 0006500; P:DNA replication; IEA.

R GO; GO: 0006500; P:DNA replication; IEA.

R InterPro; IPR0017; DNA ligase.

R InterPro; IPR0017; DNA ligase.

R InterPro; IPR0017; PPDIASe: Peptidase.

R InterPro; IPR0017; PPDIASe: Peptidase.

R Pfam; PF01364; Peptidase.

R Pfam; PF01364; Peptidase.

R Pfam; PF03785; Peptidase.

R Pfam; PF03785; Peptidase.

R Pfam; PF03785; Peptidase.
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"Cloning and characterization of hagE from P. gingivalis submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026549; AAD01810.1; -.
HSSP; P95493; ICVR.
MEROPS; C25.001; -.
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                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
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Best Local Similarity 51.6%; Pred. No. 3.5e-211;
Matches 920; Conservative 197; Mismatches 443;
                                                                                                                     NTVVYTAQGGHYAVMVVVDGKSYVEKLAVK 1732
                                                                                                                                                                      1068 NTVVYTAQGGHYAVMVVVDGKSYVEKLAVK 1097
                                                                                                                                                                                                                                                                                                                   1687
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                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                              46.3%; Score 4249.5; DB 2; Length 1097; llarity 83.2%; Pred. No. 1.1e-211; Conservative 31; Mismatches 44; Indels 91;
                                                                                                                                                                                                                                                                                                                                                                    ---INTGO---
                                                                                                                                                                         1 53 POTENTIAL.
1097 AA; 118731 MW; 73BBA337B421F8B9 CRC64;
                      InterPro; IPR000977; DNA ligase.
InterPro; IPR000531; TonB boxC.
Pfam: PF00593; TonB dep Rec; 1.
PROSTIE; P800697; DNA LIGASE A1; 1.
Membrane; Outer membrane; Receptor; Signal; TonB box.
                                                                                                                                                                      POTENT
GO:0006810; P:transport; IEA
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                                                                 1203 GSNVVSSFSW-NGMA-LNPDNYLISKDVTGATKVKYYYAVND-GFPGDHYAVMISKTGTN
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                                                                                        1394 NSTOFNPVQNLTAEQAPNSMDAILKWNAPASKRAEVLNEDFENG-IPASWKTIDADGDGN
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Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ross B., Barr I., Patterson M., Agius C., Rothel L., Mar
Hocking D., Webb E.;
"P. gingivalis polypeptides and nucleic acids.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical outer membrane protein PG27.
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ROSB B.C.;
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PVRMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYTDEAEVGTTNASIKAFIHKKYNDGLA
                                                                                                                                                               ASAAPVFLALVGDTDVISGEKGKKIKKVTDLYYSAVDGDYFPEMYTFRMSASSPEELTNI
                                                           PVRMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYTDEAEVGTTNASIKAFIHKKYNDGLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ross B.C., Czajkowski L., Hocking D., Margetts M., Webb E., Rothel Patterson M., Agius C., Camuglia S., Reynolds E., Barr I.G.;
"Identification of vaccine candidates from genomic analysis of Porphyromonas gingivalis.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AYO07522, AAG24228.1;
EMBL, AYO0522; ARG42428.1;
EMBL, SWART; SMO060; EN3; I.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Margetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357;
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                                                                                                                                                                                                                                                                                                                                                                             01-MAR.2001 (TrEMBLrel. 16, Created)
01-MAR.2001 (TrEMBLrel. 16, Last sequence update)
01-MAR.2003 (TrEMBLrel. 23, Last annotation update)
Putative outer membrane protein PG57.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%; Score 980.5; DB 2; Length 9 ilarity 28.4%; Pred. No. 2.4e-42; Conservative 109; Mismatches 264; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ross B.C., Barr I., Patterson M., Agius C., Rothel L., M. Hocking D., Webb E.;
"P. gingivalis polypeptides and nucleic acids.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              925 AA; 103632 MW; SFF2198D6914DAE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                   925 AA
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NCBI_TaxID=837;
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STRAIN=W50;
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                                                                                           7;
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                                                                                                                                                                                                                    58 NYLITPELKLPTDALVEIIYWVCTQDLTAPSEHYAVYSSSTGNNAADFVNLLYEETLTAK 117
                                                                                                                                                                                                                                                                                            177 APCPHPGGYTYSVFRDGQKIASGLSALAYIDTDVPYGTQDYCVQVNYLQGDSYKVCKNIV 236
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Best Local Similarity 47.5%; Pred. No. 1.2e-29;
Matches 150; Conservative 49; Mismatches 97; Indels 20; Gaps
EMBL; AF237555; AAF81413.1; -. SEQUENCE 312 AA; 34592 MW; 0D5792C9643A25F5 CRC64;
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Search completed: May 18, 2004, 11:35:11 Job time : 75.1557 secs

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RESULT 1
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1 MRKLLLIIAASLLGVGLYAQ......HYAVMVVVDGKSYVEKLAVK 1732
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1: /ogn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /ogn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /ogn2_6/ptodata/2/iaa/6A_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-06-330-11

US-08-141-324-14

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US-08-36-330-10

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US-08-308-11-29

US-08-490-931-10

US-08-570-311-29

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Maximum Match 100%
Listing first 45 summaries
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Sequence 3, Appli
Sequence 5999, Ap
Sequence 5503, Ap
Sequence 30227, A
Sequence 258, App
Sequence 262, App
Sequence 264, App
Sequence 564, App
Sequence 5434, App
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tumwasorn, Somying
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
CORRESPONDENCE ADDRESS:
                                                                                                                                5486, Ap
33, Appl
                                                                                                                                                                                                               4706, Ap
4, Appli
                                                                                                                                                           4, Appli
33, Appl
                                                                                                                                              Sequence 3
Sequence 4
Sequence 3
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Sequence 1
Sequence 4
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US-09-482-500A-2
US-09-442-500A-3
US-09-134-000C-5999
US-09-232-5991A-30227
US-09-071-035-258
US-09-071-035-258
US-09-071-035-258
US-09-071-035-268
US-09-071-035-268
US-09-33-258-347-36
US-09-328-352-5486
US-09-37-155-33
US-08-913-942-4
US-09-107-532A-4706
US-09-107-532A-4706
US-09-107-532A-4706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Ted W. Whitlock
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 05-DEC-1994
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION: 424
PRIOR APPLICATION: 1426
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INVERER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INVERER: UF15.C3
FELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08570311 Patent No. 5824791 GENERAL INFORMATION:
 492
507
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CITY: Gainesville
STATE: FL
COUNTRY: USA
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US-08-353-485-10
US-08-353-485-10
Sequence 10, Application US/08353485
Fatent No. 5830710
GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: 10 Probes for the Detection of Periodontal Disease
                                                                                                                                                               TLKWDAPNGTPNPNPNPNPNPGTTLSESFENGIPASWKTIDADGDGHGWKPGNAPGIAGY
                                                                               NSNGCVYSES FGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASS
                                                                                                          1021 NSNGCVYSESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASS
                                              961 TLKWDAPNGTPNPNPNPNPNPNPGTTLSESFENGIPASWKTIDADGDGHGWKPGNAPGIAGY
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ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
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LENGTH: 1732 amino acids
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Matches 1732; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                    MEDIUM TYPE: Floppy disk
Comparible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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100.0%; Score 9179;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1732; Conservative 0; Mismatches
                                                                                                                                                                                          PRIOR APPLICATION 1474
PRIOR APPLICATION 1474
PRIOR APPLICATION DATA
PRILICATION NUMBER: US 07/647,119
PRIOR PAPLICATION DATA:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-198
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: 1915.C2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
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COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-09-066-330-11

Sequence 11, Application US/09066330A

Sequence 11, Application US/09066330A

Sequence 11, Application US/09066330A

GENERAL INFORMATION:
APPLICANT: Blakeski, Nada

TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
FILE REFERENCE: Reynolds
CURRENT APPLICATION NUMBER: US/09/066,330A

CURRENT APPLICATION NUMBER: US/09/066,330A

CURRENT APPLICATION NUMBER: PS/05/066,330A

CURRENT APPLICATION NUMBER: PS/05/066,330A

SEALIER FILING DATE: 1995-10-30

BARLIER FILING DATE: 1995-10-30

MUMBER OF SEQ ID NOS: 15

SOFTWARE: PARENT PARENT ON NUMBER: PT/AU96/00673

SEQ ID NO 11

LENGTH: 1732
PVRMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYTDEAEVGTTNASIKAFIHKKYNDGLA
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                                                         1681 TVTCQGEAMIYDMNGRRLAAGRNTVVYTAQGGHYAVMVVVDGKSYVEKLAVK
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                                                                                                                                                                                                                                                                                                                                                                                                                    99.9%; Score 9167; 99.8%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-066-330-11
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 99.9
Best Local Similarity 99.8
Matches 1729; Conservative
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          TGCYSHLNTGVGFANYTAHGSETSWADPSLTATQVKALTNKDKYFLAIGNCCVTAQFDYP 120
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                                                                                                                                   LEDSYNTVNS IMWAGNLAATHAGNI GNI THI GAHYYWEAYHVLGDGSVMPYRAMPKINTY
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1621 GVTETTYRDPDLATGFYTYGVKVVYPNGESAIETATLNITSLADVTAQKPYTLTVVGKTI 1680
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                                                                                                                                                             APPLICANT: Progulske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Lantz, Mariny
APPLICANT: Lantz, Mariny
APPLICANT: Lantz, Mariny
APPLICANT: Lantz, Mariny
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whillow
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                                                      Length 1358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.0%; Score 6151.5;
85.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION 424
PRIOR APPLICATION DATA:
PILING DATE: 25-0AN-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
RAPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
                                                                                                                                                        Sequence 27, Application US/08570311
Patent No. 5824791
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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COUNTRY: US!
ZIP: 32606
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                                            181 VVANQLKVRNNIEIEVSFQGADEVATQRLYDASFSPYFETAYKQLFNRDVYTDHGDLYNT
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APPLICANT: Travis, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
APPLICANT: Pike, Robert N.
TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
TITLE OF INVENTION: Protease
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner, P.C.
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5370 Manhattan Circle, Suite 201
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                      GGTFASVSIPGARPTGEVGSPEVPAVRKLIAVPVGATPVVRVKSFTEQVYSLNQYGSEKL 120
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APPLICANT: Travis, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
APPLICANT: Pike, Robert N.
TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
TITLE OF INVENTION: Protease
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFFERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
FILING DATE: 21-OCT-1993
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08141324
Patent No. 5475097
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NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REBRENCE/DOCKET NUMBER: 44-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
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SEQUENCE CHARACTERISTICS:
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amino acid
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Matches 911; Conservative
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CORRESPONDENCE ADDRESS:
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TOPOLOGY:
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US-08-141-324-14
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APPLICANT: Progulske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Lepine, Guylaine
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: 20 Probes for the Detection of Periodontal Disease
                                                                                                                                                                                                                                                 AGDGGNOPARYDDFTFEAGKKYTFTMRRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKE
                                                                661 NYDVVITRSNYLPVIKQIQVGBPSPYQPVSNLTATTQGQKVTLKWEAPSAKKAEGSREVK
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/570,311
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/353,485
FILING DATE. 09-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08570311
Patent No. 5824791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Whitlock, Ted W. REGISTRATION INDRER: 36,965
REFERENCE/DOCKET UNDRER: UFIS TELECOMMUNICATION INFORMATION: TELEFONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 8:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS ADDRESSE: Ted W. W.
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CLASSIFICATION:
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US-08-570-311-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
52.4%; Score 4811; DB 1; Length 942;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 911; Conservative 17; Mismatches 14; Indels
                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,902
                                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1993
ATTORNEY/AGENT INFORMATION:
ZIF: 00000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OBERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                              INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 942 amino acide
                                                                                                                                                                                                                                                                      NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 942 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-541-902-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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1589 FFWINLDDVVIT-SGNAPSYTYTIYRNNTQIASGVTETTYRDPDLATGFYTYGVKVVYPN 1647
                                                                                           943 VLGIMIDDVVITGEGEGPSYTYTVYRDGTKIQEGLTETTYRDAGMSAQSHEYCVEVKYAA 1002
                                                                                                                                                                       1003 GVSPKVCVDYIPDGVADVTAQKPYTLTVVVGKTITVTCQGBAMIYDMNGRRLAAGRNTVVY 1062
                                                                                                                                           1648 GESAIETATLNITSLADVTAQKPYTLTVVGKTITVTCQGEAMIYDMNGRRLAAGRNTVVY 1707
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              ---DLPAGTKYVAFRHYNCTD 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TURMAGENT, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: Of Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.9%; Score 4673.5; DB 2; Length Best Local Similarity 81.4%; Pred. No. 1e-312; Matches 900; Conservative 56; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/33,485

FILING DATE: 09-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/06/35,485

FILING DATE: 09-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/647,119

FILING DATE: 25-JAN-1991

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/241,640

FILING DATE: 08-28P-1988

ATORNEY AGENT INFORMATION:

NAME: Whilock Ted W.

REFERENCE/POCKET NUMBER: UF15.C2

REFERENCE/POCKET NUMBER: UF15.C2

TELECOMMUNICATION INFORMATION:
         897 GTAAADF-----EVIFEETMTYTQGGANLTREK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Ted W. Whitlock
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                  1708 TAQGGHYAVMVVVDGKSYVEKLAVK 1732
                                                                                                                                                                                                                                                                   1063 TAQGGYYAVWVVDGKSYVEKLAIK 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDIUM TIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 8, Application US/08353485; Patent No. 5830710; GENERAL INFORMATION: APPLICANT: Progulske-Fox, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Progulske-Fox, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1087 amino acids
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Ted W. STREET: 2421 N.W. CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIFWVCAQDANYASEHYAVYASSTGNDASNFTNALLEETITAKGVRSPKAIRGRIQGTWR 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1178 IDADGDGQGWLCLSSGQLDWLTAHGGSNVVSSFSWNGMALNPDNYLISKDVTGATKVKYY 1237
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                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                              638 GTGVANASGVATVSMTKQITENGNYDVVITRSNYLPVIKQIQVGEPSPYQPVSNLTATTQ
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                                                                                                                                                                                                        29; Gaps
                                                                                                                                                              Length 1087;
                                                                                                                                                      50.9%; Score 4673.5; DB 2; Length
81.4%; Pred. No. 1e-312;
.ive 56; Mismatches 120; Indels
                     : 1087 amino acids
amino acid
                                                                                                                                                                              Best Local Similarity of Matches 900; Conservative
SEQUENCE CHARACTERISTICS
                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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US-08-570-311-8
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VQYDVVANQLKVRNNIEI----EVSFQGADEVATQRLYDASFSPYFETAYKQLFNRDVYTD 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 QQFVXQEYEKEGND-----LTYVLLIGDHXDIPAKITPGIKSDQV---YGQIVGNDHY 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 PEMYTFRMSASSPEELTINIIDKVLMYEKATMPDKSYLEKVLLIAGADYSWNSQVGQPTIK 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 NEVFIGRESCESKEDLKTQIDRIIHYERNITTEDKWLGQALCIASAEGGPSADNGESDIQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LLIAASLLGVGLYAQSAKIKLDAPTTRTTCTNNSFKQFDASFSFNEVELTKVETKGGTFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 SVSIPGAFPT-----GEVGSPEVPAVRKLIAVPVGATPVVRVKS--FTEQVYSINQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEKLMPHQPSMSKSDDPEKVPFVYNAAAYARKGFVGQELTQVEMLGTMRGVRIAALTINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GQVPTYTEGVNLSEKGMPTLPILSRSLAVSDTREMKVEVVSSKFIEKKAVL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGDLYNTPV-----RMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYTDEAEVGTTNASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y-GMQXXYNQEHGYIDVYNYLKAPYTGCY-----SHLNTGVSFANYTAHGSETAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTSHFGTTHVKQLTNSNQLPFIFDVACVNGDFLFSMPCFAEALMRAQKDGKPTGTVAIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HENVIANLITQYGYTKIIK-----CYDPGVTPKNIIDAFNGGISLANYTGHGSETAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 ADPLITTSQLKALTNKDKYFLAIGNCCITAQFDYVQPCFGEVITRV----KEKGAYAYIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           567 AGNI----GNITHIGAHYYWEAYH-----VLGDGSVMPYRAMPKTNTYTLPASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSPNSYWGEDYYWSVGANAVFGVQPTFEGTSMGSYDATFLEDSYNTVNSIMMAGNLAATH
                                                                                               APPLICANT: Reynolds, Eric C.
APPLICANT: Bhogal, Peter S.
APPLICANT: Bhogal, Peter S.
APPLICANT: Bhogal, Peter S.
APPLICANT: Bhogal, Peter S.
TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE FILE REFRENCE: Reynolds
CURRENT APPLICATION NUMBER: US/09/066,330A
CURRENT APPLICATION NUMBER: PW 6275
EARLIER APPLICATION NUMBER: PW 6275
EARLIER PILING DATE: 1995-10-30
SARLIER PILING DATE: 1996-10-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
46.5%; Score 4272; DB 4; Length 1706;
Best Local Similarity 50.9%; Pred. No. 8.9e-285;
Matches 932; Conservative 204; Mismatches 456; Indels 240;
                                           Sequence 10, Application US/09066330A Patent No. 6511666 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-066-330-10
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1706
                        US-09-066-330-10
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                                                                            QFLLLDADHNTFGSVIPATGPLFTGTASSNLYSANFEYLVPANADPVVTTQNIIVTGQGEV
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  GOKUTLKWEAPSAKKAEGSREVKRIGDGLFVTIEPANDVRANEAKVVLAADNVWGDNTGY
                             GEEVALKWDIPSAKKAEASREVKRIGDGLFVIIEPANDVRANEAKVVLAADNVWGDNIGY
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                                                                                                                                                                                                 Sequence 10, Application US/08336308A
Patent No. 6017532
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potemps, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
TITLE OF INVENTION: Porphyromonas gingivalis
TITLE OF INVENTION: Arginine-specific Proteinase (NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.5%; Score 4270; DB 3;
llarity 50.9%; Pred. No. 1.2e-284;
Conservative 204; Mismatches 456;
                                                                      1701 GRNTVVYTAQGGHYAVMVVVDGKSYVEKLAVK 1732
                                                                                                         1675 GRNTVVYTAQGGYYAVMVVVDGKSYVEKLAIK 1706
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APPLICATION NUMBER: US/08/336,308A
FILING DATE: 08-NOV-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/119,361
FILING DATE: 10-SEP-1993
FROM APPLICATION DATA:
APPLICATION NUMBER: US 08/265,441
FILING DATE: 24-UN-1994
ATTOCNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE DOCKET NUMBER: 21-9:
TELECOMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8080
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee,
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932; Conserv
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           PQNQASYSIQAS-AGSYVAISKDGVLYGTGVANASGVATVSMTKQITENGNYDVVITRSN
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| Qy 1203 GSNVVSSFSWNGMALNPDNYLISKDVT                          | Oy 1263 FTVVFEETPNGINKGGARFGLSTEANG                                                                                                                                                                | Qy 1323 ILLDDIQFTMGGSPTFTDYTYTVRDG                                     | 1383 VSPKKCVDVTVNST<br>    :  :  :  <br>1363 VSPKECVNVTINPT | Qy 1429VLNEDFENGIPA  Db 1421 TIEPANDVRANEAKVVLAADNVWGDNT          | 1474                                                             | OY 1524 YASSTGNDASNFANALLEEVLTAKTUV  DD 1533 -AGDGGNQPARYDDFTFE            | 1583                                                      | 1643<br>1615                                                                   | Oy 1703 NTVVYTAQGGHYAVMVVDGKSYVBKL<br>                                | RESULT 11<br>US-08-822-324-6<br>; Sequence 6, Application US/08822324                 | ; Patent No. 6129917<br>; GENERAL INFORMATION:<br>; APPLICANT: Potempa, Jan S.<br>; APPLICANT: Travis, James | APPLICANT: GENCO, CATOLINE A. ; TITLE OF INVENTION: IMMUNOGENIC COM ; TITLE OF INVENTION: METHODS ; TITLE OF INVENTION: METHODS | 1800                                                                     | ; CITY: Boulder; STARE: CO CO COUNTRY: US ZIP: 80303                    | ADABLE FORM: PE: Floppy disk IBM PC compatible SYSTEM: PC-DOS/M6           | + 8835                                                                     | ; PICOASSIFICATION: 536 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 60/013,945 ; FILING DATE: 22-MAR-1996 ; ATTORNEY/AGENT INFORMATION: |
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| ò i                                                          | g & 8                                                                                                                                                                                              | yy<br>ag                                                               | oy<br>Dp                                                    | P 64                                                              | Q <sub>y</sub>                                                   | QZ<br>Db                                                                   | QY                                                        | QZ<br>Dp                                                                       | QZ<br>Dp                                                              | SP GG                                                                                 | Qy<br>Db                                                                                                     | QV<br>DP                                                                                                                        | \$ q                                                                     | දු පු                                                                   | & A                                                                        | çy<br>Dp                                                                   | Qy<br>Db                                                                                                                                       |

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                                             SSNLYSANFEYLVPANADPVVTTQNIIVTGQGEVVIPGGVYDYCITNPEPASGKMWIAGD
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; Sequence 10, Application US/09490931
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                                                                                                                                                                                                                       46.5%; Score 4270; DB 3; Length 1704; 50.9%; Pred. No. 1.2e-284; rive 204; Mismatches 456; Indels 238
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 103-95 WO
TELECOMMUNICATION INFORMATION:
TELEPRAX: (303) 498-8080
TELEPRAX: (303) 499-8089
INFORMATION FOR SEQ ID NO. 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Alman acids
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Matches 932; Conserv
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                    APPLICANT: Forempa, Jam S.
APPLICANT: Barr, Philip J.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Madine
TITLE OF INVENTION: Prophyromonas gingivalis
TITLE OF SEQUENCES: 16
CORRESPONDENCES 16
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
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46.5%; Score 4270; DB 3; Length 1704;
Best Local Similarity 50.9%; Pred. No. 1.2e-284;
Matches 932; Conservative 204; Mismatches 456; Indels 238
                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                       3: Greenlee, Winner and Sullivan, 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/490,931
                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/336,308
FILING DATE:
                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
3Y: linear
                                                                                                                                        Colorado
: US
GENERAL INFORMATION:
APPLICANT: Travis
                                                                                                                            CITY: Boulder
STATE: Colorado
COUNTRY: US
                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                              80303
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                                                                                                                                                                                                 393 HENVIANLLTQYGYTKIIK-----CYDPGVTPKNIIDAFNGGISLVNYTCHGSETAW
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90 FIEKKUVL-----IAPSKGMIMRNEDPFKKIPYVY-GKSYSQNKFFPGEIATLDDFFIL 141
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                                                                                                                                                                                                                                                                                                                                             47 FSFNEVELTKVETKGGTFASVSIPGAFPTGEVGSPEVPAVRKLIAVPVGATPVVRVKS--
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                                                                                                                                                                                                                                                          Ouery Match
46.2%; Score 4245; DB 2; Length 1687;
Best Local Similarity 51.6%; Pred. No. 6.3e-283;
Matches 920; Conservative 197; Mismatches 443; Indels 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 474 DGKPTGTVALIASTINQSW------ASPMRG-
          UF15.C3
                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO. 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                 LENGTH: 1687 amino acids
          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                             linear
                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                              1474 VSSASHINFEG--PQNPD-----NYLVT--PELSLPGGGTLTFWVCAQDANYASEHYAV 1523
                                                                                                                                                                                          1533 - AGDGGNQPARYDDFTFE-------AGKKYTFTMK 1559
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                                                                                 ----VLNEDFENGIPASWKTIDADGDGNNWTTTPPPGGSSFAGHNSAIC 1473
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APPLICANT: Progulske-Fox, Ann
APPLICANT: Turmwascrn. Somying
APPLICANT: Turmwascrn. Somying
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
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APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                    1643 VVYPNGESAIETATLNITSLADVTAQKPYTLTVVGKTITVTCQGEAMIYDMNGRRLAAGR
                                                                                                                                                                                                                                                   1524 YASSTGNDASNFANALLEEVLTAKTVVTAPEAIRGTRAQGTWYQKTVQLPAGTKYV-AFR
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VSPKKCVDVTVNSTQFNPVQNLTAEQAPNSMDAILKWNAPASKRAE
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PRICR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDER: US 08/353,485
FILING DATE: 09-DEC-1994
PRIOR APPLICATION HAS:
APPLICATION: 424
PRIOR APPLICATION: 25-CAN-1991
CLIASSIFICATION: 25-CAN-1991
CLIASSIFICATION: 244
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTONEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
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APPLICATION NUMBER: US/08/570,311
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 29, Application US/08570311; Patent No. 5824791
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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US-08-570-311-29
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DBC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-OAN-1991
CLASSIFICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERRNCE/DOCKET NUMBER: UFIS.C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2628 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-570-311-14
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ZIP: 326
                                                                                                                           CITY:
STATE:
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972 WKPGNAPGIAGYNSNGCVYSESFGLGGIGVLIPDNYLITPALDLPNGGKLTFWVCAQDAN
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967 ESFENGIDASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSAS------YINF 1017
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APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
NUMBER OF SEQUENCES: 29
ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 YDVVANQLKVRNNIEIEVSFQ-----GADEVATQRLYDASFSPYFETAYKQLFNRDVYT 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---AAPVFLALVGDTDVISGEKGKKTKKVTDLYYSAV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHGDLYNTPVRMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYTDEAEVGTTNASIKAFIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           922 --DPVQFNPVQNLTGSAVGQKVTLK----WDAPNG---TPNPNPNPNPNPGTTTLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         419 -NYLKAPYTGCYSHLNTGVSFANYT---AHGSETAWADPLLTTSQLKALTNKDKYFLAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VL------LIAG--ADYSWNSQVGQPTIKYGMQYYNQEHGYTDVY-
                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
45.9%; Score 4217; DB 2;
Best Local Similarity 51.0%; Pred. No. 1.1e-280;
Matches 958; Conservative 114; Mismatches 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>..</del>
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| QY         1296 WIERTVDLPAGTKXVAFRHYNGSDLNYILLDDIQFTMGGSPTPTDYTYTVYRDGTKIKEG         1355           Db         2192 WIERTVDLPAGTKXVAFRHYNGSDLNYILLDDIQFTMGGSPTPTDYTYTVYRDGTKIKEG         2251           QY         1356 LIETTFEEDGVATGNHFYCVEVKYTAGVSFKKCVDVTVNSTQFNPVQNLTAEQAPNSMDA         1415           Db         2252 LIETTFEEDGVATGNHFYCVEVKYTAGVSFKCVNVTINFTQFNPVQNLTAEQAPNSMDA         2311           QY         1416 LIEKWNAPASKRAEVLANEDFENGIPASWKTIDADGDGNNWTTTPPPGGSSFAGHNSALCVS         1475           Db         2312 LIEKWNAPASKRAEVLANEDFENGIPASWKTIDADGDGNNWTTTPPPGGSSFAGHNSALCVS         1475           Db         2312 LIEKWNAPASKRAEVLANEDFENGIPSSWKTIDADGDGGNNWTTTPPPFGGSSFAGHNSALCVS         2371 | QY         1476 SASHINFEGPONPDNYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF 1535           Db         2372 SASYINFEGPONPDNYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF 2431           QY         1536 ANALLEEVLTAKTVVTAPEAIRGTRAQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD 1595           Db         2432 ANALLEEVLTAKTVVTAPEAIRGTRAQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD 2491           QY         1596 DVVITSGNAPSYTYTIYRNNTQIASGYTETTYRDPDIATGFYTYGVKVVYPNGESAIETA 1655 | 1656<br>2552<br>1716<br>2612<br>SULT 15                                        | US-09-482-500A-1    Sequence I. Application US/09482500A   Patent No. 6627193     Patent No. 6627193     GENERAL INFORMATION:   APPLICANT: Travis, James     APPLICANT: Travis, James     APPLICANT: Potempa, Jan     TILLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION     FILE REFERENCE: 235.00160101     CURRENT FILING DATE: 2001-12-17     PRIOR APPLICATION NUMBER: US 60/115,869     PRIOR PILING DATE: 1999-01-13     NUMBER OF SEQ ID NOS: 4 | SECTIMES   Patentin version 3.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Db 1136 ANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGMLCLSSGQLGWLTAHG 1186  QY 475 NCCITAQFDYVQPCFGEVITRVKEKGAYAXIGSSPNSYWGEDYYWSVGANAV 526  1187 GTNVVASFSWNGMAINPDNYLISKDYTGATKVKYYYAVNDGPPGDH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | VAISKDGVLYGTGVANASGVATVSMTKQITENGNYDVVITRSNYLPVIKQIQVG :                                                                                                                                                                                                                                                                                                                                                                                                          | 1417 GITTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASY-INFEG 1475 794YLVP | WNGM IMGIN TMGG VTVE                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 941 GSNEFAPVONLTGSSVGGKVTLKWDAPNGTPNPNPNPNPGTTLSESFENGIPASWKTI 1000  1835 -PUGFNPUQNLTGSAVGGKVTLKWDAPNGTPNPNPNPNPNPGTTLSESFENGIPASWKTI 1892  1001 DADGDGGHGWKPGNAPGLAGYNSNGCVYSESFGLGGIGVLTPDNYLLTPALDLPNGGK 1057  1893 DADGDGNNWTTPPPEGGTSFAGHNSALCVSSASY-INFEGPQNFDNYLLYTPELSLPGGGT 1951  1058 LTFWYCAQDANYASEHYAVYASSTGNDASNFTNALLEETITAKG-VRSPKAIRG-RIQGT 1115  1058 LTFWYCAQDANYASEHYAVYASSTGNDASNFTNALLEETITAKG-VRSPKAIRG-RIQGT 1011  1116 WRQKTVOLPAGTKYVAFRHFQSTDMFYI DLDEVEIKANGKRADFTETFESSTHGEAPAEW 1175  2012 WYQKTVOLPAGTKXVAFRHFGSTDMFYI DLDEVEIKANGKRADFTETFESSTHGEAPAEW 2071  1176 TTIDADGDGGGWLCLSSGQLDWLTAHGGSNVVSSFSWNGMALNPDNYLISKDVTGATKVK 1235  2072 TTIDADGDGGGWLCLSSGQLDWLTAHGGTNVVASFSWNGMALNPDNYLISKDVTGATKVK 2131  1236 YYYAVNDGFPGDHYAVWISKTGTNAGDFTVVFEETPNGINKGGARFGLSTEANGAKPQSV 1295  2132 YYYAVNDGFPGDHYAVWISKTGTNAGDFTVVFEETPNGINKGGARFGLSTEADGAKPQSV 2191 |

| q <b>Q</b>                                                   | Qy<br>Dp                                                             | Qy                                                                 | දුරු පු             | Qy<br>Gp                                                     | λõ  | qq                                                                    | Search<br>Job tin                                                                         |                                                                     |                                                                   |                                                                        |                                                                   |                                                                          |                                                                          |                                                                            |                                                                            |                                                                           |                                                                            |                                                                            |                                                                            |                                                 |                                                        |
|--------------------------------------------------------------|----------------------------------------------------------------------|--------------------------------------------------------------------|---------------------|--------------------------------------------------------------|-----|-----------------------------------------------------------------------|-------------------------------------------------------------------------------------------|---------------------------------------------------------------------|-------------------------------------------------------------------|------------------------------------------------------------------------|-------------------------------------------------------------------|--------------------------------------------------------------------------|--------------------------------------------------------------------------|----------------------------------------------------------------------------|----------------------------------------------------------------------------|---------------------------------------------------------------------------|----------------------------------------------------------------------------|----------------------------------------------------------------------------|----------------------------------------------------------------------------|-------------------------------------------------|--------------------------------------------------------|
| 172 NLLTQYGYTKIIKCYDPGVTPKNIIDAFNGGISLVNYTGHGSBTAWGTSHFG 223 | 457 TSOLKALTNKDKYFLAIGNCCITAQFDYVQPCFGEVITRVKEKGAYAYIGSSPNSY 512   : | 513 WGEDYYWSVGANAVFGVQPTFEGTSMGSYDATFLEDSYNTVNSIMWAGNLAATHAGNI 570 | MPKTNTYTLPASLPQNQAS | YSIQAS-AGSYVAISKDGVLYGTGVANASGVATVSMTKQITENGNYDVVITRSNYLPVIK | 42  | 0// Q10VCERSEYQUEVSNLIATIQQQKVTIKWEABSAKKAEGSREVKRIGDGLEVTIEP 732<br> | 733 AND-VRANBAKVVLAADNVWGDNTGYQFLLDADHNTFGSVIPA-TGPLFTG-TASSNLYS 789   : : ::     :     : | 790 ANFEXLVPANADPVVTTQNIIVTGQGEVVIPGGVYDYCITNPEPASGKWWIAGDGNQPA 849 | 546 APFBYTVPENADPSCSPTNMIMDGTASVNIPAGTYDFAIAAPQ-ANAKIWIAGQGPT 601 | 850 RYDDFTFEAGKKYTFTWRRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEE 909 - | ABLULY VERMARATIE LIMKAMGSGDGTELTISEGGGGSDYTYTVYRDGTKIKEGLTATTFEE | 910 DSVAAGNHEICVEVKYTAGVSEKVCKOVTVEGSNEFARVQNLTGSSVGGKVTLKWDAPNG 969<br> | 970 TPNPNPNPNPRG-TILSESFENGIPASWKIIDADGDGHGWKPGNAPGIAGYNSNGCVYS 1028<br> | 1029 ESFCLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASNF 1088<br> | 1089 TNALLEETITAKGVRSPKAIRGRIGGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEV 1148<br> | 1149 EIKANGKRADFTETFESSTHGEADAEWTTIDADGDGGWLCLSSGGLDWLTAHGGSNVVS 1208<br> | 1209 SFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFE 1268<br> | 1269 ETPNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDI 1328<br> | 1329 QFTWGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKKC 1388<br> | 1389   VDVTVNSTQFNPVQNLTAEQAPNSMDAILKWNAPASKRAE | VINEDFENGIPASWKTIDADGDGNNWTTPPPGGSSFAGHNSAICVSSASH 147 |
| qa                                                           | Qy<br>Db                                                             | oy<br>Oy                                                           | Qy                  | දු දු                                                        | g A | e d                                                                   | Qy<br>Dp                                                                                  | <i>\</i> 5                                                          | Db                                                                | දු දු                                                                  | 3 6                                                               | o q                                                                      | Qy<br>Db                                                                 | Oy 1<br>Db                                                                 | Qy 1<br>Db                                                                 | Oy 1<br>Db                                                                | Qy 1<br>Db                                                                 | Qy 1<br>Db 1                                                               | Oy 1<br>Db 1                                                               | Qy 1<br>Db 1                                    | 24                                                     |

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Qy 1480 INPEG--PQNPD-----NYLVT--PELSLPGGGTLTFWVCAQDANYASEHYAVYASSTG 1529

Db 1256 -NFEYLIPANADPVVTTQNIIVTGQGEVVIPGG---VYDYCITNPEPASGRWMI-AGDGG 1310

Qy 1530 NDASNFANALLEEVLTAKTVVTAPEAIRGTRAQCTWYQKTVQLPAGTKYV-AFRHFGCTD 1588

Db 13311 NQPARYDDFTFE-----------------AGKKYTFTWRRAAMGD 1338

Qy 1589 FFWINLDDVVITSGNAPSYTYTIYRNWTQIASGVTETTYRDPDLATGFYTYGVKVVYPNG 1648

Db 1339 G----TDMEVEDDSPASYTYTIYRNWTQIASGVTETTYRDPDLATGFYTYGVKVVYPNG 1649

DD 1339 G----TDMEVEDDSPASYTYTIYRNWTQIASGVTETTYRDAGSSTEYCVEKKYAG 1393

Qy 1649 ESAIETATINITSLAVAQKPYTLTVVGKTITVTCQGEAMIYDMNGRRLAAGRNTVVYT 1453

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(without alignments)
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9179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1145568
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1145568 seqs, 278261457 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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/cgn2_6/₁
                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                   | Sequence 11, Appl | Sequence 10, Appl |                 | · ~             | 9               | 105               | Segmence 100. App |                 | Sequence 99. App. | Sequence 56997. A    | Sequence 47453. A    | Semence 66335 A      | Segmence 4. Appli | Sequence 258, App |
|-------------------------------|-------------------|-------------------|-----------------|-----------------|-----------------|-------------------|-------------------|-----------------|-------------------|----------------------|----------------------|----------------------|-------------------|-------------------|
| SUMMARIES                     | US-10-229-066-11  | US-10-387-988-10  | US-10-174-695-5 | US-10-174-695-3 | US-10-174-695-6 | US-10-387-977-105 | US-10-387-977-100 | US-10-174-695-4 | US-10-387-977-99  | US-10-282-122A-56997 | US-10-282-122A-47453 | US-10-282-122A-66335 | US-10-246-330-4   | US-10-206-576-258 |
|                               | 14                | 12                | 15              | 15              | 15              | 15                | 15                | 15              | 15                | 12                   | 12                   | 12                   | 14                | 12                |
| %<br>Query<br>Match Length DB | 1732              | 805               | 419             | 419             | 231             | 736               | 491               | 196             | 507               | 1728                 | 2435                 | 2468                 | 2468              | 1638              |
| %<br>Query<br>Match           | 99.66             | 29.4              | 24.6            | 19.3            | 13.5            | 5.9               | 5.7               | 5.7             | 4.5               | 3.4                  | 3.3                  | 3.3                  | 3.3               | 3.2               |
| Score                         | 9167              | 2702              | 2254            | 1776            | 1241            | 541               | 527.5             | 521.5           | 410.5             | 309                  | 303.5                | 300.5                | 300.5             | 293               |
| Result<br>No.                 | 40                | ı m               | 4               | S               | φ               | 7                 | 80                | σ               | 10                | 11                   | 12                   | 13                   | 14                | 15                |

| 262,  | Seguence 256, App | 22616              |      |           |      | Sequence 68, Appl | Sequence 18460, A   | Sequence 33, Appl | Sequence 61210, A    |                      |      |       |      |       |      | Sequence 55546, A |                  | Sequence 909, App |       |      |        |      |      | 4490                 | 4656  | 253, A |                      |                      |
|-------|-------------------|--------------------|------|-----------|------|-------------------|---------------------|-------------------|----------------------|----------------------|------|-------|------|-------|------|-------------------|------------------|-------------------|-------|------|--------|------|------|----------------------|-------|--------|----------------------|----------------------|
| US-10 |                   | US-10-369-493-2261 | US-1 | US-10-282 |      | US-09-971-536-68  | US-10-369-493-18460 | US-09-797-862-33  | US-10-282-122A-61210 | US-10-282-122A-53633 | US-1 |       | US-1 | US-1  |      |                   | US-09-759-508B-2 | ns-               |       | us-  |        | US-  | US-  | US-10-282-122A-44901 | us-   | US-10  | US-10-282-122A-43730 | US-10-282-122A-59042 |
| 122   | 7 7               | 15                 | 15   | 12        | 12   | σ'n               | 15                  | σı                | 12                   | 12                   | 12   | 12    | 12   | 12    | 12   | 12                | σ                | 14                | 12    | 10   | 12     | 14   | 15   | 12                   | 12    | 14     | 12                   | 12                   |
| 1638  | 6310              | 1283               | 4327 | 1325      | 3930 | 1741              | 1649                | 2353              | 3217                 | 1751                 | 1308 | 1483  | 3705 | 2457  | 5559 | 1333              | 26926            | 1521              | 1920  | 1541 | 1541   | 1541 | 4283 | 1289                 | 2234  | 1539   | 1953                 | 2902                 |
| 3.5   | 9 O.              | 2.9                | 2.8  | 2.7       | 2.7  | 5.6               | 5.6                 | 5.6               | 5.6                  | 2.5                  | 2.5  | 2.5   | 2.5  | 2.5   | 2.5  | 2.5               | 2.5              | 2.4               | 2.4   | 2.4  | 2.4    | 2.4  | 2.4  | 2.4                  | 2.4   | 2.4    | 2.4                  | 2.4                  |
| 293   | 278.5             | 264                | 257  | 247.5     | 247  | 239               | 238                 | 237.5             | 237.5                | 232.5                | 231  | 229.5 | 227  | 226.5 | 226  | 225.5             | 225              | 224               | 223.5 | 223  | 223    | 223  | 223  | 222.5                | 221.5 | $\sim$ |                      | 219                  |
| 16    | 18                | 19                 | 20   | 21        | 22   | 23                | 24                  | 25                | 26                   | 27                   | 28   | 29    | 30   | 31    | 32   | 33                | 34               | 35                | 36    | 3.7  | e<br>e | 39   | 40   | 41                   | 42    | 43     | 44                   | 45                   |

## ALIGNMENTS

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Sequence 11, Application US/10229066
Publication No. US20030157637A1
GENERAL INFORMATION;
GENERAL INFORMATION;
APPLICANT: Reynolds, Eric C.
APPLICANT: Reynolds, Peter S.
APPLICANT: Blogal, Peter S.
APPLICANT: Blogal, Peter S.
APPLICANT: Blogal, Peter S.
APPLICANT: Blogal, Peter S.
APPLICANT: Blogal, Peter S.
APPLICANTON: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
FILE REFERENCE: Reynolds
CURRENT APPLICATION NUMBER: US/09/066,330
PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1996-10-30
PRIOR FILING DATE: 1996-10-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATCHTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRKLLLLIAASLLGVGLYAQSAKIKLDAPTTRTTCTNNSFKQFDASFSFNEVELTKVETK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.9%; Score 9167; Di
99.8%; Pred. No. 0;
cive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.84
Matches 1729; Conservative
                                                                                                                                                                                                                                                                                                                                                                      1732
                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-229-066-11
                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 11
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| Publication No US20030157637A1
| GENERAL INFORMATION:
| APPLICANT: Bhogal, Fate C. | APPLICANT: Bhogal, Fate C. | APPLICANT: Bhogal, Fate C. | APPLICANT: Bhogal, Fate C. | APPLICANT: Bhogal, Fate S. | APPLICANT: Bhogal, Fate S. | APPLICANT: Bhogal, Fate S. | APPLICANT: Bhogal, Fate S. | APPLICANT: Slakeski, Mada | TITLE OF INVENTION: UNMERR: US/10/229,066 | FILE REFERENCE: Reynolds | FILE REFERENCE: Reynolds | FILE REPRICATION NUMBER: US/09/066,330 | FRIOR APPLICATION NUMBER: US/09/066,330 | FRIOR FILING DATE: 1998-09-15 | FRIOR APPLICATION NUMBER: POT/AU96/00673 | FRIOR FILING DATE: 1995-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-30 | FRIOR FILING DATE: 1996-10-
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Matches 932; Conservative 204; Mismatches 456;
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| QY 1141 FYIDLDEVEIKANGKRADFTETFESSTHGEAPAEW DD 1123 FYIDLDEVEIKANGKRADFTETFESSTHGEAFAEW | Qy 1201 HGGSNVVSSFSWNGMALNPDNYLISKDVTGATKVK               | OY 1261 GDFTVVFEETPNGINKGGARFGLSTEANGAKPOSV DD 1243 GDFTVVFEETPNGINKGGARFGLSTEADGAKFOSV | Oy 1321 NYILLDDIQFTMGGSPTPTDYTYTVYRDGTKIKBG | Qy 1381 AGVSPKKCVDVTVNSTQFNPVQNLTAEQAFNSMDA Db 1363 AGVSPKKCVNVTVNSTQFNPVKNLKAQPDGGDV | QY 1429VLNEDFENGIPASWKTID. | .0y 1472 ICVSSASHINFBGPONPDNYLVTPE:                      | QY 1522 AVYASSTGNDASNFANALLEEVLTAKTVVTAPEAI)          : :   Db 1533 WI-AGDGGNQPARYDDFTFE | QY 1581 FRHFGCTDFFWINLDDVVITSGNAPSYTYTIYRNN:     | QY 1641 VKVVYPNGESAIETATLNITSLADVTAQKPYTLTVV                        | Qy 1701 GRNTVVYTAQGGHYAVMVVVDGKSYVEKLAVK 177  Db 1675 GRNTVVYTAQGGYXAVWVVDGKSYVEKLAIK 17 | RESULT 3<br>US-10-387-977-101<br>; Sequence 101, Application US/10387977 | Publication No. US20040005276Al GENERAL INFORMATION: APPLICANT: Reynolds, Eric Charles APPLICANT: O'Brien-Simpson, Neil Martin | // APPLICANT: SIAKESKI, Nada i TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCT i TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF i TITLE OF INVENTION: PORPHYROMONAS GINGIYALIS | FILE REFERENCE: 52928200301 CURRENT APPLICATION NUMBER: US/10/387,977 CURRENT FILING DATE: 2003-07-18 PRIOR APPLICATION NUMBER: US 09/423,056 | /AU98/003<br>?O 6528                                              | HION FILING DATE: 1997-44-30 NUMBER OF SEQ ID NOS: 105 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 101 | ; LENGIH: 509<br>; TYPE: PRT<br>; ORGANISM: Porphyromonas gingivalis<br>US-10-387-977-101 |
|-----------------------------------------------------------------------------------------|-----------------------------------------------------------|-----------------------------------------------------------------------------------------|---------------------------------------------|---------------------------------------------------------------------------------------|----------------------------|----------------------------------------------------------|------------------------------------------------------------------------------------------|--------------------------------------------------|---------------------------------------------------------------------|------------------------------------------------------------------------------------------|--------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------|
| 117 SEKLMPHQPSMSKSDDPEKVPFVKNAAAXARKGFVGQELTQVEMLGTWRGVRIAALTINP 176                    | VQYDVVANQLKVRNNIEIEVSFQGADEVATQRLYDASFSFYFETAYKQLFNRDVYTD | AKEKEALKPWLTWKAQKGFYLDVHYTDBABVGTTNASI  : :                                             |                                             |                                                                                       |                            | ADPLITTSQLKALTNKDKYFLAIGNCCITAQFDYVQPCFGEVITRVKEKGAYAYIG | 507 SSPNSYMGEDYYMSVGANAVFGVQPTFEGTSMGSYDATFLEDSYNTVNSIMWAGNLAATH 566                     | AGNIGNITHIGAHYYWEAYHVLGDGSVMPYRAMPKTNTYTLPASL 61 | DGVLYGTGVANASGVATVSMTKQITENGNYDVVITESN :  :: :         ::        :: |                                                                                          | 727 FVTIEBAND-VRANBAKVVIAADNVWGDNTGYQELLDADHNTFGSVIPA-TGPLFTG-TA 783<br> | 784 SSNLYSANFEYLVPANADPVVTTONIVTGQGEVVIPGGVYDYCITNPEPASGKOMIAGD 843<br>                                                        | 844 GGNQPARYDDFTFEAGKKYTFTMRRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLT 903     :     :                   :                                                                           | 904 ATTFEEDGVAAGNHEYCVBVKYTAGVSPKVCKDVTVEGSNEFAPVQNLIGSSVGQKVTLK 963<br>                                                                      | 964 WDAPNGTPNPNPNPNPRGTTLSESFENGIPASWKTIDADGDGHGWKPGNAPGIAGY 1020 | 1021 NSNGCVYSESFCLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASS 1080<br>                                     | 1081 IGNDASNFTNALLEETITAKGYRSPKAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDM 1140<br>                |
| \( \frac{1}{2} \)                                                                       | QY                                                        | Sy<br>B                                                                                 | oy<br>G                                     | Oy<br>Ob                                                                              | Qy<br>Dp                   | op 63                                                    | ζ, dg                                                                                    | oy<br>Pp                                         | & g                                                                 | DP 54                                                                                    | <i>₹</i>                                                                 | oy<br>G                                                                                                                        | oy<br>Og                                                                                                                                                                       | S S                                                                                                                                           | & 8                                                               | PP ON                                                                                                          | Qy<br>Dp                                                                                  |

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                                                                                                                                BGLTETTFEEDGVATGNHEYCVEVKYT 1380
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DVVLKWEAPSAKKTEGSREVKRIGDGL 1420
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                                                                                                                                                                                                                                     L-LDADHNTFGSVIPATGPLFTGTASS 1479
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                                                                                                                                                                                                                                                                                                             IRGTRAQGTWYQKTVQLPAGTKYV-A 1580
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                                                                                                                                                                               241 NPNPGTTLSESFENGIPASWKTIDADGDGHGWKPGNAPGIAGYNSNGCVYSESFGLGGIG 300
                                                                   61 ANADEVUTTQNIIVTGQGEVVIPGGUYDYCITNPEPASGROWIAGDGGUQPARYDDFTFE 120
                                                                                                                                                                                                                                                           918 EYCVEVKYTAGVSPKVCKDVTVEGSNEFAPVQNLTGSSVGQKVTLKWDAPNGTPNPPNP 977
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                                198 ANADPVVTTQNIIVTGQGEVVIPGGVYDYCITNPEPASGYMIAGDGGNQPARYDDFTFE
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APPLICANT: Slakeski, Nada
APPLICANT: Chen Clao Guang
APPLICANT: Chen, Clao Guang
APPLICANT: Chen, Clao Guang
APPLICANT: Brit, Ian George
ITILE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REPERENCE: 529242000700700
FILE REPERENCE: 229242000700700
FILE REPERENCE: 229242000700700
FILE REPERENCE: 22000-106-18
FRICH APPLICATION NUMBER: DCT/AU00/01588
FRICH FILING DATE: 2000-12-21
FRICH FILING DATE: 1999-12-24
FRICH FILING DATE: 1999-12-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10174695
Publication No. US20030232022A1
GENERAL INFORMATION:
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Best Local Similarity
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ORGANISM:
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SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                    MSASSPEELTNIIDKVLMYEKATMPDKSYLEKVLLIAGADYSWNSQVGQPTIKYGMQYYY 408
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                                                                                                         DVYTDHGDLYNTPVRMLVVAGAKFKEALKPWLTWKAQKGFYLDVHYTDEAEVGTTNASIK
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  Length 509;
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| Publication No. US2003023202A1
| GENERAL INFORMATION:
| APPLICANT: Reviolds, Eric Charles
| APPLICANT: Glakeski, Nada
| APPLICANT: Chen, Cheo Guang
| APPLICANT: Chen, Cheo George
| TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
| TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
| CURRENT APPLICATION NUMBER: US/10/174,695
| CURRENT APPLICATION NUMBER: WET/AU0/01588
| PRIOR FILING DATE: 2000-12-21
| PRIOR FILING DATE: 2000-12-21
| PRIOR FILING DATE: 1999-12-24
| NUMBER OF SEQ ID NOS: 8
| SEGIFFARE: FastSEQ for Windows Version 4.0
                                                          Indels
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Score 2702; DB 15;
Pred. No. 6.3e-199;
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Pred. No. 1.4e-164;
1; Mismatches 0;
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                                                       Mismatches
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29.4%; Score 2702;
100.0%; Pred. No. 6
ive 0; Mismatches
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US-10-174-695-5
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99.8%;
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Best Local Similarity 99.8³
Matches 418; Conservative
                                                       Conservative
                          Similarity
                          Best Local Sim
Matches 509;
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  Query Match
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62 GTFASVSIPGAFPTGEVGSPEVPAVRKLIAVPVGATPVVRVKS--FTEQVYSLNQYGSEK 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 KY----NDGLAASAAPVFLALVGDTDVISGE--KGKKTKKVTDLYYSAVDGDYFPEMYTF 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 RMSASSPEELTNIIDKVIMYEKATMPDKSYLEKVILLIAGADYSWNSQVGQPTIKY-GMQY 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 DVVANQLKVRNNIEIEVSFQGADEVATORLYDASFSPYFETAYKOLFNRDVYTDHGDLYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 GVAQVPTFTEGVNISEKGTPILPILSRSLAVSETRAMKVEVVSSKFIEKKDVL-
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ilarity 25.1%; Pred. No. 3.2e-32;
Conservative 130; Mismatches 328;
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CURRENT FILING DATE: 2003-07-16
PRIOR PELLOR TOWNER: US 09/423,056
PRIOR APPLICATION NUMBER: US (20/423,056
PRIOR APPLICATION NUMBER: ECT/AU98/00311
PRIOR PELLING DATE: 1998-04-30
PRIOR PILLING DATE: 1998-04-30
PRIOR PILLING DATE: 1997-04-30
PRIOR PILLING DATE: 1997-04-30
PRIOR FILLING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                             Porphyromonas gingivalis
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Best Local Similarity
Matches 200; Conser
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US-10-387-977-105
                                                                                                                                                                                                                                       SEQ ID NO 105
LENGTH: 736
                                                                                                                                                                                                                                                                                       TYPE: PRT
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Publication No. US20040005276A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric Charles
APPLICANT: Slakeski, Nada
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TERATMENT OF PERIODONITIES ASSOCIATED WITH
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
FILE REFERENCE: 529282000301
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236 NPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPGIAGYNSNGCVYSESFG 295
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                                             LGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASNFTNAL
                                                                                                                                      LEETITAKGVRSPKAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKA
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99.6%; Pred. No. 5.5e-87;
tive 1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Reynolds, Eric Charles
APPLICANT: Slakeski, Nada
APPLICANT: Slakeski, Nada
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
APPLICANT: Barr, Ian George
TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REPRENCE: 5.29282000700
CURRENT APPLICATION NUMBER: US/10/174,695
CURRENT PILING DATE: 2002-06-18
PRIOR PILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: AU PQ 4859
PRIOR PILING DATE: 1999-12-24
NUMBER: PSEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 231
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Publication No. US20030232022A1
GENERAL INFORMATION:
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Best Local Similarity 99.6
Matches 230; Conservative
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US-10-387-977-99
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APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
FILE REFERENCE: 552925000301
CURRENT APPLICATION NUMBER: US/10/387,977
CURRENT FILING DATE: 2003-07-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 EYEKEGND-----LTYVLLIGDHKDIPAKITPGIKSDQV---YGQIVGNDHYNEVFIG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 RMSASSPEELTNIIDKVLMYEKATMPDKSYLEKVLLIAGADYSWNSQVGQPTIKY-GMQY 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 107; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR PEDICATION NUMBER: US 0/423,056
PRIOR PELING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: US CT/AU98/00311
PRIOR APPLICATION NUMBER: AU PO 6528
PRIOR FILING DATE: 1998-04-30
PRIOR PILING DATE: 1997-04-30
PRIOR PILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                      Sequence 100, Application US/10387977
Publication No. US20040005276A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Porphyromonas gingivalis US-10-387-977-100
| | : | | | 698 NGRRVATAKNRMVFEAON 715
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                                                                                                                    US-10-387-977-100
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APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Meil Martin
APPLICANT: Slakeski, Nada
TITLE CP INVENTION: SYTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
CURRENT APPLICATION NUMBER: US /10/387,977
CURRENT FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: PCT/AU98/00311
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1997-04-30
PRIOR FILING DATE: 1997-04-30
SPING FILING DATE: 1997-04-30
SEQ ID NOS: 105
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SEQ ID NOS: 105
SEQ ID NOS: 105
SEQ ID NO SELECT WINDOWS VERSION 4.0
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4.5%; Score 410.5; DB 15; Length 507;
Best Local Similarity 25.4%; Pred. No. 1.9e-22;
Matches 142; Conservative 86; Mismatches 209; Indels 121; Gaps
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                                                                                     APPLICANT: Reynolds, Eric Charles
APPLICANT: Slakeski, Nada
APPLICANT: Slakeski, Nada
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
APPLICANT: Barr, Ian George
TITLE OF INVENTON: P. GINGTVALIS ANTIGENIC COMPOSITION
FILE REFERENCE: 529282000700
CURRENT APPLICATION NUMBER: US/10/174,695
CURRENT FILING DATE: 2002-06-18
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.7%; Score 521.5; DB 15; Length Best Local Similarity 92.2%; Pred. No. 1.1e-31; Matches 94; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   989 FENGIPASWKTIDADGDGHGWKPGNAPGIAGYNSNGCVYSES 1030
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ORGANISM: Porphyromonas gingivalis
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Publication No. US20040005276A1
GENERAL INFORMATION:
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Sequence 4, Application US/10174695
Publication No. US20030232022A1
GENERAL INFORMATION:
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TYPE: PRT ORGANISM: Enterococcus faecalis US-10-282-122A-56997
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294 KY----NDGLAASAAPVFLALVGDTDVISGE--KGKKTKKVTDLYYSAVDGDYFPEMYTF 347
                          62 EYEKEGND-----LTYVLLVGDHKDIPAKITPGIKSDQV---YGQIVGNDHYNEVPIG 111
                                                                                                                                   407 YYNOEHGYIDVYNYLKAPYIGCY-----SHLNTGVSFANYIAHGSEIAWADPLLI 456
                                                                                                                                                                                                                                                                                                          284 W------ASPMRG-------ODEMNEI-------LCEKHPNNIKR 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              677 QIQVGEPSPYQPVSN---LIATIQGQKVTLKWEAPSAKKAEGSREVKRIGDGLFVTIEPA 733
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                                                                                                                                                                                                                                                                     513 WGEDYYWSVGANAVFGVQPTFEGTSMGSYDATFLEDSYNTVNSIMWAGNLAATHAGNI---
                                                                                                                                                                                                                              571 --GNITHIGAHYYWEAYH------VLGDGSVMPYRAMPKTNTYTLPASLPQNQAS
                                                                                                                                                                       ----CYDPGVTPKNIIDAFNGGISLANYTGHGSETAWGTSHFG
                                                                                                                                                                                                       TSQLKALTNKDKYFLAIGNCCITAQFDYVQPCFGBVITRV----KEKGAYAYIGSSPNSY
                                                                                                                                                                                                                                                                                                                                                                                                            618 YSIQAS-AGSYVAISKDGVLYGTGVANASGVATVSMTKQITENGNYDVVITRSNYLPVIK
                                                                   348 RMSASSPEELTNIIDKVLMYEKATMPDKSYLEKVLLIAGADYSWNSOVGQPTIKY-GMQY
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PELING DATE: 2000-03-21

PRIOR PELING DATE: 2000-03-21

PRIOR PELING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PILING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 56997, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                     172 NLLTOYGYTKIIK----
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
3.4%; Score 309; DB 12; Length 1728;
Best Local Similarity 21.3%; Pred. No. 1e-13;
Matches 375; Conservative 163; Mismatches 617; Indels 604;
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FLING DATE: 2001-02-02
PRIOR PLLING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PRILING DATE: 2001-02-16
Remaining Prior Application data removed - S
NUMBER OF SEQ ID NOS: 78614
SEQ ID NO 56997
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| 10 cc cc cc cc cc cc cc cc cc cc cc cc cc                                | UNITED DATE: 2003-02-05  TREPLICATION NUMBER: US/10/282, TRILING DATE: 2003-02-00  TRILING DATE: 2000-03-21  APPLICATION NUMBER: 60/191,078  FILING DATE: 2000-05-23  APPLICATION NUMBER: 60/206,848  FILING DATE: 2000-05-26  FILING DATE: 2000-05-26  FILING DATE: 2000-05-26  APPLICATION NUMBER: 60/230,335  FILING DATE: 2000-09-06  APPLICATION NUMBER: 60/230,335  FILING DATE: 2000-09-06  APPLICATION NUMBER: 60/230,335  FILING DATE: 2000-09-06  APPLICATION NUMBER: 60/230,335  FILING DATE: 2000-09-06 | CKK H.ZO                                                                                                              | Query Match  Best Local Similarity 21.5%; Pred. No. 4.8e-13; Matches 309; Conservative 121; Mismatches 538; Indels 467; Gaps  531 PTFEGTSMGSYDATFLEDSYNTVNSIMWAGNLAATHAGNIGNIT  244 PTLGGTAEAGSRVSYYDGTTLLGTTTADSSGKWFTPTTTGLGEGAHSITVTATDAAGNVS  575 HIGAHYYWBAYHVLGDGSVMPYRAWPKTNTYTLPASLPQNQASYSIQASAGSYVAI  304TPSAAFELTIDTTABA-LPTVNATDGTSLSGTAEAGATVNI | Db 344 DINGDGTPDATUTADPSGVAT-CONTINENTERNIENTERNIENTERNIENTERNIENTERNIENTERNIENTERNIENTERNIENTERNIENTERNIENTERNIENTERNIENTERNIENTERNIENTERNIENTERNIENTERNIEGE 37  Qy 727 FVITEPRANDVRANERKVUL |
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| 710 PNTPVATPIV 901 GLTATTFEED 761 GKYTVTL-DS 955 S-VGCKVTLK   1:       : | 8666<br>1036<br>905<br>1090<br>947<br>1149<br>980                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | OY 1198 LTAHGGSNUVSSFSWNGMAINPDNYLISKDVTGATKVKYYAVNDGFPGDHYAVMISKTG 1257  DD 1037 ATAKQTVMVVAK.NDTGLESQPTTAMTPDNYTTPT | Db 1231 SNPTAFKTPÅDPDÅPVATPTVÖKLTGSTTNGYQVVGAABVGTTVEVRDÅDGTVLGMATTG 1290  QY 1450 -DGNNWTTTPPPGGSSFAGHNSALCYSSASHINPEGPQNPDNYLVTP-ELSLPGGGTLF 1507  Db 1291 TDG-KYTVTLEFGKASANETITVVAKNATGKESQPATATTPVDLATFTIDSIT- 1342  QY 1508 WVCAQDANYASEHY                                                                                                             | SPYTYGVKVYYPNGESAIETATLNITSLADVTA SPYNSSEQLLASGNTTTGGTFSVHIAAGLAT A                                                                                                                           |

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red. No. 4.8e-13;
Mismatches 538; Indels 467; Gaps
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                                                                            GTVTDDAGSVVGALASGGSTDDATPTLSGTAEAGSTVSVY-DGTTL---LGTTTADPSGN
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                                                    DFTFEAGKKYTFTMRRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEEDG-
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DGPLMAGY---IPQESLAGFESLTGAGVLGGMSAGTALLVGAAAIGAGVAISNSSGGGGG 155
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CURRENT FILING DATE: 2003-02-20

FRIOR PELICATION NUMBER: 60/191,078

PRIOR PELICATION NUMBER: 60/191,078

PRIOR PLING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/200,848

PRIOR PLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/200,727

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-12-23

PRIOR PLING DATE: 2000-12-23

PRIOR PLING DATE: 2000-12-23

PRIOR PLING DATE: 2000-01-23

PRIOR PLING DATE: 2000-01-23

PRIOR PLING DATE: 2000-01-23

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PRIOR PLING DATE: 2000-01-23

PRIOR PLING DATE: 2001-02-09

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Sequence 66335, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
ARPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                      Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT:
APPLICANT:
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|                                                                                                            | RESULT 14 US-10-246-330-4 ; Sequence 4, Application US/10246330 ; Publication NO. US20030166030A1 ; GENERAL INFORMATION: ; APPLICANT: O'TOOLe, George A. ; APPLICANT: MAIN, Thien-Fah ; TITLE OF INVENTION: METHODS TO STUDY AND MECHANISMS OF ; TITLE OF INVENTION: BIOFILM-SPECIFIC ANTIBIOTIC RESISTANCE ; TITLE THE REPREMENCE: 14537-002001 ; FILE REPREMENCE: 14537-002001 | ATTICN NOMERS: 020-18  ATION NUMBER: US 60/323,241  DATE: 2001-09-18  Q ID NOS: 32  stSEQ for Windows Version 4.  8  seudomonas aeruginosa                                                                     |                                                     |                                        | Qy 638 GTGVANASGVATVSMTKQITENGNYDVUITRSNYLPVIKQIQVGEPSPYQPVSNLTAT 695                                                                                                                                                                          | Db 263 PDGSSVJGKAEPGSTVGVIDGDGQPDIT/VVGPGGSFEVPLNPPLINGETVTV 316  QY 745 LAADNVWGDNIGYQFLLDADHNIFGSVIPATGPLFTGTASSNLYSANFEYLVPANADPVV 804  : | Qy 805 TTQNIIVTGGGEVUIPGGVYDYCITNPEPASGKMMIAGDGGNQPARYD 852                             | Db 421 DPPDAPQVNASNGSVLSGTAEAGVTIVITDGNGNFIGGTSADANGNWSFTPG 472  Qy 896 TXIXEGLTATTPEBDGVAAGNHEXCVEVKXTAGVSPKVCKDVTVGGSNBFAPVQ 949  :::: | 577 PASVTVDAVAPATPTVDPSNGTTLSGTABPGSSVTLTDGNGNPIGQVTADGSGN-WTF 633 |
|------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------|----------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------|
| QY         805 TTQNIIVTGQGEVVIPGGVPDYCITNPEDASGKMMIAGDGGNQPARYD 852           Db         :             : : | ### SQLFDGTATTFEEDGVAAGNHEYCVEVKXTAGVSPKVCKDVTVEGSNEFAPV0 949  ###                                                                                                                                                                                                                                                                                                               | TPSTPLPNGTVVNATATDPSGNASPASVTVDAVAPATEVVNASGHTISGTAETGYNSNGCVYS  ESFGLGG-IGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGND  LTDGNGNPIGQVTADGSGNWSFTPTTPLENGTVVNATATD  LTDGNGNPIGQVTADGSGNWSFTPTTPLENGTVVNATATD | 1085 ASNFINALIEETITAKGVRSPKAIRGRIQGTWRQKTVDLPA 1125 | QGWLCLSSGQLDWLTAHCGSNVVSSFSWNGWALNPD : | 993VVAQDAAGNSSCASVTVDSQAPAAPVVNPSNGTTLSGTAEPGAL 937 1281 FGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMG 1333 1281 FGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMG 1333 938 VTL-TDGNGNPIGQVTADGSGNWSFTPGTPLANGTVVNATASDPTGNTSA 986 | 1334 GSPTPIDYTYTVYRDGTKIKEGLIETTFEBDGVATCNHEYCVE 1376                                                                                        | 1047 TPLADGTVVNATATDPAGN-TGGQGSTTVDAIAPATPTVNLSNGSSLS 1093 1437 GIPASWKT-IDADGDGNNWTTTP | 1459PP                                                                                                                                   | 1612YRNNTQIASG-VTETTYRDPDLATGFYTYGVKVVYPNGESAIETATLNIT 1660        |

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388 GTVIGTGTADGTGAFTV--TVPAGEAGANETLTA-----VAKNASGTEXTPTTFQTPAD 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 21.5%; Pred. No. 1.6e-12; Matches 293; Conservative 140; Mismatches 499;
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21.5%; Pred. No. 1.6e-12;
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                                                                                                                                                                                                                                                                                                                         FILING DATE: 1998-05-04
APPLICATION NUMBER: US 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: US 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: US 60/066,009
FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PB369P1D1
                                                                                                                                                                                                                APPLICATION NUMBER: US/10/206,576
FILING DATE: 29-Jul-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 258:
US-10-206-576-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
                                                                                                                            COMPUTER: Dell Latitude
OPERATING SYSTEM: Windows
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1638 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                 COMPUTER READABLE FORM:
                                                                                                          MEDIUM TYPE: CD-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPE: amino acid
CITY: Rockville
STATE: Maryland
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Publication No. US20030017495A1
GENERAL INFORMATION:
APPLICANT: Choi et al.
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 497
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1556
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                      KPGNAPGIAGYNSNGCVYS 1028
                                                                                                      ESFGLGG-IGVLTPD---NYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGND 1084
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                                                                                                                                               694 LTDGNGNPIGOVTADGSGNWSFTPTTPLPNG
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550 845 877 652 934 446 ------

Search completed: May 18, 2004, 11:38:32 Job time: 74.1557 secs

us-08-570-311-2.rag

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

May 18, 2004, 11:33:39 ; Search time 51.2572 Seconds (without alignments) 2739.638 Million cell updates/sec Run on:

US-08-570-311-2

2641 1 MRKLNSLFSLAVLLSLLCWG.....QNLTGSAVGQKVTLKWDAPN 497 Title: Perfect score: Sequence:

Scoring table:

1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1586107

of hits satisfying chosen parameters: ,

Total number

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_29Jan04:\* Database

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2001s:\* geneseqp2000s:\* geneseqp20048:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| so,       | ription       | Aar96025 P. gingiv | Aaw69483 Haemadglu | Aar96030 P. gingiv | Aaw69488 Haemagglu | Aaw24786 PrtR anti |          | Aaw34843 Arg-gingi | Aay67396 Arg-gingi |          | Aar96033 P. gingiv | Aaw69495 Haemagglu | Aar96032 P. gingiv | Aaw69494 Haemagglu | Aar96029 P. gingiv | Aaw24787 PrtK anti | Aaw69487 Haemagglu | Aar96028 P. gingiv | Aaw69486 Haemagglu | Aau03572 P. gingiv | Aau03574 P. gingiv | Aar96021 P. gingiv | Aaw69489 Haemagglu | Aar96023 P. gingiv | Aar96022 P. gingiv | Aaw69491 Haemagglu |
|-----------|---------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | ID            | AAR96025           | AAW69483           | AAR96030           | AAW69488           | AAW24786           | AAR70188 | AAW34843           | AAY67396           | AAU08938 | AAR96033           | AAW69495           | AAR96032           | AAW69494           | AAR96029           | AAW24787           | AAW69487           | AAR96028           | AAW69486           | AAU03572           | AAU03574           | AAR96021           | AAW69489           | AAR96023           | AAR96022           | AAW69491           |
|           | DB            | ~                  | 7                  | 7                  | N                  | 7                  | C)       | ~                  | m                  | 4        | N                  | N                  | (1                 | N                  |                    |                    | 7                  | ~                  | 7                  | 4                  | 4                  | 7                  | C)                 | (7                 | Ŋ                  | N                  |
|           | Length        | 497                | 497                | 2628               | 2628               | 1706               | 1704     | 1704               | 1704               | 1704     | 1687               | 1687               | 1358               | 1358               | 1732               | 1732               | 1732               | 1087               | 1087               | 419                | 419                | 450                | 450                | 456                | 456                | 456                |
| o\c       | Query         | 100.0              | 100.0              | 100.0              | 100.0              | 36.0               | 35.8     | 35.8               | 35.8               | 35.8     | 35.7               | 35.7               | 30.9               | 30.9               | 0                  | 30.8               | 30.8               | 30.5               | 30.5               | 30.0               | 25.1               | 20.7               | 20.7               | 20.7               | 20.7               | 20.7               |
|           | Score         | 2641               | 2641               | 2641               | 2641               | 951.5              | 944.5    |                    | 944.5              | 944.5    | 943.5              | 943.5              | 816                | 816                | ď.                 | 812.5              | 812.5              | .90                | 806.5              |                    | 7                  | 46.                | 9                  | 4                  | 4                  | 546.5              |
|           | Result<br>No. |                    | ~                  | ĸ                  | 4                  | 2                  | 9        | 7                  | æ                  | σ        | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24                 | 25                 |

| Aaw69490 Haemagglu | Aar72458 Porphyrom | Aar77313 Porphyrom | Aar96024 P. gingiv | Aaw69492 Haemagglu | Aau03575 P. gingiv | Aay34359 Porphorym | Aay34484 Porphorym |          | Aay34521 Porphorym | Aay34520 Porphorym | Aay34392 Porphorym | Aab14942 Porphyrom | Aay34483 Porphorym | Aay34358 Porphorym | Aau03573 P. gingiv | Abp55081 Porphyrom | Aab49217 Peptide u | Aaw34805 Arg-speci | Adc01014 Enterohae |  |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--|
| AAW69490           | AAR72458           | AAR77313           | AAR96024           | AAW69492           | AAU03575           | AAY34359           | AAY34484           | AAY34522 | AAY34521           | AAY34520           | AAY34392           | AAB14942           | AAY34483           | AAY34358           | AAU03573           | ABP55081           | AAB49217           | AAW34805           | ADC01014           |  |
| 2                  | 7                  | N                  | 7                  | 2                  | 4                  | N                  | N                  | 7        | 7                  | 7                  | 7                  | 'n                 | 7                  | 7                  | 4                  | 9                  | 4                  | 7                  | 7                  |  |
| 456                | 970                | 991                | 439                | 439                | 231                | 377                | 312                | 921      | 922                | 925                | 938                | 148                | 293                | 299                | 196                | 135                | 134                | 49                 | 5291               |  |
| 20.7               | 19.8               | 18.8               | 17.4               | 17.4               | 17.3               | 16.1               | 14.4               | 12.8     | 12.8               | 12.8               | 12.8               | 10.3               | 8.1                | 8.1                | 7.1                | 6.7                | 6.7                | 9.9                | 5.8                |  |
| 546.5              | 522                | 495.5              | 458.5              | 458.5              | 457.5              | 425.5              | 379                | 337      | 337                | 337                | 337                | 272.5              | 213.5              | 213.5              | 188.5              | 177.5              | 176.5              | 175                | 153                |  |
| 26                 | 27                 | 28                 | 29                 | 30                 | 31                 | 32                 | 33                 | 34       | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |  |

## ALIGNMENTS

Haemagglutinin; hagA; periodontal disease; vaccine; antibody Porphyromonas gingivalis; strain 381. AAR96025 standard; protein; 497 AA. P. gingivalis haemagglutinin hagA. (revised)
(first entry) 16-OCT-2003 04-SEP-1996 AAR96025; RESULT 1 AAR96025 

WO9617936-A2. 13-JUN-1996.

94US-00353485. 95WO-US016108. 11-DEC-1995; 09-DEC-1994;

(UYFL ) UNIV FLORIDA. (UABR-) UAB RES FOUND.

Patti Lantz M, Han N, Lepine G, Progulske-Fox A, Tumwasorn S, WPI; 1996-287181/29. N-PSDB; AAT30649.

Ę,

Porphyromonas gingivalis genes and proteins - used in the detection and vaccination against periodontal disease.

Claim 5; Page 47-51; 153pp; English.

A portion (AAR96025) of P. gingivalis 381 haemagglutinin hagA (see also AAR96030) was identified as the product of clone ST2 (AAT30649) isolated from a P. gingivalis 318 genomic library. The haemagglutinin can be obtd. from transformed host cells and used as a vaccine to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of a live vaccine. The haemagglutinin can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)

Sequence 497 AA;

0;

Gaps

0;

120 120 180 180 240 240 300 300 360 360 420 420 480 480

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This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagA haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
Porphyromonas gingivalis genes - encoding haemagglutinin and/or poly:peptide(s)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTP
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                                                                                                                                                                                    100.0%; Score 2641; DB 2; Length 497; 100.0%; Pred. No. 2.5e-194; ive 0; Mismatches 0; Indels 0;
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/label= Sig_peptide
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                                      Col 37-44; 101pp; English

    P. gingivalis haemagglutinin hagA.

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(first entry)
                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 497; Conservative
                                                                                                                                                             Sequence 497 AA;
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04-SEP-1996
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                                                                                                         ARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDPFEYKVPVNA
                                                     MRKLINSLFSLAVLLSLLCWGQTAAAQGGPKTAPSVTHQAVQKGIRTSKVKDLRDPIPAGM
                            Gaps
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 Length 497;
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                          Indels
Score 2641; DB 2;
Pred. No. 2.5e-194;
Mismatches 0;
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91US-00647119.
94US-00353485.
 100.0%;
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            Similarity 100.
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(UABR-) UAB RES FOUND.
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25-JAN-1991;
09-DEC-1994;
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Best Local Simi
Matches 497;
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                                                                                                                                                                                              Porphyromonas gingivalis genes and proteins - used in the detection and vaccination against periodontal disease.
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0; Mismatches 0;
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Les 497; Conservative
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N-PSDB; AAT30654.
                                                                                                                                     Progulske-Fox A,
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         WO9617936-A2
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    encoding haemagglutinin and/or

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100.0%; Pred. No. 2.9e-193;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated Porphyromonas gingivalis genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Col 91-110; 101pp; English.
                       Ā
                       AAW69488 standard; protein; 2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-00241640.
91US-00647119.
94US-00353485.
                                                                                                                                                                                                                                                                                                                                                                                                                          95US-00570311
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                                                                                                                                                                      Haemagglutinin protein hagA
                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patti JM, Han N, Lantz
                                                                                                                                                                                                                                                                        Porphyromonas gingivalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protease poly:peptide(s))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         497; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UABR-) UAB RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYFL ) UNIV FLORIDA
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09-DEC-1994;
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                                                                                                                       22-DEC-1998
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Best Local S
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AAW69488
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09 9 120 120 180 180

us-08-570-311-2.rag

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A PrtR-PrtK cell surface protein of Porphyromonas ginivalis (PG)
                                 Example 1; Fig 8b; 68pp; English
                                                                                                                                                                                                                                                                                                                              186 PGDAASVV------
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 237; Conserv
                                                                                                                                                                                   Sequence 1706 AA;
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PrtR; PrtR45; PrtR44; PrtR15; PrtR17; PrtR27; haemagglutinin; adhesin;
therapy; diagnosis; vaccine; antigen.
420
                                        420
                                                                       480
                                  SEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTV
                                                       YRDNVVIAQNLAATIFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL
                                                                      421 YRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL
                        SEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTV
                                                                                                                                                                                                                                                                                             228. .719
/label= prtR45
/note= "45 kDa Arg-specific thiol protease"
719. .720
                                                                                                                                                                                                                                                                                                                          720. 1138
/label= PrtR44
/note= "44 kDa adhesin"
1138. 1139
                                                                                                                                                                                                                                                                       . .227
label= Pro-pro_peptide
                                                                                                                                                                                                                                                                                                                                                                           /note= "15 kDa adhesin'
1273. .1274
                                                                                                                                                                                                                                                                                                                                                                                                         'note= "17 kDa adhesin
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "27 kDa adhesin
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VICTORIAN DAIRY IND AUTHORITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Slakeski N;
                                                                                                                                                                                                                                                Porphyromonas gingivalis; strain W50.
                                                                                                                                           AAW24786 standard; protein; 1706 AA
                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                 PrtR antigenic protein complex.
                                                                                                                                                                                                                                                                                                                                                            139. .1273
label= PrtR15
                                                                                      TGSAVGQKVTLKWDAPN 497
                                                                                                    TGSAVGOKVTLKWDAPN 497
                                                                                                                                                                                                                                                                                                                                                                                           274. .1431
label= PrtR17
                                                                                                                                                                                                                                                                                                                                                                                                                                 'label= PrtR27
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                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                      227. .228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reynolds EC, Bhogal PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-272112/24.
N-PSDB; AAT78850.
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Protein
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(VICT-) VICTO
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                                                                                                                                                                           17-OCT-2003
25-NOV:1997
                                       361
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                        361
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                                                                                                                                                                                                                                                                      Peptide
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New antigenic protein complex from Porphyromonas gingivalis - comprising Arg- and Lys- specific thiol endo-peptidase(s), used in the detection, prevention and treatment of periodontal disease.

comprises a 300 kDa complexed a 45 kDa arginine specific thiol protease and 44, 15, 17 and 27 kDa adhesins encoded by the prtR gene (AATYB850), and a 148 kDa 19sine-specific thiol protease and 39, 15 and 4 kDa 19sine-specific thiol protease and 39, 15 and 4 kDa adhesins (see AAW4787) encoded by the prtK gene (AAY78851). A claimed antigenic complex comprises at least one adhesin domain, the complex of prtR and prtK each containing at least one adhesin domain, the complex of prtR and prtK each containing at least one adhesin domain, the complex baving a mol.wt. of over 200 kDa, and preferably comprises all 9 proteins of the PrtR-PrtK complex (see also AAW24780-85). It can be used in a claimed composition to elicit an immune response directed against of PG, and in a claimed method of reducing the prospect of PG infection and/or severity of disease. Antibodies directed against the complex are claimed for use in treating PG infection. Unlike whole PG cells or other PttK complex or component parts are safe and effective antigens. (Updated on 17-OCT-2003 to standardise OS field)

970 SFE-NGIPASWKTIDADGDGHGW-KPGNAPGIAGYNSNGCVYSESF-GLGGIGV-LIPDN 1025 20; SPEAMRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETF 1145 1206 ISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGL 1265 ESSTHGEAPAEWITIDADGDGQGWLCLSSGQLDWLTAHGGTNVVSSFSWNGMALNPDNYL 1205 295 TNFVLDGTASADIPAGTYDYVIINPNPGI-IYIVGEGVSKGNDYVVEAGKTYHFTVQRQG 185 910 PKVCKDVTVEGSNEFAPVQNLTGSAVGQKVTLKWDAPNGTPNPNPNPNPNPNPNFGTTTLSE 969 296 YLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETL---GSD 351 850 SCHGIELTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVATGNHEYCVEVKYTAGVS 909 671 TATTÓGOKVTLKWDAPSTKTNATTNTARSVDGIRELVLLSVSÓAPELLRSGOAEIVLEAH ----EGVKLPAPYQERTIDLSAYAGQQVXLAFRHFNSTGIFRLYLDDV--AVSGEGSSND 22 TAAAQG------GPKTAPSVTHQAVQK--GIR---TSKVKDLRDPIPAGMARIILEAH 69 DVWEDGTGYQMLWDADHNQYGASIPEE--SFWFANGTIPAGLYDPFEYKVPVNADASFSP SFDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN Gaps 36.0%; Score 951.5; DB 2; Length 1706; 31.9%; Pred. No. 1.3e-63; ive 74; Mismatches 156; Indels 275; ----VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS--

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193

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1085
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                            730
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                      790 TIMIMDGTASVNIPAGTYDFALAAPQANAKIWIAGGGPTKEDDYVFEAGKKYHFLMKKMG
                                                                                                                                                                                                                                                                      850 SCHOLTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVATGNHEYCVEVKYTAGVS
                                                                                                                                                                                                      -----DKRTYVLNESF
                                                                                                                                                                                                                                                       238 DIQILPNGWIMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYL
                                                                                                                                                                                                                                                                                                                       -----GPKTAPSVTHQAVQK--GIR---TSKVKDLRDPIPAGMARIILEAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 YRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL
                                                    69 DVWEDGTGYQMLWDADHNQYGASIPEE -- SFWFANGTIPAGLYDPFEYKVPVNADASFSP
                                                                                                     TNFVLDGTASADI PAGTYDYVI INPNPGI-IYIVGEGVSKGNDYVVEAGKTYHFTVQRQG
                                                                                                                                                                                                                           910 PKVCKDVTVEGSNEFAPVQNLTGSAVGQKVTLKWDAPNGTPNPNPNPNPNPNPGTTTLSESF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYTYTV
                                                                                                                                                                                                                                                                                                       298 VIPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arg-specific gingipain protease; gingivalis; periodontal disease; vaccine; infection.
                                                                                                                                                                                                                                                                                                                                                          -KSEGVKL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arg-gingipain high molecular weight prepolyprotein sequence

    1. .227
    /note= "precursor protein"

                                                                                                                                                                                                                                                                                                                                                         ----DKPAPMNLV---
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1. .227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1385 KAQPDĠGDVVĽKWEAPS 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 TGSAVGQKVTLKWDAPN 497
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                                                                                                                                                    186 PGDAASVV--
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Protein
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              1323 YTYTVXRDGTKIKEGLIETTFEEDGVATGNHEYCVEVKYTAGVSPKKCVNVTV-NSTQFN 1381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A low mol.wt. arginine-specific gingipain (AG-1) and high mol.wt. AG (AG-2) were isolated from P. gingivalis strains H66 (ATCC 33277) and W50 (ATCC 53373). The sequences of the proteins were used to design PCR primers and probes to isolate AG DNA. Lambda DASH and lambda ZAP libraries were screened with a probe based on amino acids 11-22 of the AG protein to obtain DNA encoding AG-1 (AAQ83484) and AG-2 (AAQ83489). AG-2 correct PN field.)
YTYTVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1704;
                                                                                                                                                                                                                                                    Arg-gingipain-2; gingivalis; periodontal disease; vaccine; arginine-specific protease.
                                                                                                                                                                                                                                                                                                                          228. .719
/label= Protease
/note= "corresponds to Arg-gingipain-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.8%; Score 944.5; DB 2; Best Local Similarity 31.9%; Pred. No. 4.4e-63; Matches 235; Conservative 75; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pavloff N;
                                                                                                                                                                                                                                                                                                                                                            720. .1091
/label= Hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                       1092. .1429
/label= Hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                               1430. .1704
/label= Hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 70-77; 89pp; English
                                                              AAR70188 standard; protein; 1704 AA
                                                476 HVQNLTGSAVGQKVTLKWDAPN 497
                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                           Arg-gingipain-2 prepolyprotein
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93US-00141324.
94US-00265441.
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                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                        Porphyromonas gingivalis
                                                                                                                                                                                        (revised)
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N-PSDB; AAQ83489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 1704 AA;
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24-JUN-1994;
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21-SEP-1995
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  416
                                                                                                                                                              AAR70188;
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Protein
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AAR70188
ID AAR7
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from gingivitis and/or periodontal diseases
                                                                                                              Disclosure; Page 68-73; 95pp; English.
                                        (UYGE-) UNIV GEORGIA RES FOUND INC. (MORE-) MOREHOUSE SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                            ------DKPAPMNLV-
                                                                                                                                                                                                               35.8%; Scor
31.9%; Pred
                  97WO-US004635
                             96US-0013945P.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ----PAPYOERTID--
                                                                                                                                                                                                                             Matches 235; Conservative
                                                          Travis J,
                                                                     WPI; 1997-479993/44.
                                                                                                                                                                                                                                                                                                              PGDAASVV--
                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                      Sequence 1704 AA;
                                                                           N-PSDB; AAT93872
                21-MAR-1997;
                                                          Potempa J,
                                                                                                                                                                                                                                                                                                  790
                                                                                                   diseases.
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1326 YRDGTKIKEGLIETTFEEDGVATGNHEYCVEVKYTAGV9PKECVNVTI-NPTOFNPVKNL 1384 Arginine specific proteinase; Arg-gingipain; gingipain-2; haemagglutinin; immunogenic component; vaccine; inflammatory response; tissue damage; periodontal disease. 421 YRDNVVIAQNIAATIFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL 480 This sequence represents a Porphyromonas gingivalis arginine-specific proteinase known as Arg-gingipain/gingipain-2 amino acid sequence. Gingipain-2 consists or a 50kD protease component non-covalently associated with a 44kD haemagglutinin component. The proteinase is stimulated by glycine containing peptides and glycine analogues. It is stimulated by cysteine protease group specific inhibitors. The protease preparation can be used in immunogenic compositions and vaccines against inflammatory response and tissue damage caused by P. gingivalis in periodontal disease. It can also be used to screen for agents that 720. .1185 /note= "Amino acids 720-1185 are specifically claimed" .206 KDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLST -----AVSGEGSSNDYTYTV New Porphyromonas gingivalis arginine-specific protease preparation useful for preparing vaccines against periodontal disease and for screening for Arg-gingipain inhibitors. 229. .719 /note= "Amino acids 229-719 are specifically Arg-gingipain-2 amino acid sequence. AAY67396 standard; protein; 1704 AA. Location/Qualifiers (UYGE-) UNIV GEORGIA RES FOUND INC. Claim 1; Col 29-42; 55pp; English. 1385 KAQPDGGDVVLKWEAPS 1401 481 TGSAVGQKVTLKWDAPN 497 94US-00265441. 94US-00336308 (first entry) Porphyromonas gingivalis. WPI; 2000-136659/12. N-PSDB; AAZ60181. 08-NOV-1994; 25-APR-2000 24-JUN-1994; US6017532-A. 25-JAN-2000. Potempa JS, Region Region q g à à ਨੇ ò The present sequence represents an arginine-specific protease of Porphyromonas gingivalis. The following peptides, derived from Arg- and Lys-specific high molecular weight proteases, offer protection against infection: YTYTOYRDEX INEGETATE DOWNTGNE YOURYTAGS VERVOR (1); YTYPUEKCOR RMIVIVAKKY (11); OLDFIFDNAC WOEDFLESMP CREALMRAQ (111); GENPRYQPON NITATIOGOK VILKMDAPSTK (VIV); GNNEYCUEVK YTAGVSPRVC (VI); TKIKEGLIAT TFEEDGVATG NUMFYCUEVK TRAGFERS (VII); DYTYTOYRDG TKIKEGLIATTF FEEDGVATG NUMFYCUCVKY TAGYSPRVC (VIII); DYTYTOYRDG TKIKEGLIATTF FEEDGVATG NETTEEBOGV ATGN (X); KIKEGLIATT FEEDGVATGH HEY (XII); ATHITEEDGVATG HEY (XII); ATHITEEDGVATG HEY (XII); ATHITEEDGVATG HEY (XII); ATHITEEDGVATG HEY (XIII); THEY ALL USED HEY WOND TO ACCIDE XIII); ATHITEEDGVATGH HEY (XII); AND YTPUEREKING RMIVIVARKY (XIII); THEY ALL USED ALL USED ACCIDES AND ACCIDED TO ACCIDE AND ALL USED ACCIDED TO ACCIDE AND ALL USED ACCIDED TO ACCIDE AND ALL USED ACCIDED TO ACCIDE AND ALL USED ACCIDED TO ACCIDE AND ALL USED ACCIDED TO ACCIDE AND ALL USED ACCIDED TO ACCIDE AND ALL USED ACCIDED TO ACCIDE AND ALL USED ACCIDED TO ACCIDE AND ALL USED ACCIDED TO ACCIDE AND ALL USED ACCIDED TO ACCIDE AND ALL USED ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDE ACCIDE AND ACCIDED TO ACCIDE AND ACCIDED TO ACCIDE AND ACCIDE EAIRGRIOGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETFES 1145 730 849 297 DVWEDGTGYQMLWDADHNQYGASIPEE -- SFWFANGTIPAGLYDPFEYKVPVNADASFSP 126 TNFVLDGTASADIPAGTYDYVIINPNPGI-IYIVGEGVSKGNDYVVEAGKTYHFTVQRQG 185 SGDGTELTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVATGNHEYCVEVKYTAGVS 909 68 Porphyromonas gingivalis Arg-specific gingipain protease peptide(s) -useful for protecting animals and humans from gingivalis and periodontal DTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYL ----VIGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS------DKRTYVLNESF TAAAQG------GPKTAPSVTHQAVQK--GIR---TSKVKDLRDP1PAGMARIILEAH TATTOGOKVTLKWDAPSTKTNATTNTARSVDGIRELVLLSVSDAPELLRSGQAEIVLBAH 910 PKVCKDVTVEGSNEFAPVONLTGSAVGÓKVTLKWDAPNGTPNPNPNPNPNPGTTTLSESF VIPKVIVPENGKLSYWVSSQ-VPWINEHYGVFLSTIGNEAANFIIKLLEETLGS-----------KSEGVKL-----Indels 267; Length 1704; ----LSAYAGQQV----Score 944.5; DB 2; Pred. No. 4.4e-63; ; Mismatches 160;

Porphyromonas gingivalis

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                                                          35.8%; Score 944.5; DB 3; Length 1704; 31.9%; Pred. No. 4.4e-63; live 75; Mismatches 160; Indels 267;
modulate Arg-gingipain proteinase activity inhibitors
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                                Sequence 1704 AA;
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Periodontitis; antiinflammatory; Arg-gingipain-2; AG-2; immunogen.

P. gingivalis high molecular weight Arg-gingipain-2.

(first entry)

18-DEC-2001

AAU08938 standard; protein; 1704 AA.

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The invention relates to a recombinant DNA molecule encoding high molecular weight (mature) Arg-gingipain (AG) protein, which has an enzymatically active protease component (AG-2) and a haemagglutinin component, from P. gingivalis. The nucleic acid is useful for producing mature Arg-gingipain protein. Immunogenic compositions comprising Arg-gingipain are useful for immunising animals including humans against inflammatory response and tissue damage caused by an archaebacterium Porphyromonas gingivalis, which causes progressive periodontitis. Arg-gingipain is also useful for identifying agents that modulate Arg-gingipain is also useful for identifying agents that modulate Arg-gingipain proteinase activity, whether by acting on the protein in the preventing the interaction of the proteinase with the protein in the gingival area, such as complement factors C3 or C5. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant DNA molecule which encodes high molecular weight (mature) May-gingipain protein, useful for immunization against inflammation and tissue damage, comprises enzymatically active protease component and hemaglutinin component.
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                                                                      Indels 267;
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| Jabel= HGP_17kDa
| Jnote= "Haemagglutinin protein component"
                                                                                                                                                              /label= HGP_44kDa
/note= "Haemagglutinin protein component"
                                                                                                                                                                                                                                                                                                "Haemagglutinin protein component"
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                                                                                                                  'label= Proteolytic component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barr PJ, Pavloff N;
                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                  27kDa
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94US-00265441.
94WO-US010283.
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24-JUN-1994;
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1067 SPBAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETF 1126
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                                                                                                              Porphyromonas gingivalis genes and proteins vaccination against periodontal disease.
    Lepine G,
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                                                                                                                                                                                  Claim 5; Page 138-143; 153pp; English.
    Tumwasorn S,
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                                            WPI; 1996-287181/29
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  Progulske-Fox A,
                                                                    N-PSDB; AAT30656
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product of the second open reading frame of the hagD gene (AAR30655)
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    P. gingivalis hagD haemagglutinin.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagE haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gingivalis genes - encoding haemagglutinin and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lepine G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      771 TNMIMDGTASVNIPAGTYDFAIAAPQANAKIWIAGQGPTKEDDYVFEAGKKYHFLMKKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      831 SÜGTELTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVATGNHEYCVEVKYTAGVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVWEDGTGYQMLWDADHNQYGASIPEE--SFWFANGTIPAGLYDPFEYKVPVNADASFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFVLDGTASADIPAGTYDYVIINPNPGI-IYIVGEGVSKGNDYVVEAGKTYHFTVQRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- DKRTYVLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 TAAAQG------GPKTAPSVTHQAVQK--GIR---TSKVKDLRDPIPAGMARIILEAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.7%; Score 943.5; DB 2; Length 1687; ilarity 31.8%; Pred. No. 5.2e-63; Conservative 75; Mismatches 160; Indels 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Progulske-Fox A,
                                                                                                                                                                                                                                     Haemagglutinin protein; periodontal disease; vaccine; hagE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --VTGEGGNEFAPVONLQWSVSGOTVTLTWQAPAS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Col 167-182; 101pp; English.
                                                                                                          AAW69495 standard; protein; 1687 AA
                             NLKAQPDGGDVVLKWEAPS 1384
 497
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91US-00647119.
94US-00353485.
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NLTGSAVGQKVTLKWDAPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patti JM, Han N, Lantz M,
                                                                                                                                                                                                     Haemagglutinin protein hagE
                                                                                                                                                                       (first entry)
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protease poly:peptide(s))
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Best Local Similarity
Matches 235; Conserv
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                                                                                                                                                                                                                                                                      Porphyromonas
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25-JAN-1991;
09-DEC-1994;
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(UABR-) UAB F
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                                                                                                                                                                                                                                                                                                                           383 DNVWGDNIGYQFLLDADHNIFGSVIPAIGPLF-IGIASSNLYSANFEYLIPANADPVVIT 441
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derived from P. gingivalis 318 genomic DNA. A first open reading frame coded for hagD protease (see also AAR96031). The protease and haemagglutinin can be obtd. from transformed host cells and used in vaccines to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of live vaccines. The haemagglutinin and protease can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGVSPKVCKDVTVEGSNEFAPVONLTGSAVGQKVTLKWDAPNGTPNPNPNPNPGTTTLSE
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                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                   Indels 274;
                                                                                                                                                                       Length 1358;
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                                                                                                                                                                    30.9%; Score 816; DB 2; L 29.6%; Pred. No. 2.4e-53; ive 75; Mismatches 171;
                                                                                                                                                                                                                                TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD-
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                                                                                                                                                                                                     Conservative
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                                                                                                                                                                  Query Match
Best Local Similarity
Matches 219; Conserv
                                                                                                                                        Sequence 1358 AA;
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68 HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||:|| : : || || : : || : || : || 678 YLITPALDLANGKUTFWVCAQDANXASEHYAVYASSTGNDASNFTNALLEETITAKGVR 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagD haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as

    encoding haemagglutinin and/or

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFVLDGTASADIPAGTYDYVIINPNP--GIIYIVGEG---VSKGNDYVVEAGKTYHFTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gabs
                                                                                                                                                                                                                                                                                                                Lepine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75; Mismatches 171; Indels 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1358;
                                                                                                                                                                                                                                                                                                               Progulske-Fox A,
                                                                      hagD.
                                                                       vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.9%; Score 816; DB 2; 29.6%; Pred. No. 2.4e-53;
                                                                      disease;
                                                                                                                                                                                                                                                                                                                Tumwasorn S,
                                                                                                                                                                                                                                                                                                                                                                                     gingivalis genes
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Col 145-158; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccines against periodontal disease
                                                                      protein; periodontal
                                                                                                                                                                                                           88US-00241640.
91US-00647119.
94US-00353485.
                                                                                                                                                                                   95US-00570311
                                        Haemagglutinin protein hagD
                                                                                                                                                                                                                                                                                                               Patti JM, Han N, Lantz M,
              (first entry)
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                                                                                                 Porphyromonas gingivalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1358 AA;
                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV58880
                                                                      Haemagglutinin
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09-DEC-1994;
                                                                                                                                                                                 11-DEC-1995;
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AAW69494 standard; protein; 1358

RESULT 13 AAW69494
ID AAW6
XX
AC AAW6

AAW69494

| NPI; 1996-287181/29.  N-PSDB; AAT30653.  XX  PT  Porphyromenas gingivalis genes and proteins - used in the detection and vaccination against periodontal disease.  XX  Claim 5; Page 76-81; 153pp; English.  XX  C gingivalis W12 cysteine protease, porphypain (AAR96029), was C dentified as the product of the prtp gene (AAT30653) isolated from P. C dentified as the product of the prtp gene (AAT30653) isolated from P. C gingivalis W12 genemic DNA. The porphypain shows homology to the haemagglutinins (see also AAR96026-28 and AAR96030-33) of P. gingivalis C G 318. It can be obtd. from transformed host cells and used as a vaccine to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of a live vaccine. The porphypain and C c haemagglutinins can also be used to detect the presence of anti-P. C gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field) | Duery Match 30.8%; Score 812.5; DB 2; Length 1732; Sest Local Similarity 30.0%; Pred. No. 6.4e-53; Atches 222; Conservative 70; Mismatches 172; Indels 277; Gaps | QY 22 TAAAQGGPKTAPSVTHQAVQKGIRTSKVKDLRDPIPAGMARIILEA 67                                                      | QY         127 TNFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSKGNDYVVBAGKTYHFTV 181           Db         807 QNIIVTGQGEVVIPGGVYDYCITNPEPASGKMMIAGDGGNQPARYDDFTFEAGKKYTFTM 866           QY         182 QRQGFGDASXV | 194VICEGGNEFAPVONLOWSVSGQTVTLTWQAPASDKRTYVLN | QY         295 NYLVTPRVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS 350 |                                                                                                                                                                      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------|------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Qy         351                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Qy         479 NLTGSAVGQKVTLKWDAPN 497           bb         1037 NLKAQPDGGDVVLKWEAPS 1055                                                                        | RESULT 14 AAR96029 ID AAR96029 standard; protein; 1732 AA. XX AC AAR96029; XX XX XX DT 16-OCT-2003 (revised) | 04-SEF-1996 (III) P. gingivalis po Porphypain; haem Porphyromonas gin                                                                                                                                     | Region 688                                   | Monte                                                                        | XX W09617936-A2. XX XX PD 13-JUN-1996. XX XX XX XX XX XX XX XX XX YABEC-1994; 94US-00353485. XX XX YABEC-1994; 94US-00353485. XX YX XX YX XX YX YX YX XX XX YX YX YX |

QNLTGSAV--GQKVTLKWDAP

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A PITR-PITK cell surface protein of Porphyromonas ginivalis (PG) comprises a 300 kDa complex composed a 48 kDa lysine-specific thiol protease and 39, 15 and 44 kDa adhesins encoded by the pirk gene (AAT78851), and a 45 kDa arginine-specific thiol protease and 44, 15, 17 and 27 kDa adhesins (see AAW24786) encoded by the pirk gene (AAT78850). A claimed antigenic complex comprises at least one multimeric protein complex of Pirk and Pitk each containing at least one adhesin domain, the complex having a mol.wt. of over 200 kDa, and preferably comprises all 9 proteins of the Pitk complex (see also AAW24780-85). It can be used
                                                                                                                                                                                     dontal disease; cell surface protein; thiol protease; endopeptidase;
PrtK48; PrtK39; PrtK15; PrtK44; haemagglutinin; adhesin; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antigenic protein complex from Porphyromonas gingivalis - comprising Arg- and Lys- specific thiol endo-peptidase(s), used in the detection, prevention and treatment of periodontal disease.
                                                                                                                                                                                                                                                                                                                        /note= "48 kDa Lys-specific thiol protease" 737. .738 738. .1156
                                                                                                                                                                                                                                                                               1. .228
/label= Pro-pro_peptide
                                                                                                                                                                                                                                                                                                                                                                       738. .1156
/label= PrtK39
/note= "39 kDa adhesin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "44 kDa adhesin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "15 kDa adhesin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYME ) UNIV MELBOURNE.
(VICT-) VICTORIAN DAIRY IND AUTHORITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ż
                                                                                                                                                                                                                                          Porphyromonas gingivalis; strain W50.
                                                                   AAW24787 standard; protein; 1732 AA
                                                                                                                                                                                                                                                                   Location/Qualifiers
    ONLTAEQAPNSMDAILKWNAP 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Slakeski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 9b; 68pp; English
                                                                                                                                                             PrtK antigenic protein complex.
                                                                                                                                                                                                                                                                                                                     229. .737
/label= PrtK48
                                                                                                                                                                                                                                                                                                                                                                                                                                     Tabel= PrtK15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= PrtK44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-AU000673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95AU-00006275
                                                                                                                                                                                                                vaccine; antigen
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                                                                                                                       (revised)
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N-PSDB; AAT78851.
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Protein
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                                                                                                                                                                                      Periodontal
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                                                                                                                       17-0CT-2003
                                                                                                                                                                                                                diagnosis;
  1402
                                                                                             AAW24787;
                                                                                                                                                                                                                                                                              Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NYLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS--- 350
                                                                               (Updated
in a claimed composition to elicit an immune response directed against by, and in a claimed method of reducing the prospect of RG infection and/or severity of disease. Antibodies directed against the complex are claimed for use in treating PG infection. Unlike whole PG cells or other perviously prepared antigens based on fimbriae or the capsule, the PtR. PtK complex or component parts are affe and effective antigens. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                                                     1043 NYLITPALDLENGGKLTFWVCAQDANYASEHYAVYASSTGNDASNFTNALLEETITAKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP
                                                                                                                                                                                                                                                                                                              748 DNVWGDNTGYQFLLDADHNTFGSVIPATGPLF-TGTASSNLYSANFBYLVPANADPVVTT
                                                                                                                                                                                                                                                                                                                                                  INFVLDGTASADIPAGTYDYVIINPNP--GIIYIVGEG---VSKGNDYVVEAGKTYHFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                             RRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEEDGVAAGNHEYCVEVKYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           927 AGVSPKVCKDVTVEGSNEFAPVQNLTGSSVGQKVTLKWDAPNGTPNPNPNPNPNPGTTLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1283 LSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSPTPTDYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHV
                                                                                                                                                                                                                        22 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD------PIPAGMARIILEA
                                                                                                                                                                                                                                                    693 TATTOGOKVTLKWEAPS----AKKAEGSREVKRIGDGLFVTIEPANDVRANEAKVVLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---KSEGVKL----
                                                                                                                                                                                            Gaps
                                                                                                                                                                                          Indels 277;
                                                                                                                                                             Length 1732;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --VIGEGGNEFAPVONLOWSVSGOTVTLTWQAP-
                                                                                                                                                         30.8%; Score 812.5; DB 2; 30.0%; Pred. No. 6.4e-53; ive 70; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----DKPAPMNLV-
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Best Local Simil
Matches 222; (
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Search completed: May 18, 2004, 11:42:39 Job time : 56.2572 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

May 18, 2004, 11:37:00 ; Search time 12.9765 Seconds (without alignments) 3684.135 Million cell updates/sec Run on:

US-08-570-311-2 2641 1 MRKINSLFSLAVLLSLLCWG......QNLTGSAVGQKVTLKWDAPN 497 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283366 seqs, 96191526 residues Searched: 283366

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_78:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description    | aqqlı       | ٠.   | gingipain R (EC 3. |      | arginyl endopeptid |      | hypothetical prote | endo-1,4-beta-xyla | probably celluloso | hypothetical prote | probable secreted | hypothetical prote | endo-1,4-beta-xyla | probable peptidogl | bacillopeptidase F | hypothetical prote | outer membrane pro | hypothetical prote | surface protein pr | internalin protein | cell surface prote | surface | chetical | probable RIX famil | - CIC | 5   | ď     | pro    | cycloinulo-oligosa |
|-----------|----------------|-------------|------|--------------------|------|--------------------|------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|---------|----------|--------------------|-------|-----|-------|--------|--------------------|
| SUMMARIES |                | i<br>!<br>! |      |                    |      |                    |      |                    |                    |                    |                    |                   |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |         |          |                    |       |     |       |        |                    |
| SUMM      | ID             | Ñ           | 4976 | A55426             | 3083 | 4022               | 4849 | 6906               | 7264               | 9701               | 8664               | 14                | 341                | S19011             | 148                | 73                 | E97835             | 34                 |                    |                    | 74                 | 47                 | AH1115  | AH2515   | B85547             | 9     |     | 63    | AD1374 | 56                 |
|           | DB             |             | 7    | N                  | ~    | 7                  | Н    | 7                  | 7                  | 7                  | 7                  | 7                 | 7                  | 7                  | 7                  | ٦                  | ~                  | N                  | ~                  | 7                  | 7                  | 7                  | 0       | N        | ~                  | ~     | 7   | 7     | 7      | N                  |
|           | Length         | 262         | 52   | 1704               | 73   | 991                | 23   | 5291               | 23                 | 48                 | 1983               | 781               | 2468               | 635                | 0                  | 43                 | 1655               | 65                 | 725                | 1873               | 940                | 34                 | 34      | 93       | 5188               | 71    | 908 | 4     | 940    | 0                  |
| æ         | Query<br>Match | 100.0       | Ġ.   | 35.8               | Ö    | 8                  | •    |                    |                    |                    |                    |                   |                    | •                  | •                  | •                  | •                  | •                  | •                  | •                  | •                  | •                  | •       | •        | 4.8                | •     | •   | •     | •      | •                  |
|           | Score          | 26          | 50   | 944.5              | 12   | 94                 | 156  | 153                | 152                | 150                | 147                | <b>T</b> #        | 138.5              | 7                  | 137                | 135.5              | 135                |                    | 131.5              |                    | 129                | 129                | 128     | 128      | 127.5              | 127   | 26  | 126.5 | 25     | 125                |
|           | sult<br>No.    | ı           | 7    | ٣                  | 4    | IJ                 | 9    | 7                  | œ                  | δ                  | 10                 | Ħ                 | 12                 | 13                 | 14                 | 12                 | 16                 | 17                 | 18                 | 19                 | 20                 | 21                 | 22      | 23       | 24                 | 25    | 56  | 27    | 28     | 29                 |

| autotransporter pr | proteinase [import | S-layer protein - | probable peptidogl | hypothetical prote | probable glycosyl | alpha-glucosidase | peptidoglycan anch | levanase/invertase | transferred entry | Subtilase family p | fungal stress prot | probable S-layer p | chitinase (EC 3.2. | aggregation factor | hypothetical prote |
|--------------------|--------------------|-------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| AF3204             | H90371             | T17884            | AD1129             | AF1718             | T35028            | F97177            | AH1396             | C97080             | A55368            | A12007             | JE0292             | D97316             | A38368             | T08615             | B84331             |
| ~                  | 8                  | 7                 | 7                  | 7                  | 7                 | 7                 | 7                  | 7                  | 7                 | 7                  | н                  | 7                  | 7                  | N                  | 7                  |
| 89                 | 875                | 1616              | 2013               | 208                | 729               | 1217              | 1530               | 1142               | 587               | 1448               | 364                | 1939               | 669                | 2205               | 694                |
| æ                  |                    |                   |                    |                    |                   |                   |                    |                    |                   |                    |                    |                    |                    |                    |                    |
|                    | 4.7                | 4.7               | 4.7                | 4.7                | 4.6               | 4.6               | 4.6                | 4.6                | 4.6               | 4.6                | 4.5                | 4.5                | 4.5                | 4.5                | 4.5                |
| 4.7                | 124.5 4.7          |                   |                    |                    |                   |                   |                    |                    | 120.5 4.6         |                    |                    | 120 4.5            |                    | 119 4.5            | 118.5 4.5          |

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| RESULT 1                                                                                  |
|-------------------------------------------------------------------------------------------|
| 128651                                                                                    |
| hemagglutinin A - Porphyromonas gingivalis                                                |
| C;Species: Porphyromonas gingivalis                                                       |
| C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 03-Aug-2001               |
| C;Accession: T28651                                                                       |
| R; Han, N.; Whitlock, J.; Progulske-Fox, A.                                               |
| Infect. Immun. 64, 4000-4007, 1996                                                        |
| A; Title: The hemagglutinin gene A (hagA) of Porphyromonas gingivalis 381 contains four : |
| A; Reference number: Z20494; MUID:97047672; PMID:8926061                                  |
| A; Accession: T28651                                                                      |
| A;Status: preliminary; translated from GB/EMBL/DDBJ                                       |
| A; Molecule type: DNA                                                                     |
| A;Residues: 1-2628 <han></han>                                                            |
| A; Cross-references: EMBL: U41807; NID: g1552410; PID: g1469916; PIDN: AAB17128.1         |
| C;Genetics:                                                                               |
| A,Gene: hagA                                                                              |
|                                                                                           |

|                                                                                                      | Ö                                                 | 0.9                                                            | 09                                                              | 120                                                                 | 120                                                                 | 180                                                                  |
|------------------------------------------------------------------------------------------------------|---------------------------------------------------|----------------------------------------------------------------|-----------------------------------------------------------------|---------------------------------------------------------------------|---------------------------------------------------------------------|----------------------------------------------------------------------|
|                                                                                                      | 0; Gaps                                           | PIPAGM                                                         | PIPAGM                                                          | KVPVNA                                                              | KVPVNA                                                              | KTYHFT                                                               |
| 2628;                                                                                                | ;<br>0                                            | VKDLRD                                                         | VKDLRD                                                          | YDPFEY                                                              | YDPFEY                                                              | YVVEAG                                                               |
| Length                                                                                               | Indels                                            | KGIRTSK                                                        | KGIRTSK                                                         | GTIPAGI                                                             | GTIPAGI                                                             | GVSKGN                                                               |
| DB 2;<br>-e-163;                                                                                     | .,                                                | VTHOAVC                                                        | VTHOAV                                                          | ESFWFAN                                                             | ESFWFAN                                                             | SILYIVGE                                                             |
| 2641;<br>No. 2.1                                                                                     | natches                                           | GGPKTAPS                                                       | GPKTAP                                                          | CYGASIP                                                             | ZYGASIPE                                                            | VIINPNPC                                                             |
| Score<br>Pred.                                                                                       | ); Mism                                           | SOTABAO                                                        | GOTABAOC                                                        | MDADHN                                                              | WDADHIN(                                                            | PAGTYDY                                                              |
| Ouery Match 100.0%; Score 2641; DB 2; Length 2628; Best Local Similarity 100.0%; Pred. No. 2.1e-163; | Matches 497; Conservative 0; Mismatches 0; Indels | 1 MRKLNSLFSLAVLLSLLCWGQTAAAQGGPKTAPSVTHQAVQKGIRTSKVKDLRDPIPAGM | MRKLNSIFSLAVILSILCWGQTAAAQGGPKTAPSVTHQAVQKGIRTSKVKDLRDPIPAGM 60 | 61 ARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDFFEYKVPVNA 120 | 61 ARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDPFEYKVPVNA 120 | 121 DASFSPTNEVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSKGNDYVVEAGKTYHFT 180 |
| ilarity                                                                                              | Conserva                                          | KLNSLFSLA                                                      | KLNSLFSLA                                                       | ILEAHDU                                                             | ILEAHDW                                                             | SFSPTNFVI                                                            |
| ch<br>l Sim                                                                                          | 497;                                              | L MR                                                           | - M                                                             | 61 AR                                                               | 61 AR                                                               | 21 DP                                                                |
| Query Match<br>Best Local S                                                                          | fatches                                           |                                                                |                                                                 |                                                                     |                                                                     |                                                                      |
| ОЩ                                                                                                   | 4                                                 | ò                                                              | qq                                                              | ŏ                                                                   | Dp                                                                  | ð                                                                    |

121 DASFSPINFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSKGNDYVVEAGKTYHFT 180

| 121 DASFSPTNFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSKGNDYVVEAGKTYHFT 180 | 181 VQRQCPGDAASVVVTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPASDKRTYVLNESFDTQ 240 | 181 VQRQEPGDAASVVVTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPASDKRTYVLNESFDTQ 240 | 241 TLPNGWTMIDADGDGHWMLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTP 300 | 241 TLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTP 300 | 301 KVTVPENGKLSYMVSSQVPWTNBHYGVFLSTTGNBAANFTIKLLEETLGSDKPAPMLVK 360 | 301 KVTVPENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDKPAPMNLVK 360 | 361 SEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTV 420 | 361 SEGVKLPAFYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTV 420 |
|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|---------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|
| qa                                                                   | Qy                                                                   | qa                                                                   | ολ                                                                   | qq                                                                   | δλ                                                                  | qq                                                                   | δλ                                                                   | qq                                                                   |

421 YRDNVVIAQNLAATTENQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVBGSNEFAHVQNL 480

ð

| qu                                                   | 421 YRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL 480                                                                                                                                                |                                                                                                                                                                                                                                                                                                            |
|------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>&gt;</b>                                          | TGSAVGOKVITIKMUMAN 497                                                                                                                                                                                              | OY 416 YIYTVYRDNVVIAQNLAATTENQENVAPGQYNYCVEVKYTAGVSPKVCKDVIVEGSNEFA 475                                                                                                                                                                                                                                    |
| 7 A                                                  | TGSAVGQKVTLKWDAPN                                                                                                                                                                                                   | GVATGNHEYCVEVKYTAGVSPKKČV                                                                                                                                                                                                                                                                                  |
| RESULT                                               | 2                                                                                                                                                                                                                   | QY         476 HVQNLTGSAVGQKVTLKWDAPN 497           Db         1382 PVKNLKAQPDGGDVVLKWEAPS 1403                                                                                                                                                                                                            |
| S49763<br>gingip<br>C;Spec:<br>C;Date                | ain R (EC 3.4.22.37) precursor - Porphyromonas gingivalis (fragment) des: Porphyromonas gingivalis (5-Mar-1995 #sequence_revision 12-May-1995 #text_change 31-Mar-1997                                              | RESULT 3<br>A55426                                                                                                                                                                                                                                                                                         |
| C; Acce.<br>R; Adus:<br>submit(<br>A; Desci          | Ssion: S4976.<br>Opoku, J.; Muir, J.; Slaney, J.M.; Rangarajan, M.; Curtis, M.A.<br>ed to the EMBL Data Library, November 1994<br>iption: Cloning, sequence analysis and expression in Escherichia coli of prpRl of | gingipain R (EC 3.4.22.37) precursor - Porphyromonas gingivalis N;Alternate names: 50K high molecular mass arginine-specific cysteine proteinase; HGP; C;Species: Porphyromonas gingivalis C;Species: Porphyromonas gingivalis C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 08-Oct-1999 |
| A; Accel<br>A; Stati<br>A; Molec                     | reace inducer: 349763 assion: S49763 as: preliminary ule type: DNA                                                                                                                                                  | C.Accession: AD3420; D33113<br>R.Pavolff, N.; Potempa, J.; Pike, R.N.; Prochazka, V.; Kiefer, M.C.; Travis, J.; Barr, J. Biol. Chem. 270, 1007-1010, 1995<br>A;Title: Molecular cloning and structural characterization of the Arg-gingipain protein                                                       |
| A, Resi<br>A, Cros<br>C, Gene<br>A, Gene<br>C, Keywo | A.Residues: 1-1526 <adu> A.Cross-references: EMBL:X82680 C.Genetics: A.Gene: prpR1 C.Keywords: cysteine proteinase: hydrolase</adu>                                                                                 | A; Reference number: A55426; MUID:95138080; PMID:7836351 A; Accession: A55426 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-1704 < PAV>                                                                                                                                                      |
| Quer<br>Best<br>Match                                | Query Match  Best Local Similarity 31.8%; Pred. No. 1.1e-53; Match And Similarity 31.8%; Pred. No. 1.1e-53; Match And Similarity 31.8%; Pred. No. 1.1e-53;                                                          | 57068<br>an ainainalia Tahl                                                                                                                                                                                                                                                                                |
| %<br>%                                               | AQGGFKTAPSVTHQAVQKGIRTSKVKDLRDPIPAGMARIILEAH 6                                                                                                                                                                      |                                                                                                                                                                                                                                                                                                            |
| Qy<br>Db                                             | DVWEDGTGYQMLWDADHNQYGASIPESSFWFANGTIFAGLYDFFEYKVPVNADASFSP                                                                                                                                                          | A;Residues: 228-249 <pik> A;Residues: 228-249 <pik> A;Derimental source: H66 A;Note: sequence extracted from NCBI backbone (NCBIP:141694) C;Reywords: cysteine proteinase; hydrolase</pik></pik>                                                                                                           |
| Qy                                                   | 127 TNFVLDGTASADIPAGTYDXVIINPNPGI-IYIVGEGVSKGNDYVVBAGKTYHFTVQRQG 185<br>                                                                                                                                            | Query Match 35.8%; Score 944.5; DB 2; Length 1704;<br>Best Local Similarity 31.9%; Pred. No. 3.2e-53;<br>Matches 235; Conservative 75; Mismatches 160; Indels 267; Gaps 20;                                                                                                                                |
| Q.y.<br>D.b.                                         | 186 PGDAASVV 193                                                                                                                                                                                                    | Qy 22 TAAAQGGEKTAPSVTHQAVQK-GIRTSKVKDLRDFIPAGMARIILEAH 68                                                                                                                                                                                                                                                  |
| oy.                                                  | 194VTGEGGNEFAPVQNLQMSVSGQTVTLTWQAPASDKRTYVLNE 235<br>                                                                                                                                                               | Qy 69 DVWEDGIGYQMLWDADHNQYGASIPEESFWPANGTIPAGLYDPFEYKVPVNADASFSP 126                                                                                                                                                                                                                                       |
| Qy<br>Db                                             | 236 SFDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN 295                                                                                                                                                | Qy 127 TNFVLDGTASADIPAGTYDYVINPNPGI-IYIVGEGVSKGNDYVVEAGKTYHPTVQRQG 185     ::                                                                                                                                                                                                                              |
| Oy<br>Dp                                             | 296 YLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS 350                                                                                                                                                    | Qy 186 PGDAASVV 193      :                                                                                                                                                                                                                                                                                 |
| λ                                                    | 351 354                                                                                                                                                                                                             | Qy 194VTGEGGNEFAPVQNLOWSVSGQTVTLTWQAPASDKRTYVLNESF 237                                                                                                                                                                                                                                                     |
| Ωp                                                   | 1086 SPEAIRGRIQSTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETF 1145                                                                                                                                              | Db 910 PKVCKDVTVEGSNEFAEVQNLTGSAVGQKVTLKWDAPNGTENENENENENEPREGTTTLSESF 969                                                                                                                                                                                                                                 |
| රු අ                                                 | 355PMNLV 359<br>    :<br>1146 ESSTHGEATAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVSSFSWNGMALNPDNYL 1205                                                                                                                     | Qy 238 DTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYL 297 :                                                                                                                                                                                                                                  |
| ογ                                                   | 360 359                                                                                                                                                                                                             | OY 298 VTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVELSTTGNEAANFTIKLLEETLGS 350                                                                                                                                                                                                                                          |
| Db                                                   | 1206 ISKDVIGATKVKYYYAVNDGFPGDHYAVMISKIGTNAGDFTVVFEETPNGINKGGARFGL 1265                                                                                                                                              | Db 1026 ITPALDLENGGKLTFWVCAQDANYASEHYAVYASSTGNDASNFTNALLEETITAKGVRSP 1085                                                                                                                                                                                                                                  |
| ZO<br>Dp                                             | 360KSEGVKLPAPYQERTIDLSAYAGQOYYLAFRHFNSTGIFRLYLDDVAVSGEGSSND 415 :::    ::                                                                                                                                           | Qy 351 366                                                                                                                                                                                                                                                                                                 |
|                                                      |                                                                                                                                                                                                                     |                                                                                                                                                                                                                                                                                                            |

| Qy         22 TARAAQGGPKTARENTHQAVQKGIRTSKVKDLRD | Qy         295 NYLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS 350           Db         1043 NYLITPALDIPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASNFTNALLEETTTAKGV 1102           Qy         351                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | RESULT 5 140229 arginyl endopeptidase - Porphyromonas gingivalis C,Species: Porphyromonas gingivalis C,Species: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 08-Oct-1999 C;Accession: 140229 R;Okamoto, K.; Misuni, Y.; Kadowaki, T.; Yoneda, M.; Yamamoto, K.; Ikehara, Y. Arch. Biochem. Biophys. 316, 917-925, 1995 A;Title: Structural characterization of argingipain, a novel arginine-specific cysteine A;Reference number: 140229, MUID:9516884; PMID:7864651 A;Reference number: 140229 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-991 «RES> A;Residues: 1-991 «RES> A;Residues: 1-991 «RES> A;Cross-references: GB:D26470; NID:9927644; PIDN:BAN05484:1; PID:g927645 Query Match Best Local Similarity 25.5%; Pred. NO. 2:9e-24; Matches 124; Conservative 41; Mismatches 90; Indels 231; Gaps 7; |
|--------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                                                  | lysine-specific cysteine proteinase porphypain (EC 3.4.22) - Porphyromonas gingivalis Nathernate names: lysine-specific cysteine proteinase 1, 60K (Species: Porphyromonas gingivalis C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 17-Nov-2000 (Accession: T30836, T30826, A53113 (Accession: T30836, T30826, A53113 (Accession: T30836, T30826, A53113 (Accession: T30836, T30826, A53113 (Accession: T30836, T30826, A53113 (Accession: T30836, T30826, A2110: PMID:8631659 (Accession: T30836, T30836, MUD:96213011; PMID:8631659 (Accession: T30836, T30836, MUD:96213011; PMID:8631659 (Accession: T30836, T30836, MUD:96213011; PMID:8631659 (Accession: T30836, T30836, T30836, T30836, T30836, T30837 (Accession: T30836, T30836, T30836, T30836, T30836, T30836, T30837 (Accession: T30837, Tanslated from GB/EMBL/DDBJ (Accession: T30837) (Accession: T30837 (Accession: T30837) (Accession: T30837 (Accession: T30837) (Accession: T30837 (Accession: T30837) (Accession: T30837 (Accession: T30837) (Accession: T30837 (Accession: T30837) (Accession: T30837 (Accession: T30837) (Accession: T30837 (Accession: T30837) (Accession: T30837 (Accession: T30837) (Accession: T30837 (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: T30837) (Accession: | A;Residues: 1-1350, NV, 1352-1363, YY, 1365-1447, 'H', 1449-1732 <lew> A;Residues: 1-1350, NV, 1352-1363, YY, 1365-1447, 'H', 1449-1732 <lew> A;Cross-references: EMBL:AF017059; NID:92738802; PID:92738803; PIDN:AAC26523.1  R;Pike, R.; McGraw, W.; Potempa, J.; Travis, J. J. Biol. Chem. 269, 406-411, 1994 J. Biol. Chem. 269, 406-411, 1994 J. Biol. Chem. 269, 406-411, 1994 J. Biol. Chem. 269, 406-411, 1994 J. Ricesahon: A53113 J. MUID:94103245; PMID:8276827 J. Ricesahon: A53113 J. Molecule type: protein J. Residues: 229-249 J. Residues: 229-249 J. Residues: 229-249 J. Residues: 229-249 J. Molecule type: protein J. Residues: 239-249 J. Molecule type: protein J. Residues: 239-249 J. Molecule type: J. J. J. J. J. J. J. J. J. J. J. J. J.</lew></lew>                                                               |

| P;537,539/Binding site: substrate (ABP, Asn) #status predicted  Querry Match Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Local Similarity 20.4%; Fred. No. 0.0431; Best Tronslogy Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantilarity Cantil | RESULT 7  F90656  Proportetical protein ECs0542 [imported] - Escherichia coli (strain 0157:H7, substrain R. C.5pecies: Escherichia coli C.5pecies: Bacherichia coli C.5pecies: Bacherichia coli C.5pecies: Bacherichia coli C.5pecies: Escherichia coli C.5pecies: Escherichia coli C.5pecies: Bacherichia coli C.5pecies: Bacherichia coli C.5Accession: F90656 R.Häysshi, T.: Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishli, K.; Yokoyama, K.; Han, C.G Gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.: DNA Res: B, 11-22, 2001 A,;Hitle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gent A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Molecula type: DNA A,;Mo |
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83

-GDAASV--

408

-NVVIAQNLAA 433

----EIAHNMKMRĞH---- 433

355

---EETLGSDKPAP--

---ANFTIKLL--

287

327 227

----DSWTTVSGTYTLDYTGT----LKTLYMY

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288 YIQVNDFVNVNKGEWTEIKGSF---TLPVTDYSGVSIYVESQ--NPT--LEFYIDDFSVI 340
                                                                                                                                          WQAPASDKRIYVINESFDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 GEISNNQITIQNDIPDLYSVFKDYFPIGVAVDSSRLNDADPHAQLTAKHFNMLVAEN--- 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 TTFNQENVAPGQYNYCVE----VKYTAGVSPKVCKDVTVEGSNEFAHVQNLTGSAVGQK 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 GGYSLLTTGRIANNGPSYDLTGKIVPGQQYNVDFWVKFVNGNDTEQIKATVKATSNKDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------MNLVKSEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                       169 -VESPDPTLEYYIDDVVVTPQNPIQVGNVITNGTFENGNTSGWVGTGSSVVKAVYGVAHS
28 IRAFADDININLVSNG----DFEIGTIDGMIKQGNPTLEVTTEQAIGQYSMKVTGRIQIY
                                                                                                                                                                                                                                                                                                                                                                     WTASGGAKIDLSPDNYLVTPKVTVP------ENGKLSYWVSSQVPWTNEHYGV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 -AMKPESLOPTEGNFTFDNADKIVDY-
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Matches 127; Conserv
                                                                                                                                                                                                                                                                                  138 WOKOVŠE--
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A; Status: preliminary
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C;Keywords: glycosidase; hydrolase
F;1-32/Domain: signal sequence #status predicted <SIG>F;133-1234/Product: endo-1,4-beta-xylanase A maino-terminal repeat homology <TXA1>F;195-339/Domain: Thermotoga xylanase A amino-terminal repeat homology <TXA2>F;195-339/Domain: Streptomyces endo-1,4-beta-xylanase A homology <XXX>F;885-675/Domain: Streptomyces endo-1,4-beta-xylanase A cellulose-binding repeat homology <TXC1>F;887-1042/Domain: Thermotoga xylanase A cellulose-binding repeat homology <TXC2>F;1055-1108/Domain: S-layer repeat homology <SIR>F;1055-1108/Domain: S-layer repeat homology <
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A;Description: Characterization of genes from Thermoanaerobacterium thermosulfurigenes A;Reference number: S72640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Accession: $72640

A, Roceaule type: DNA
A, Residues: 1-1234 <Amatus
A, Cross-references: EMBL:U50952; NID:g1255235; PIDN:AAB08046.1; PID:g1255238
A, Experimental Source: strain EMI
A, Experimental Source: strain EMI
R, Matuschek, M.; Sahm, K.; Zibat, A.; Bahl, H.
Mol. Gen. Genet. 252, 493-496, 1996
A, Title: Characterization of genes from Thermoanaerobacterium thermosulfurigenes EM1 the Accession: $72622
A, Accession: $72622
A, Residues: 815-1234 <AMAW>
A, Residues: 815-1234 <AMAW>
A, Cross-references: EMBL:U50952
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      --ISGDNLIN----AAE 3450
                                                                                                                                                                                                                                                      ---AEAGSALTLSGTGTNFATGTVVTVLLNGKGYSATIQSNGSWSVNVPAADVAALSDGT 3608
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                                                                                                                                                                                                                                                                                                                                          323
                                                                        173 AGKTYHFTVQRQGPGDAASVVVT----GEGGNEFAPVQ-NLQWSVSGQTVTLTWQAPASD 227
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Date: 29-Jul-1997 #sequence_revision 29-Jul-1997 #text_change 16-Jul-1999
Accession: S72640; S72622
                                                                                                               --YLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTVYRDNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIAONLAATTFNOENVAPGOYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVONLTG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 HYGVFLS---TTGNEAANFTIKLLEETLGSDKPAP---MNLVKSEGVKLPAPYQERTIDL
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20.0%; Pred. No. 0.078;
tive 66; Mismatches 138; Indels 184; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3662 NGSTSAEVGQTVTVTFGGKTYTATVAANGTWALNVPAVDLAALGQG------
                                                                                                                                                                                                                                                                                                                                          280 SWIASGGAKIDLS--PDNYLVIPKVIVPENGK-LSYWVSSQVPWI
                                                                                                                                                                                                         228 KRTYVLNESFDTQTLPNGWTMIDADGDGHNWLSTINV-YNTA-
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          ----SAGNSSTQTHNVQVNTAAVSLSVST-
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C;Superfamily: Thermoanaerobacterium
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Best Local (
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   and
probably cellulosomal scaffolding protein precursor, secreted, cellulose-binding C;Species: Clostridium acetobutylicum C;Sacess: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: C97012 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: C97012 #serton, G:, Omelhenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, S.Nolling, J.; Breton, G.; Omelhenko, M.V.; Smith, D.R.
                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AE001437; PIDN:AAK78886.1; PID:g15023809; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            578 LSQSYLAGLALGQYTLTLDFNGGGASQTITINVVKNETVKLSVGTVSGNPGD--TVKVPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%; Score 150; DB 2; Length 1483; 20.2%; Pred. No. 0.14;
                                                                                                                                                                                                            A,Title: Genome Sequence and Comparative Analysis of the A,Reference number: A96900; MUID:21359325, PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81; Mismatches
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Conservative

97;

Matches

Similarity

23;

| Db 325 SGSAKVYEATINKNGTYTLGAEVTSDMGIKIVESKGSVKVEL-PDGSTKAYVLIFETS 881  Qy 304 VPENGKLSYWVSSQVPWTNEHYGVPLSTTGNE | RESULT 11 T36143 probable secreted proteinase - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2003 C; Accession: T36143 R; Seeger, K.; Haris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999 A; Reference number: 221598 A; Reference number: 221598 A; Reference T36143 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA | A; KESTONES: 1-741 CASES A; KENDELIAGE SERIES ALOS 6852; PIDN: CABSIOOI.1; GSPDB:GNOOO70; SCOEDB:SCE19A.20c A; Experimental source: strain A3(2) A; Experimental source: strain A3(2) C; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Generics: A; Ge | OY 119 NADASESPINEVLOGIASADIPAGITUY LITENED 1.1 INCECTOR CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT IN CONTRACT |
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|                                                                                                                | Qy         392 FNSTGIFRLYLDDDAAVSGEGSSNDYT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | RESULT 10 G86643  Hypothetical protein ybeF [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis C;Accession: G86643 R;Accession: G86643 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Residues: Draliminary A;Rolecule type: DAA A;Residues: 1-1983 <ato> A;Cross-references: GB:ABC05176; PID:g12723000; PIDN:AAK04249.1; GSPDB:GN00146 A;Experimental source: strain IL1403 A;Genetics: A;Genetics:</ato>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Query Match         5:6%; Score 147; DB 2; Length 1983;           Best Local Similarity         21:7%; Pred. No. 0.32;           Matches 117; Conservative 77; Mismatches 181; Indels 164; Gaps 30;           QY         39 AVOKGIRTSKVKDLRDPIPAGMARIILEAHDVMEDGTCYQMLWDADHNQXGASIPEESFW 98           Db         628 ATQQGIVKMIDGDIDYSNREIPWKIDINSPGYW 660           QY         99 FANGTIPAGLYDPFEYKVPVNADASFSPTNF-VLDGTASADIPAGTYDYVINPNPGITY 157           Db         661 MENWSL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |

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A; Reference number: $19011; MUID: 92041687; PMID: 1938968
                                        A; Status: preliminary
                      A; Accession: S19011
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 15-Oct-1999
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 15-Oct-1999
C;Accession: S1901
R;Gosalbes, M.J.; Perez-Gonzalez, J.A.; Gonzalez, R.; Navarro, A.
J. Bacteriol. 173, 7705-7710, 1991
A;Title: Two beta-glycanase genes are clustered in Bacillus polymyxa: molecular cloning,
                                                                                                                                                                                                                                                       M.J., Br
K., Lim,
                                                                                                                                                                                                                                                                                                                                       A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A,Reference number: A82950; MUID:20437337; PMID:10984043
A,Accession: A83412
                                                                                                                                                                                                                                                                                                                                                                                                                        A, Molecule type: DNA
A, Residues: 1-2468 <STO>
A, Cross-references: GB:AE004613; GB:AE004091; NID:g9947856; PIDN:AAG05263.1; GSPDB:GN001
                                                                                                                                                                                                                                                       P.; Hickey,
A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 VS-KGNDYVVEAGKTYHFTVQRQGPGDAASVVVTGEGGNEFAPVQNLQWSVSGQTVTLTW 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352 SSVTGN---AEPGAT--VGVDTDGDGQPDTTVVVGPGGSFEVPLN--PPLTNGETVTVIV 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405 TDPAGNSSTPVTAEAPDFPDAPQVNASNGSVLSGTAEAGVTIVITDGNGNPIGQTSADAN 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---FSKSWTASG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 GAKIDLSPDNYLVTPKVTVPENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAANFTIKLLE 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVSGEGSSNDYTYT----VYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         622 QVTADGSGN-WTFTPSTPLPNGTVV---NATATDPSGNASSPAS----VTVDAVAPATFV 673
                                                                                                                                                                     hypothetical protein PA1874 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                           C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #seguence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 GNWSFTPGSQLPDGTVVNVVARDAAGNSSPATSITVDGVAPNAPVVEPSNGSELSGTAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 ETLGSDKPAPMNLVKSEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 IIPAGLYDPFEYKVPVNADASFSPTNFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         580 VTVDAVAPATPTVDPSNGT-----TLSGTAEPGSSVTLTDGNGNPIG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 131; Gaps
                                                                                                                                                                                                                               C,Accession: A83412
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, I.; Lorry, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2468;
                                              ---VIAONLAATTFNOENVAPGOYNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -INVY-----NTATH-TGDGAM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Bacillus polymyxa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 5.2%; Score 138.5; DB 2; Best Local Similarity 23.7%; Pred. No. 1.6; Matches 107; Conservative 47; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V--CKDVTVEGSNEFAHVQNLT---GSAVGQ 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNPSNGTTLSGTAEPGATVTLTDGNGNPIGQ 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 QAPASDKRTYVLNESFDTQTLPN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endo-1,4-beta-xylanase (EC 3.2.1.8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary A;Molecule type: nwn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 -NWLST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PA1874
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A. Molecule type: DNA
A. Residues: 1-635 < GOS
A. Residues: 1-635 < GOS
A. Residues: 1-635 < GOS
A. Cose-references: EMBL:X57094; NID:948815; PIDN:CAA40378.1; PID:948816
A. Molec: the authors translated the codon GAA for residue 78 as Gly, CCT for residue 272
C. Function:
A. Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans
A. Description: catalyzes the hydrolysis of 1,4-beta-xylosidic linkages in xylans
C. Superfamily: Clostridium xylanase A repeat homology
C. Keywords: glycosidase; hydrolase; polysaccharide degradation
F;408-502/Domain: Clostridium xylanase A repeat homology < CXA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----NPG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---EGVSKGNDYVVEAGKTY---HFT-VQRQGPGDAA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 TPFGVGGNNHHAVFNFKNEMYVVYHAQTVSKAQ---IGAGKGYRSPHINKLVHKEDGSIS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 SVV--VIGEGGNEFAPVQNLQMSVSGQTVTLTWQAPASDKRTYVLNESFDTQTLPNGWTM 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 -QASGGP---ISNLNVTN--IHNGDWIAVGKADFGSAGAKTFKANVATNVGGNIEVRLDS 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 DNYLVTPKVTVPENGKLSYW--VSSQVPWTNEHYGVFLSTTGNEAAN-----FTIKL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 LFEDSGIHKYNGKYYYSYCINFA--GTHPQQYPAGEIGYMVSDNPMGPFTYKGHFLKNPY 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402 LDDVAVSGEGSSNDYTYTVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: || || || ::| || || 201 --LYS------GGGIPNES------DPASIANPKTARVIKLGADMISVIGSATTIDAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452 ETGPLVGSLKVPSTGGMQTWREVETTINNATGVHNIYLVFTGSGSGNLLNLDAWQFTPNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LS6 TADTPIGPWTDPLGKALVTHST------PGMAGVTWLFDPAVLVDDDGTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 TAAAQGGPKTAP----SVTHQAVQKGIRTSKVKDLRDPIPAGMARIILEAHDVWEDGTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65; Mismatches 176; Indels 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 SFSPT-------NFVLDGTASADIPAGTYDYVII-NP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 VCKDVTVEGSNEFAHVQNLTGSAVGQKVTL-----KNDA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V-----QTLSNITHATGDQEIKLALTSDDGTWDA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 OMLWDADHNOYGASIPEESFWFANGTIPAGLYDPFEYKV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 IDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAK-
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 137.5; DB 2;
Pred. No. 0.27;
                                                                                                                                                                                                                                                                                                                                                                                                                                      5.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 21.24
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 IIYIVG----
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probable peptidoglycan bound protein (LPXTG motif) lin0457 [imported] - Listeria innocus C.Species: Listeria innocus C.Species: Listeria innocus C.Species: Listeria innocus C.Spacies: Listeria innocus C.Spaces: Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001 C.Accession: A11489

R.Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Katef, U. Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669

us-08-570-311-2.rpr

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1567 ARLDVTDNNDDTT-----NLIITSNFA-----ËKVNLNKPGKYEVTISATDTKG--NQ 1612
                                                                                                                                                                                                                                                                                                                                                                                                                   1185 GODYEIALFDKDGKEVQSAIKTNNKGEFSFSD----VAIKNPADFKLKVTAP---TRINF 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1238 VY----SAKNPLFNMSTKEYTLNSVVPGV-----GGVAE--IYITETSKPTTKIILDKAV 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1397 ITPVVDYŠKVKWDVLGTYPVTVTAŤDASĆNKATQTVNLRIVĎTTSPTILIŤ------NN 1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1450 PLTYSIENWRKLTEQELYKAAGLIGGDNYDLAPGQSVQPNKQPMVFTSNFS--TIFSDIA 1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1508 SVKPGQYQVQVNLADSSGNQAIPQTITINVVDTMGPVIKADNVSY-HVNTTKTEAEFFQD 1566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1287 TPNA----ITIESSDEATEVTN-EWTVVDSNGTVVYSGTGNTIRIPNDEGTYIAKNTATD 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          404
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                                                       A;Residues: 1-2013 <GLA>
A;Residues: 1-2013 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC95689.1; PID:g16412898; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 QA--PASDKRTYVLNESFDTQTLPNGWTMIDADGDGH-----NWLSTINVYNTATHTGD 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -TASGGAK-----IDLSPDNYLVTPKVTVPENG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLSYWVSSQVPWTNEHYGVFLSTTGNE-------AANFTIKLLEETLG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 VLDGTASADIP---AGTYDYVIINPNPGIIYIVGEGVSKGNDYVVEAGK-TYHFTVQRQG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----TLTW 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDKP----APMNLVKSEGVK-LPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405 VAVSGEGSSNDYTYTVYRDNVVIAQNLAATTFNQENV---APGQYNYCVEVKYTAGVSPK
                                                                                                                                                                                                                                                                                                                                                                               GTGYOM-LWDADHNOYGASIPEES---FWFANGTIPAGLYDPFEYKVPVNADASFSPTNF
                                                                                                                                                                                                                                                                                                             82; Mismatches 163; Indels 144;
                                                                                                                                                                                                                                                  5.2%; Score 137; DB 2; Length 2013; 20.9%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SGOTV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 PGDAASVVVTGEGGNEFAPVQNLQWSV---
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1613 TTKEITVQVSKD 1624
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                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 103; Conserv
A;Status: preliminary
A;Molecule type: DNA
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A; Scards: preliminary; translated from GB/EMBL/DUBU
A; Rolecule type: DNA
A; Residues: 1-211 cRES.
A; Rolecule type: DNA
A; Rolecule type: DNA
A; Robidues: 1-211 cRES.
A; Cross-references GB: W12230; NID: G142938; PIDN: AAA22458.1; PID: GSZ1705
C; Bron, S.; Broullet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch.
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Perrari, E.
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Perrari, E.
A; Authors: Poulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle:
i.ech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee.
Y, M.; Ogawa, K.; Ogiwara, A.; Oduega, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sado, T.; Scanlon,
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sckiguchi, J.; Sckowska, A.; Scanlon,
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sckiguchi, J.; Sckowska, A.; Scanlon,
A; Authors: Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A.
A; Hulbors: Yoshikawa, H.F.; Zumstein, B.; Yoshikawa, H.; Danchin, A.
A; Reference nuuber: A69580; MUD: 98044033; PMID: 9384377
A; Accession: B69596
A; Recidues: 1-1433 <a href="mailto: kumb-rieferences: GB: Z99111; GB: Z99112; GB: AL009126; NID: G2633902; PIDN: CAB13404.1; P. A; Conserient Bource: Strain 168
C; Genetics: Lesson 168080; MID: Garain 168
C; Genetics: Lesson 168080; MID: Garain 168
C; Genetics: Lesson 168080; MID: GB: Z99111; GB: Z99112; GB: AL009126; NID: G2633902; PIDN: CAB13404.1; P. Conserient Lesson 268080; MID: Garain 168
C; Genetics: Lesson 268080; MID: GB: Z99112; GB: AL009126; NID: G2633902; PIDN: CAB13404.1; P. C. Conserient Lesson 268080; MID: Garain 168080; MID: Garain 168080; MID: Garain 168080; MID: Garain 168080; MID: Garain 168080; MID: Garain 168080; MID: Garain 168080; MID: Garain 16808
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Biosot. Biotechnol. Biochem. Sc. 1166-1168, 1992
A;Title: Purification of a new extracellular 90-kba serine proteinase with isoelectric I
A;Reference number: JN0335; MUID:93005071; PMID:1368833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 195-218, A' < KAT>
A; Residues: 195-218, A' < KAT>
A; Residues: 195-218, A' < KAT>
A; Note: source of this material was Bacillus subtilis (natto)
B; Beall, B.; Lowe, M.; Luckenhaus, J.
J. Bacteriol. 170, 4855-4864, 1988
A; Title: Cloning and characterization of Bacillus subtilis homologs of Escherichia coli
A; Reference number: 139846; MUID:89008108; PMID:3139638
A; Recension: 139849
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Note: this sequence has been corrected R;Masuda, E.S.; Anaguchi, H.; Sato, T.; Takeuchi, M.; Kobayashi, Y. Nucleic Acids Res. 18, 657, 1990 A;Title: Nucleotide sequence of the sporulation gene spoilGA from Bacillus subtilis. A;Reference number: S08223; MUID:90174995; PMID:2106671
                                                        J. Biol. Chem. 265, 6845-6850, 1990
A.Title: Cloning, genetic organization, and characterization of a structural gene A.Reference number: A35750; MUID:90216713; PMID:2108961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 876-935,'CG' <WU2>
A;Cross-references: GB:J05400; NID:g142607; PIDN:AAA83363.1; PID:g1119197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1410-1433 < MAS>
A; Cross-references: EMBL:X17344; NID:940165; PIDN:CAA35224.1; PID:9809661
                                                                                                                                                                                                                A,Gene: bpr; bpf
A,Map position: 135 (degrees)
C,Superfamily: bacillopeptidase F; subtilisin homology
C;Keywords extracellular protein; hydrolase; serine proteinase
F;130/Domain: signal sequence #status predicted <SIG>F;31-194/Domain: propeptide #status predicted <PRO>F;31-194/Domain: propeptide #status predicted <PRO>F;195-1433/Product: bacillopeptidase F #status experimental <MATF;213-466/Domain: subtiliain homology <SBT>F;227,274,452/Active site: Asp, His, Ser #status predicted
X.C.; Nathoo, S.; Pang, A.S.H.; Carne, T.; Wong, S.L.
51. Chem. 265, 6845-6850, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: JN0335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S08223
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DB 1; Length 1433;

Score 135.5;

5.1%;

Search completed: May 18, 2004, 11:47:45 Job time : 15.9765 secs

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GenCore version 5.1,6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 18, 2004, 11:35:14 ; Search time 9.08355 Seconds (without alignments) 2848.981 Million cell updates/sec

Title: Perfect score: Sequence:

US-08-570-311-2 2641 1 MRKINSLFSLAVLLSLLCWG......QNLTGSAVGQKVTLKWDAPN 497

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB sed length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt 42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description           |            | ın   | 3784  | 5071       |            |            |            |            | Q97z97 sulfolobus |            | P59809 chlamydophi |            |            | bacillus   | _     |            | P14914 rickettsia | Q53047 r outer mem |            |            |           |            | _          |            | P09333 bacillus br | P56199 homo sapien | P24821 homo sapien | esche      | O14556 homo sapien | P07589 bos taurus | Q9phw6 campylobact | ۰,  | P44596 haemophilus |
|-----------|-----------------------|------------|------|-------|------------|------------|------------|------------|------------|-------------------|------------|--------------------|------------|------------|------------|-------|------------|-------------------|--------------------|------------|------------|-----------|------------|------------|------------|--------------------|--------------------|--------------------|------------|--------------------|-------------------|--------------------|-----|--------------------|
| SUMMARIES | ΩI                    | HGA2 PORGI |      |       | PRTH PORGI | XXNA_THESA | XYND PAEPO | SUBF BACSU | OMPB RICCN | YA33 SULSO        | OMPB RICJA | OXAA CHLCV         | TOXA CLODI | SLAP_BACCI | CTA1 BACCI |       | CHII_BACCI | 120K RICRI        | OMPB_RICRI         | G3P1_SCHPO | G3PC GRAVE | PHB_ALCFA | TKT2_YEAST | GELA DICDI | YEEJ_ECO57 | SLPO BACBR         | ITA1_HUMAN         | TENA_HUMAN         | YEEJ ECOLI | G3PT HUMAN         |                   | FLID CAMJE         |     | HAP1_HAEIN         |
|           | DB                    | -          | Н    | Н     | Н          | Н          | Н          | Н          | Н          | Н                 | Н          | Н                  | Н          | н          | Н          | Н     | Н          | Н                 |                    |            |            |           | Н          | Н          | H          | М                  | Н                  | rH                 | r          | н                  | н                 | Н                  | Н   | eч                 |
|           | Query<br>Match Length | 2628       | 2164 | 991   | 989        | 1157       | 635        | 1433       | 1655       | 725               | 1656       | 794                | 2710       | 1616       | 972        | 587   | 669        | 1300              | 1654               | 336        | 335        | 488       | 681        | 857        | 2660       | 1004               | 1151               | 2201               | 2358       | 408                | 2265              | 642                | 827 | 1409               |
| æ         | Query                 | 100.       | 8.76 | 8     | 7          | •          | ٠          |            |            | •                 |            |                    | •          | •          |            | 4.6   |            |                   | •                  | 4.4        |            | 4.3       | ٠          | •          | •          | •                  | ٠                  | •                  | •          | •                  | •                 | •                  | 4.2 | 4.2                |
|           | Score                 | 2641       | 2583 | 494.5 | 472        | 156        | 137.5      | 135.5      | 135        | 131.5             | 131        | 129                | 127        | 124        | N          | 120.5 | 119        | 118.5             | 118.5              | 115.5      | 114.5      | 114.5     | 114.5      | 114.5      | 114.5      | 113.5              | 113.5              | 111                |            | 110.5              |                   | 110                | 110 | 110                |
|           | Result<br>No.         | -1         | 7    | ю     | 4          | ហ          | 9          | 7          | œ          | σ                 | 10         | 11                 | 12         | 13         | 14         | 15    | 16         | 17                | 18                 | 13         | 20         | 21        | 22         | 23         | 24         | 25                 | (1)                | 27                 | 28         | 29                 | 30                | 31                 | 32  | 33                 |

| Q9y5h0 homo sapien | Q52657 rickettsia | P35806 caulobacter | P35830 thermus the | P76072 escherichia | P32637 podospora a | Q11176 caenorhabdi | P21647 klebsiella | Q91740 xenopus lae | P16950 t amylopull | P04937 rattus norv | Q60053 thermoactin |
|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|
| CDG3 HUMAN         | OMPA_RICCN        | FLGE CAUCR         | SLAP THETH         | STFR ECOLI         | G3P PODAN          | WDRI CAEEL         | MRKC KLEPN        | FINC XENLA         | APU THETY          | FINC RAT           | NEP1_THEVU         |
| Н                  | Н                 | Н                  | 7                  | 7                  | ÷                  | 7                  | Н                 | Н                  | Н                  | Н                  | Н                  |
| 932                | 2021              | 591                | 917                | 1120               | 337                | 611                | 828               | 2481               | 1475               | 2477               | 999                |
|                    |                   |                    |                    |                    |                    |                    |                   |                    |                    |                    |                    |
|                    | 4.1               | 4.1                | 4.1                | 4.1                | 4.1                | 4.1                | 4.1               | 4.1                | 4.1                | 4.1                | 4.1                |
| 4.1                | 109.5 4.1         |                    |                    |                    | •                  |                    |                   |                    |                    |                    |                    |

## ALIGNMENTS

|                  | ALIGNMENTS                                                                                                 |
|------------------|------------------------------------------------------------------------------------------------------------|
| RESULT<br>HGA2_P | LT 1<br>PORGI                                                                                              |
| a d              | HGAZ PORGI STANDARD; PRT; 2628 AA.<br>O51845;                                                              |
| TO E             | 2000 (Rel. 39, Creat                                                                                       |
| Z E              | 10-OCT-2000 (Rel. 32, Last annotation update)                                                              |
| E E              | rsor.                                                                                                      |
| SS               | hyromonas gingivalis (Bacteroides gingival                                                                 |
| )<br>0<br>0      | Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;<br>Pornhyromonadaceae: Pornhyromonae          |
| 888              | TaxID=837;                                                                                                 |
| R P              | [1]<br>SEOUENCE FROM N.A.                                                                                  |
| RC               | STRAIN=381;                                                                                                |
| X :              | MEDLINE=97047672; PubMed=8926061;                                                                          |
| RT               | Han N., Whitlock J., Progulske-Fox A.;<br>"The hemagalutinin gene A (haga) of Porphyromonas ginginalis 381 |
| RT               | s four large, contiguous, direct repeats.";                                                                |
| R.               |                                                                                                            |
| ဗ္ဗ ဗ္ဗ          | -!- FUNCTION: Agglutinates erythrocytes.                                                                   |
| 38               | -:- SIMILMAKIII: Belongs to pepciaase ramily C25.                                                          |
| SS               | SS-PROT entry is copyright. It is produced throug                                                          |
| ပ္ပ              | informatics and the EMBL outstatio                                                                         |
| ខ្លួ             | the European Bioinformatics Institute. There are no restrictions on its                                    |
| 38               | ified and this statement is not removed.                                                                   |
| S                | requires a license agreement (See http://www.isb-sib.ch                                                    |
| 8                | Wisb-sib.ch).                                                                                              |
| ၁ ဥ              | DMD1. IIV1607, XXD141.00 1.                                                                                |
| ž ž              | BMBD; U4100/; AMBI/128:1;<br>PIR: T28651: T28651.                                                          |
| K                | glutinin; Virulence; Hyd                                                                                   |
| FT               | 1 24 POTENTIAL.                                                                                            |
| H                | 25 2628 HEMAGGLUTININ A.                                                                                   |
| H .              | 25 539 PEPTIDASE C25-LIKE                                                                                  |
| H E              | PEPTIDASE                                                                                                  |
| - L              | 1451 PEPTIDASE C25-LIKE<br>1452 1907 DEPTIDASE C25-LIKE                                                    |
| H                | 2074 2628 PEPT                                                                                             |
| SO               | 628 AA; 283324 MW; 61C4DE32540C99DA                                                                        |
| 8                | Query Match 100.0%; Score 2641; DB 1; Length 2628; Boet 1003 Charley 100.0%.                               |
| Ma               | 7; Conservative 0;                                                                                         |
| δ                | 1 MRKLNSLFSLAVILSILCWGQTAAAQGGPKTAPSVTHQAVQKGIRTSKVKDLRDPIPAGM 60                                          |
| qq               | 1 MRKLNSLFSLAVLLSLLCWGQTAAAQGGPKTAPSVTHQAVQKGIRTSKVKDLRDPIPAGM 60                                          |
| δ                | 61 ARILLEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDPFEYKVPVNA 120                                        |
| g                | 61 ARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDFFEYKVPVNA 120                                        |
|                  |                                                                                                            |

us-08-570-311-2.rsp

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09 9 180 180 240 240 300 300 360 360 420 420 480

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41 ARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDPFEYKVPVNA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 YRDNVVIAQNLTATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAPVQNL 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRKLNSLFSLAVLLSLLCWGQTAAAQGGPKTAPSVTHQAVQKGIRTSKAKDLRDPIPAGM
                                                                                                                                                                                                                                           ARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDPFEYKVPVNA
                                                                                                                                                                                                                                                                                                                                                                 VQRQGPGDAASVVVTGEGGNEFAPVQNLQMSVSGQTVTLTWQAPASDXRTYVLNESFDTQ
                                                                                                                                                                                                                                                                                                                                                                                                     101 VQRQGPGDAASVVVTGEGGNEFAPVQNLQMSVSGQTVTLTWQAPASDKRTYVLNESFDTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASSGAKIDLSPDNYLVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 KVTVPENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDKPAPMNLVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 SEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 SEGVKAPAPYQERTIDLSAYAGQQVYLAFRHFGCTGIFRLYLDDVAVSGEGSSNDYTYTV
                                                                                                                                        A MRKINSLFSLAVILSLICWGQTAAAQGGPKTAPSVTHQAVQKGIRTSKVKDLRDPIPAGM
                                                                                                                                                                                                                                                                                        DASFSPINFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSKGNDYVVEAGKTYHFT
                                                                                                                                                                                                                                                                                                                              121 DASFSPINFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSKGNDYVVEAGKTYHFT
                                                                                                                                                                                                                                                                                                                                                                                                                                           TLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
dingipain R1 precursor (EC 3.4.22.37) (Gingipain 1) (Arg-gingipain)
                                                                                                    0;
                                                                 Length 2164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ikehara Y.;
"Structural characterization of argingipain, a novel
arginine-specific cysteine proteinase as a major periodontal
pathogenic factor from Porphyromonas gingivalis.";
Arch. Biochem. Biophys. 316:917-925 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=HG66;
MEDLINE=92406812; PubMed=1527017;
Chen Z., Potempa J., Polanowski A., Wikstrom M., Travis J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ž
                                                                                                    10; Indels
     PEPTIDASE C25-LIKE 3.
W; 6DPAB22832586C63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95168884; PubMed=7864651;
Okamoto K., Misumi Y., Kadowaki T., Yoneda M., Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 228-290 AND 517-541 STRAIN=381;
                                                             Score 2583; DB 1;
Pred. No. 4.9e-159;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    991 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porphyromonadaceae; Porphyromonas.
                         233387 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGSAVGQKVTLKWDAPN 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 TGSAVGOKVTLKWDAPN 497
                                                                               98.0%;
                                                               97.8%;
                                                                             Local Similarity 98.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
         1443
       992 14.
2164 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 228-270.
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       DOMAIN
SEQUENCE
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                                                               Query Match
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                                                                                                                                                                                                                                                   KVIVPENGKLSYWVSSQVPWINEHYGVFLSTIGNEAANFIIKLLEETLGSDKPAPMLVK 360
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                                                                                                        VQRQGPGDAASVVVTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPASDKRTYVLNESFDTQ
                                                                                                                                                                        YRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL
DASFSPINFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSKGNDYVVEAGKTYHFT
                     DASFSPINFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSKGNDYVVEAGKTYHFT
                                                                         VQRQGPGDAASVVVTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPASDKRTXVLNESFDTQ
                                                                                                                                                                                                                                                                                                    SEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTV
                                                                                                                                                  TLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E., Bisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M., Haft D.H., Kolonay J.F., Nelson W.C., Mason T., Tallon L., Gray J., Dewhirst F.E., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gingivalis). (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivals strain W83.";
J. Bacteriol. 185:5591-5601(2003).
-!- FUNCTION: Agglutinates erythrocytes (By similarity).
-!- SIMILARITY: Belongs to peptidase family C25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.4
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PEPTIDASE C25-LIKE
PEPTIDASE C25-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2164 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porphyromonas gingivalis (Bacteroides
Bacteria, Bacteroidetes, Bacteroides (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE017178; AAQ66831.1; ALT_INIT.
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MEDLINE=22829867; PubMed=12949112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 42, Created)
(Rel. 42, Last seq
(Rel. 43, Last ann
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P59915;
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HGA1_PORGI
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               --EGGGSDYTYTVYRDGT 875
                                              426 VIAQNLAATTENQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNLTGSAV 485
                                                                                 876 KIKEGLIETIYRDAGMSAQSHEYCVEVKYAAGVSPKVCVDYIPDGVADVTAQKPYLLTVV 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 QGWLCLSSGQLDWLTAHGGTNVVSSFSWNG-----NALNPDNYLLSKDVTGATKVKYYA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 GTEICCFPSLPKAPICSTSTLMRLRSKTNAKRADFTETFESSTHGEAPAEWTTIDADGDG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 HNW--LSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTPKVTVPENGKLSYW 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P.GINGIVALIS TO EVADE COMPLEMENT MEDIATED KILLING DURING THE IMMUNE RESPONSE. PLAYS AN IMPORTANT ROLE IN SOFT TISSUE INFECTIONS AND IS A VIRULENCE FACTOR.

-!- SUBCELLULAR LOCATION: In membrane vesicles.
-!- SIMILARITY: Belongs to peptidase family C25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 GNEFAPVQNLQWSVSGQTVTLTWQAPASDKRTYVLNESFDTQT---LPNGWTMIDADGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fletcher H.M., Schenkein H.A., Macrina F.L.; "Cloning and characterization of a new protease gene (prtH) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAY ENABLE
                                                                                                                                                                                                                                                                                                                                                                                       Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.9%; Score 472; DB 1; Length 989 38.6%; Pred. No. 5.7e-23; Live 45; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110238 MW; FA85FE8A3AC8944C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fletcher H.M., Schenkein H.A., Macrina F.L.,
Infect. Immun. 62:5707-5707(1994)
-!- FUNCTION: CLEAVES HUMAN COMPLEMENT COMPONENT C3.
                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Protease prtH (EC 3.4.22..).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00551; formyl transf; 1.
Hydrolase; Thiol protease; Repeat; Virulence.
                                                                                                                                                                                                                                                      989 AA.
                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                        Porphyromonadaceae; Porphyromonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Infect. Immun. 62:4279-4286(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95012612; PubMed=7927685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L27483; AAA51298.1; -.
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GKTITV 941
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                                                                                                                      GOKVTL 491
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MEROPS; C25.001; -.
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P46071;
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           960
                                                                                                                      486
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PRIM PORGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68
                                                                                                                                            CATALYTIC ACTIVITY: Cleavage of proteins, including collagens and immunoglobulins, with a preference for Arg in Pl, and hydrophobic residues in P2 and P3.

ENZYME REGULATION: Requires cysteine for activation and Ca(2+) and/or Mg(2+) for stabilization. It is stimulated by glycine-containing dipeptides. It is resistant to inhibition by proteinase inhibitors in human plasma.

SIMILARITY: Belongs to peptidase family C25.
                                                    intracellular degradation and turnover of proteins. Its proteolytic activity is a major factor in both periodontal tissue destruction and in bacterial host defense mechanisms. Activates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAAAQG------GPKTAPSVTHQAVQK--GIR---TSKVKDLRDPIPAGMARIILEAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 WIMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTPKVTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 ENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDKPAPMNLVKSEGVK
"Purification and characterization of a 50-kDa cysteine proteinase (gingipain) from Porphyromonas gingivalis.";
J. Biol. Chem. 267:18896-18901(1992)
-!- FUNCTION: Thiol protease which is believed to participate in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virulence; Hydrolase; Thíol protease; Calcium; Signal; Zymogen. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.7%; Score 494.5; DB 1; Length 991; 25.5%; Pred. No. 2e-24; Live 41; Mismatches 90; Indels 231.
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GINGIPAIN R1.

PROTON DONOR (BY SIMILARITY)

NUCLEOPHILE (BY SIMILARITY).

865

R1 -> TK (IN REF. 2).

108782 MW; 03EE3F43CEBE2544 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IRR007110; Ig-like.
InterPro; IRR00176; Peptidase C25.
InterPro; IPR005536; Peptidase C25.
Pfam; PF01364; Peptidase C25, I.
Pfam; PF03785; Peptidase C25, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D26470; BAA05484.1; -.
PIR; 140229; 140229;
HSSP; P95493; ICVR.
MEROPS; C25.001; -.
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ACT_SITE
CONFLICT
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                                                                                                                                    287
VSSQVPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDK-PAPMNL-VKSEGVKLPAPYQ 371
                           489
                                                                                                                                                                                                     288 GLTETTFEEDGVATGNHEYCVEVKYTAGVSPKKCVNVTV-NSTQFNPVKNLKAQPDGGDV 346
                                                                                      ERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYTYTVYRDNVVIAQ
                                                                                                             430 NLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNLTGSAVGQKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linkages in xylans.
-!- PATHWAY: Xylan degradation.
-!- INDUCTION: By xylan and xylose.
-!- SIMILARITY: Belongs to cellulase family F (family 10 of glycosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee Y.-E., Lowe S.E., Zeikus J.G.,
"Gene cloning, sequencing, and biochemical characterization of
endoxylanase from Thermoanaerobacterium saccharolyticum B6A-RI.";
Appl. Environ. Microbiol. 59:3134-3137(1993).
[2]
ACTIVE SITE, AND MUTAGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    xylobiose.
CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacteriaceae, Thermoanaerobacterium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydrolases),
SIMILARITY: Contains 2 S-layer homology (SLH) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 34-41.

    4-beta-D-xylan xylanohydrolase A)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermoanaerobacter saccharolyticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94028940; PubMed=8215382
                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                  490 TLKWDAPN 497
                                                                                                                                                                                                                                                                                                         347 VLKWEAPS 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=B6A-RI;
                                                                                                                                                                                                                                                                                                                                                                                                                       XYNA THESA P36917;
                                                                                      372
                                                                                                                                  231
                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
XYNA THESA
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EMBL; M97882; AAA21812.1; ALT\_SEQ. HSSP; P10478; 1XYZ. InterPro; IPR008960; CBD9-like.

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106 AGLYDPFEYKVPVNADASFSPTNFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 EDDNGKHYDTIVWOKOVSEDSWTTVSGTYTLDYIGTLKTLYMYVESPDPTLEYYIDDVVV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WTAS-GGAKIDLSPDNYLVTPKVTVPENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAANF 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 TIKLLEETLGSDKPAPM-----NLVKSEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFN 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 PT--LEFYIDDFSVIGEISNNQITIQNDIPDLYSVFKDYFPIGVAVDPSRLNDADPHAQL 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 TTQNPIQVGNVIANETFENGNT-----SGWIGTGSSVVKAVXGVA-HSGDYSLLTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 GNDYVVEAGKTYHFTVQRQGP-----GDAASV----VVTGE-GGNEFAPVQNLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TQTLPNGWTMIDADGDGHNWLSTIN----VYNTATHTGDGAMFSKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 RTÅNWNGPSYDL------TGKIVPGQQYNVDFWVK-------FVNGNDTEQIKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 ASLFSP----PIRVFADDININLVSNG----DFESGTIDGWIKQGNPTLAVTTEQAIGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.9%; Score 156; DB 1; Length 1157;
20.4%; Pred. No. 0.019;
iive 64; Mismatches 128; Indels 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 WSVSGQTV-TLTWQAPASD-------KRTYVLNESFD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
14, Last annotation update)
Endo-1,4-beta-xylanase D precursor (EC 3.2.1.8) (Xylanase D)
(1,4-beta-b-xylan xylanohydrolase D).
                                                                                                                                                                                                                                                                                                                                                                                             PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                   Xylan degradation; Hydrolase; Glycosidase; Signal; Repeat.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128379 MW; 51FA6004497EC58B CRC64;
                                                                                                                                                                                                                                                                                                           ENDO-1,4-BETA-XYLANASE A. CATALYTIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 STGIFRLYLDDVAVSGEGSSNDYT-----YTVYRD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     D->N: LOSS OF ACTIVITY.
E->Q: LOSS OF ACTIVITY.
D->N: LOSS OF ACTIVITY.
InterPro; IPR003305; CBM CenC.
InterPro; IPR008979; Gal bind like.
InterPro; IPR008979; Gal bind like.
InterPro; IPR001000; GlyCo_hydro_10.
InterPro; IPR001119; SLH.
Pfam; PF00311; GlyCo_hydro_10; 1.
Pfam; PF00331; GlyCo_hydro_10; 1.
Pfam; PF00335; SLH; 2.
PRINTS; PR00134; GLHYDRLASE10.
SWART; SW00531; GlyCo_10; 1.
PROSITE; PS00551; GLYCOSYL_HYDROL_F10; 1.
PROSITE; PS01072; SLH DOWAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   635 A.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387 TAKHFNMLVAEN----AMKPESLQPTEGNF 412
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOPHILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92; Conservative
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                                                                                                                                                                                                                                                                                                                                 649
11113
11157
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61157 AA;
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XYND PAEPO
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ACT_SITE
ACT_SITE
MUTAGEN
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DOMAIN
DOMAIN
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462 VCKDVTVEGSNEFAHVQNLTGSAVGQKVTL-
                                                                           561 -HNISVRG-ASSNAGTAKV---DLVIG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                  and cloning of the gene.";
J. Bacteriol, 172:1470-1477(1990),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90170864; PubMed=2106512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriol. 172:5520-5521(1990)
                                                                                                                                                                                                                                 01-AUG-1990 (Rel. 15, Created)
                                                                                                                                                                                                                                                                                          (90 kDa serine proteinase).
                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                         OR BPF OR BSU15300.
illus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                         SUBF_BACSU
ID SUBF_BACSU
AC P16397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=168
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                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 --LYS-----GGGIPNES-----DPASIANPKTARVIKLGADMTSVIGSATTIDAPY 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---EGVSKGNDYVVEAGKTY---HFT-VQRQGPGDAA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 SVV--VTGEGGNEFAPVQNLOWSVSGQTVTLTWQAPASDKRTYVLNESFDTQTLPNGWTM 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QASGGP---ISNINVIN--IHNGDWIAVGKADFGSAGAKTFKANVATNVGGNIEVRLDS 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 LFEDSGIHKYNGKYYYSYCINFA--GTHPQQYPAGEIGYMVSDNPMGPFTYKGHFLKNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 TFFGVGGNNHHAVFNFKNEMYVVYHAQTVSKAQ---IGAGKGYRSPHINKLVHKEDGSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 TAAAAQGGPKTAP----SVTHQAVQKGIRTSKVKDLRDPIPAGMARIILEAHDVWEDGTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- PVNADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 LEETLGSDKPAPMNLVKSEGVKLPAPYQERTIDLSAYAGQQVYLAFRHF--NSTGIFRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.2%; Score 137.5; DB 1; Length 635;
21.2%; Pred. No. 0.14;
Live 65; Mismatches 176; Indels 217; Gaps
           Paenibacillus polymyxa (Bacillus polymyxa).
Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
                                                                                                          Gosalbes M.J., Perez-Gonzalez J.A., Gonzalez R., Navarro A., "Two beta-giycanase genes are clustered in Bacillus polymyxa: molecular cloning, expression, and sequence analysis of genes encoding a xylanase and an endo-beta-(1,3)-(1,4)-glucanase.", J. Bacteriol. 173:7705-7710(1991).

-! FUNCTION: SHOWS XYLANASE ACTIVITY AS WELL AS ALPHA-L-ARABINOFORANOSIDASE ACTIVITY.

-! CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
                                                                                                                                                                                                                                       -!- PATHWĀY: Xylan degradation.
-!- SIMILARITY: Belongs to family 43 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----NFVLDGTASADIPAGTYDYVII-NP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 DNYLVTPKVTVPENGKLSYW--VSSQVPWTNEHYGVFLSTTGNEAAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 OMLWDADHNOYGASIPEESFWFANGTIPAGLYDPFEYKV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENDO-1,4-BETA-XYLANASE D. F9DEC69967323316 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 IDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03422; CBM 6; 1.
SMART; SM00606; CBD IV; 1.
Xylan degradation; Hydrolase; Glycosidase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR005084; CBM-6.
InterPro; IPR008979; Gal_bind_like.
                                                                                                MEDLINE=92041687; PubMed=1938968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67914 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S19011; S19011.
InterPro; IPR006584; CBD IV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
es 123; Conserv
                                                                     FROM N.A.
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                                         NCBI_TaxID=1406;
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Azevedo V. Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brightell S.C., Bron S.,
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R. Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Serkowska A., Serror S.J., Serror P., Shin B.S., Soldo B.,
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01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Bacillopeptidase F precursor (EC 3.4.21.-) (Esterase) (RP-I protease)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pero J.; "Bacillus subtilis: purification of the protein
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Sloma A., Rufo G.A. Jr., Rudolph C.F., Sullivan B.J., Theriault K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sloma A., Rufo G.A. Jr., Rudolph C.F., Sullivan B.J., Theriault K.A.,
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VCDI_TaxID=1423;
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-!- SUBCELLULAR LOCATION: Secreted.
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-!- SIMILARITY: Belongs to peptidase family S8.
                                                                                                                                                                                                                                                   MEDLINE=90174995; Púbmed=2106671;
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"Nucleotide sequence of the sporulation gene spoilGA from Bacillus
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SIMILARITY).
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Escherichia coli cell division genes ftsZ and ftsA.";
J. Bacteriol. 170:4855-4864(1988).
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A -> V (IN REF. 3).
KHQNKA -> N (IN REF. 3).
QPQVLP -> RTRLYS (IN REF. 3).
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InterPro; IPR00209; Peptidase S8.
InterPro; IPR009209; Protease Inhib.
Pfam; PF05647; Peptidase M6; I.
Pfam; PF05647; Peptidase S8; I.
PRINTS; PR00723; SUBTILIASE ASP; FALSE NEG.
PROSITE; PS00134; SUBTILASE ASP; FALSE NEG.
PROSITE; PS00134; SUBTILASE ASP; FALSE NEG.
PROSITE; PS00138; SUBTILASE SER; I.
Hydrolase; Serine protease; Zymogen; Signal;
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MEDLINE=89008108; PubMed=3139638;
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SEQUENCE OF 1410-1433 FROM N.A.
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EMBL; J05400; AAA83362.1; --
EMBL; Z99111; CAB13403.1; --
EMBL; M20530; AAA22458.1; --
EMBL; X17344; CAA35224.1; --
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HSSP; P00782; 2SBT.
MEROPS; S08.017; -.
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136
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Outer membrane protein B precursor (168 kDs surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDs surface-exposed protein (Surface protein antigen) (120 kDs outer membrane protein ompB); 32 kDs beta peptide].
                                                                                                                                                              Gaps
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Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Racult D.;
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Rickettsiaceae; Rickettsieae; Rickettsia.
     FCRSRHKSV (IN REF.
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                                SING (IN REF. 3).
98DF6846897807C9 CRC64;
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                                                                                                                                                         58; Mismatches 150;
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Pred. No. 0.54;
AQVSVVETG -> FCI
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                                                 1433 AA; 154577 MW;
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Matches 112; Conservative
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SEQUENCE FROM N.A.

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SEQUENCE TRAIN=ATCC 35092 / DSM 1617 / P2;

MEDINE=21332329; bubMed=11427736;

A She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

A Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

A Awayez M.J., Strauso G., Fletcher C., Gordon P.M.K.,

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A Thi-Ngoc H.E., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

A Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

A Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

"The complete genome of the crenarchaeon sulfolobus solfataricus P2.";

RL Proc. Natl. Acad. Sci. Us.A. 98:7835-7840(2001).

CC. -- SIMILARITY: Contains 3 fibronectin type III domains.
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                                                                                                                                                                                                    594 QTGVV-----DASSLTNAQTLTINGKIGTVGANNKTLGQFNIGSSKTVLSDGDVAINELV 648
                ----APASD 227
                                                                       534 AALQGITLANDATKTLTLGGANIIGANGGTINFQANGGTIKLTSTQNNIVVDFDLAIATD 593
                                                                                                                                       228 KRIYVLNESFDTQTLPNGWTM----IDADGDGHNWLSTINVYNTATHTGDGAMFSKSWT 282
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                                                                                                                                                                                                                                                                                                         343 ILBETLGSDKPAPMNLVKS--EGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRL 400
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                ---NLOWSVSGOTVTLTWO----
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein SSO1033 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR008957; FN III-like.
InterPro; IPR00361; FN III.
InterPro; IPR006652; Kelch_rep.
Pfam; PF00041; fn1; S.
Pfam; PF01344; Kelch; S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE006722; AAK41296.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2287;
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097297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                             Stenos J., Walker D.;
"The rickettsial outer membrane protein A and B genes of Rickettsia australis, the most divergent rickettsia of the spotted fever group."; Submitted WAT-1999) to the EMBL/GenBank/DDBA databases.
-!- FUNCTION: THE 120 kba SIRRACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-layer with hexagonal symmetry (By similarity).
-:- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P -> A (IN STRAIN INDIAN TICK TYPHUS).

G -> S (IN STRAIN INDIAN TICK TYPHUS).

V -> A (IN STRAIN INDIAN TICK TYPHUS).

V -> A (IN STRAIN INDIAN TICK TYPHUS).

N -> D (IN STRAIN INDIAN TICK TYPHUS).

I -> V (IN STRAIN INDIAN TICK TYPHUS).

A -> T (IN STRAIN INDIAN TICK TYPHUS).

R -> L (IN STRAIN INDIAN TICK TYPHUS).

KD -> GH (IN REF. 3).

E -> S (IN REF. 3).

G -> S (IN REF. 3).

H -> R (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439 ANGTLAS------ASADANVAVINNITAIEASGAGVVQLSGTHAAELRLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
(By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53; Mismatches 189; Indels 184; Gaps
                                                                                                                                                                                          "Phylogenetic analysis of members of the genus Rickettsia using the gene coding the outer-membrane protein rOmpB (ompB)."; Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wall; Complete proteome.
120 kba SURFACE-EXPOSED PROTEIN.
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                                                      SEQUENCE OF 33-1649 FROM N.A.
STRAIN=Indian tick typhus, and Malish 7;
MEDLINE=20393643; PubMed=10939649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.1%; Score 135;
19.3%; Pred. No. 0
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TIGRFAMs; TIGR01414; autotrans_barl; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR005315; Autotransport.
InterPro; IPR005546; Autotransporter.
                                                                                                                                                           Roux V., Raoult D.;
"Phylogenetic analysis of members of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 353-1655 FROM N.A.
Science 293;2093-2098(2001).
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1655 A.A.;
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Matches 102;
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                                                                                                                                                                                                                                                            175 K-----TYHFTVQRQG----PGDAASVV-----VTGEGGNEFAPVQNLQ----
                                                                                                                                                                                                                                                                                                                   322 FPPLPPKITSYSAGNESVTLGW--------NPVRLSSGYEILYWNNMGFN--
              proteome
                                                                                                                                                                                                                                                                                                  ------WSVSGQTVTLTWQAPASDKRTYVLNESFDTQTLPNGWTMIDADGDGHNWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DDVAVSGEGSSNDYTYTVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEV
                                                                                                                                                                                   -----FVLDGTASADI
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptidel.
           repeat; Repeat; Signal; Complete
POTENTIAL.
HYPOTHETICAL PROTEIN SSO1033.
                                                                                                                                              DB 1; Length 725;
                                                                                                                                                                Indels
                                                                                             FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FEBF1220D013BAB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             ----TASG----TASG-----GAKIDLSPDNYLV-----
                                                                                                                                                       Pred. No. 0.4;
61; Mismatches 134;
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                                                                                                                                                                                 101 NGTIPAGLYDPFEYKVPVNADASFSPTN----
                                                                                                                                            Score 131.5;
Pred. No. 0.4
                                     KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
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                                                                                                                         78465 MW;
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                                                                                                                                             5.0%;
         Kelch
                                                                                                                                                               Conservative
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                   SM00060; FN3; 3
       Hypothetical protein; SIGNAL
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Rickettsia japonica.
                                                                                                                           A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 ANGTIPAGLYDPFEYKVPVNADASFSPTNFV------LDGTASADIPAGT---- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    488 FKLADGTVINGKVNQTVLVG-GVLAAGAITLDGSATITGDIGNGGGGAALQSITLANDAT 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191 SVVVTGEGGNEFAPVONLOMSVSGQTVTLTWQ------APASDKRTYVLNESFDTQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLPNGWTM-----IDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            713 ADTVINVGEGVNL---YATNITTTDANVGSFV-----FNAGG------KNIVSGTVGG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                757 QQGNXFNTVALDNGTTVKFLGNATFNGNTTIAANSTLQISGNYTADFIASADGTGIVEFV 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           547 KTLTLGGANIISANGGTINFQANGGTIKLTSTQNNIVVDCDLAIATDQTGVV----DAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 YLVTPKVTVPENGKLSYMVSSQVPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDKPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        356 MNLVKS--EGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGE--G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLUTAR LOCATION: Cell wall. This bacterium is covered by a layer with hexagonal symmetry.
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                            Uchiyama T.;
"Sequencing of the gene encoding the protein rOmp B of Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45; Mismatches 198; Indels 122;
                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 kDa SURFACE-EXPOSED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 ---YDYVIINPNPGIIYIVGEGVSKGNDYVVEAGKTYHFTVQRQGPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GVSPKVCKDVTVEGS----NEFAHVQNLTGS 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168097 MW; 3132A69C9DD5999F CRC64;
                                                                                                                                                                                                                                                                                                japonica.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 SSNDYTYTVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 kDa BETA PEPTIDE. POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cn 5.0%; Score 131; DB 1; 95; Conservative 4. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006315; Autotransport.
InterPro; IPR005346; Autotransporter.
Pfam; PF03797; Autotransporter; 1.
TIGRPAMS; TIGR01414; autotrans_barl; 2.
Antigen; S-layer; Cell wall.
1 1338 120 kDa sum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB003681; BAA20138.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1338
1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          528 53
1656 AA;
                                                                                                                                                            SEQUENCE FROM N.A.
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817 NTGPINVTLNKQAVPVNALKQITVSGPGNVVVNEIGNAGNYHGA 860

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 TASAD--IPAGTYDYVIINPNPGIIYIVGEGV----SKGNDYVV-EAGKTYHFTVQRQG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: Required for the insertion of integral membrane proteins into the membrane. Probably plays an essential role in the integration of proteins of the respiratory chain complexes. Involved in integration of membrane proteins that insert dependently and independently of the Sec translocase complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Specifically interacts with transmembrane segments of nascent integral membrane proteins during membrane integration (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 LWDADHNQYGASIPEESFW-FANGTIPAGLYDPFEYK-----VPVNADASFSPTNFVLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63; Mismatches 154; Indels 106; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22569155; PubMed=12682364;
Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.
Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC)
                                                                                                                                                                                                                                           Chlamydophila caviae.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                examining the role of niche-specific genes in the evolution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the OXA1/oxaA family. Subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9EDCF05E73709133 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      membrane; Complete proteome.
                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.9%; Score 129; DB : 21.0%; Pred. No. 0.65;
                                   794 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydiaceae.";
Nucleic Acids Res. 31:2134-2147(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_01810; -; 1.
InterPro; IPR011709; 6) PEfan; PF02096; 60KD iMP; 1.
Transmembrane; Inner membrane; Compl
                                                                                            (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE016995; AAP05217.1; -.
TIGR; CCA00472; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88951 MW;
                                                                                                                                                                                     Inner membrane protein oxaA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                               STANDARD;
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713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     NCBI_TaxID=83557;
                                                                                                                                                                                                               OXAA OR CCA00472
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740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity
                                                                                         10-OCT-2003
                                                                                                                                                  5-MAR-2004
                                                                                                                     .0-OCT-2003
                            OXAA CHLCV
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                                                  P59809;
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OXAA_CHLCV
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                                                                                                                                                                       | | | | :::: : | | | | ::: : 389 WITSGIPEVEIMSNAF--TPAIXXHVIKKNKGQLDKVKLPKAKDPLALRSGVYPQWILN- 445
                                                                                                           SGRELTNSVASGYR-VSTFNSTMLELESNDGSIKKTYKLPQQQPYAFEVEVGVNRASDDL 388
                                                                                                                                                281 WTASGGAKIDLSPDNYLVTP-----KVTVPE-----NGKLSYWVSSQ 317
                                                                                                                                                                                                                                                 PGDAASVVVTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPASD--KRTYVLNESFDTQTLP 243
                                   278 PSEASFPGLPSVGANN-QPVSD----TVGGYYPLLRRGILSDAKKRT----PSSYHALNIV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Only after the enteral delivery of the enterotoxin A may the characteristic disease called pseudomembranous colitis be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: THE C-TERMINAL PART OF TOXIN A CONSISTS OF A 833 AA REPETITIVE STRUCTURE. THIS PART OF TOXIN A IS COMPOSED OF FIVE DIFFBRENT OLIGOPEPTIDES.
                                                                                                                                                                                                                        318 VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDKPAPMNLVKSEG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium difficile.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular characterization of the Clostridium difficile toxin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=VPI 10463;
MEDLINE=90129305; PubMed=2105276;
Dove C.H., Wang S.Z., Price S.B., Phelphs C.J., Lyerly D.M., Wilkins T.W., Johnson J.L.;
                                                                                                                                                                                                                                                                                                                           500 LPLPQKEGTHRFLVYAGPLADPTLRVLDKAYTNSKGESPQYLDCITFRG
                                                                                                                                                                                                                                                                                                LPAPYQERTIDLSAYAGQQVYLAFR-----HFNSTGIFRLYLDDVAVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=VPI 10463;
MEDLINE=90221894; PubMed=2109310;
Sauerborn M., von Bichel-Streiber C.;
"Nucleotide sequence of Clostridium difficile toxin A.";
Nucleic Acids Res. 18:1629-1630(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       2710 AA.
                                                                          244 NGWIMIDADGDGHNWLSTINVYNTATHTGDGAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infect. Immun. 58:480-488(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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von Eichel-Streiber C.;
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EMBL; X51797; CAA36094.1; -. EMBL; M30307; AAA23283.1; -.

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2622
                                                                                                                                                           EAATGWQTI----DGKKYYFNTNTALASTGYTIINGKHFYFNTDGIMQIGVFKGPNGFEYF 2173
                                                                                                                                                                                                                                                     2234 HLCTINNDKYYFSYDGILQ-NGYITIERNNFYFDANNE-----SKMVTGVFKGPNGFEY 2286
                                                                                                                                                                                                                                                                                         --IPEESFWF-ANGTIPAGLY---DPFEYK 115
                                                                                                                                                                                                                                                                                                                        NWLSTINVYNTAT--HTGDGAMF----SKSWTASGGAKIDLSPDNYLVTPKVTVP 305
                                                                                                                                                                                                                                                                                                                                                                   ENGKLSYWVSSQVPWTNEHYGVFLSTTG-----NEAAN------FTIKLLE 345
                                                                                                                                                                                                                                                                                                                                         2335 KYYFNLNTABAATGWQTIDGKKYYFNINTABAATGWQTIDGKKYYFNTNTFIASTGYT-S
                                                                                                                                                                                                                                                                                                                                                                                                                                   2450 YYFGSDSKAVTGLRTIDGKK----YYFNTNTAVAVTGWQTINGKKYYFNTNTSIASTGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2506 IISGKHFYFNTDGIMQIGVFKGPDGFEYFAPANTDANNIBGQAIRYONRFLYLHDNIYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2566 GNNSKAATGWVTIDGNRYYFEPNTAMGANGYKTIDNKNFYFRNGLPQI---GVFKGSNGF
                                                                                                                                                                                  116 VPVNADAS-----INPNPGIA---SADIPAGTYDYVI-----INPNPGI---
                                                                                                                                                                                                                              ----IYIVGEGVSKGNDYVVEAGKTYHFTVQRQGPGDAASVVVTG-----EGGNE
                                                                                                                                                                                                                                                                            FAPVONLOWSVSGQTVT----LTWQAPASDKRTYVLNESFDTQTLPNGWTM1DADGDGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                             386 YLAFRH--FNSTGIFRLYL--------DDVAVSGEGSSNDYTYTVYRDNV-VI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        428 AQNLAATT-----FNQENVAPGQYNY-CVEVK--YTAGVSPKVCKDVTVEGSNEF
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MEDLINE=94374689; PubMed=7522196;
Aubert-Pivert E., Davies J.;
Blosynthesis of butirosin in Bacillus circulans NRRL B3312:
identification by sequence analysis and insertional mutagenesis the butB gene involved in antibiotic production.";
                                                                                            DB 1; Length 2710;
                                                                    2710 AA; 308052 MW; 0A6E52CE84C14421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                 66; Mismatches 200;
                                                                                                                                                                                                                                                                                                                                                                                                               346 ETLGSDKPAPMNLVKSEGVKLPAPYQERTIDLSAYAGOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 29, Last sequence update)
                                                                                          Score 127; DB Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1616 AA
                                                                                                                                       EDGTGYQMLWDADHNQYGAS------
EMBL, X92982; CAA63564.1; -.
InterPro; IPR002479; CW binding.
Pfan: PF01473; CW binding.
Pfam: PF01473; CW binding.1; 28.
Pfam: PF0488; Cly_transf_sug; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     475 AH-----VQNLTGSAV 485
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                                                                                        4.8%;
                                                                                                                114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                         Toxin; Enterotoxin
                                                                                                    Local Similarity
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SLAP_BACCI
ID SLAP_BACCI
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01-FEB-1996
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SEQUENCE 1
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                                                                 SEQUENCE
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                                                                                         Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPVGHINVNVDAP---POKTNYVALFTS-----GAQVTNSQETDKVFVKKTNTALAVDKH 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 TG-----QAPASDKRTYV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 NGTEAALKADGAFQSAVRLTAGTNAISVKLLKDGREIVSSTVTVTYNDAQQPA----- 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---IINPNPGIIYIVGEGVSKGNDYVVEAGKTYHFTVQRQGPGDAASVVV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 INESFDIQILPNGWIMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 PDNYLVTPKVTVPENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDK 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 -----GPQITVPQ-----FNVAVQV------DAGSKVTKVVNPSIDGKT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 PAWTGPIDLEIPSGGYVLVA--QD-----TSYAGKNIKKYLATYFKVGDAIKLRKNGFAV 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 LRKWNGMMIIALVISLLTPAWGKASAQSLGQESGGV---QPQSAGVTDDVYVLSRDGTFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 IPAGMARIILEAHDVWEDGTGYQMLWDADHNQYGASI---PEESFWFANGTIPAGLYDPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: THE S-LAVER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. MAY PLAY A ROLE IN THE EXPORT OF BUTIROSIN FROM THE ORGANISM.

SUBCELLULAR LOCATION: Cell Wall. This bacterium is covered by a slayer with hexagonal symmetry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 --DLIEVEAAPIDIT-ISIEGPAHA-IGYVD-ODIAGIDDTVALFTNDW------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFKTSYTLAEGINYLDLV-----VTKEGKEQDSKDLVVYSRPGFSTGKKVJL-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 124; DB 1; Length 1616;
; Pred. No. 3.5;
78; Mismatches 214; Indels 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 S-LAYER RELATED PROTEIN.
172874 MW; 1F03FF7A4F113AA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 PA---PMNL-VKSEGVKLPAPYQERTIDLSAYAGQQV--YLA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L20421; AAA62588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02368; Big 2; 1.
Pfam; PF00395; SLH; 1.
SMART; SM00635; BID 2; 1.
Signal; Cell wall; S-layer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR, T17884, T17884.
InterPro, IPR003343; Big 2.
InterPro, IPR001119; SLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 20.19
watches 120; Conservative
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Pseudomonalisin precursor (EC 3.4.21.100) (Pepstatin-insensitive
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IGA4; 11-FEB-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wlodawer A., Li M.,
Dunn B.M., Oda K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1GA6; 11
                                                                                                                                                                                                                                                                                                           Hara S.;
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 KSWTASGGAKIDLSPDNYLVTPKVTVPENGKLSYWVSSQVPWTNEHYGVFLSTTGNEAAN 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 FIIKLLEETLGSDKPAPMNLVKSEGVKLPAPYQERTIDL-----SAYAGQQVYLAFRHF 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 ---KMIKRIGGSIDSTWLDLFNRE---ISWSTLONQIDAVHDVNGKAMAYAMIYASRENY 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       393 NSTGI---FRLYLDDVAVS-----GEGSSNDYTYTVYRDNVVIAQNLAATTFNQENVAP 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283
                                                       15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Cycloisomaltooligosaccharide glucanotransferase precursor (EC 2.4.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 RQGPGDAASVVVTGEGGN-----EFAPVQNLQWSVS-----GQ--TVTLTWQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PASDKRIYVLNESFDIQILPNGWIMIDADGD-----GHNWLSTINVYNTAIHTGDGAMFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109; Gaps
                                                                                                                                                                                                                              Oguma T., Kurokawa T., Tobe K., Kobayashi M.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PRODUCES CYCLOISOMALTOOLIGOSACCHARIDE FROM DEXTRAN.
-!- SIMILARITY: Belongs to family 66 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
CYCLOISOMALTOOLIGOSACCHARIDE
GLUCANOTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ed. No. 2.6;
Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----HINAWOFYDWMRHD---
                                                                                                                                         Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 SPLGISPTWGIÝEDSSHTNQFDVDFGDGS----TYLYMSD----PON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           972 AA; 107431 MW; 2827BEA61782CC22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 GQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNLTGSAV 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 NWQNY-IHAEYIDSINTAGFDGIHVDQMGQRSNVYDYNGNSI 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
            972 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.6%; Score 121.5; 20.8%; Pred. No. 2.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR005084; CBM 6.
InterPro; IPR008979; Gal_bind_like.
Pfam; PF03422; CBM 6; 2.
Transferase; Glycosyltransferase; Signal.
          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
                                          Created)
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        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                            Bacillus circulans
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Matches 71; Conserv
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                            NCBI_TaxID=1397;
                                                                                                                                                                                                              STRAIN=T-3040;
                                        .5-JUL-1998
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PICP PSESR
ID PICP PSESR
AC P42790;
       CTA1_BACCI
P94286;
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Last sequence update)
Last annotation update)

(Rel. 32, Created) (Rel. 32, Last sequ (Rel. 43, Last anno

01-NOV-1995 ( 01-NOV-1995 ( 15-MAR-2004 (

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21614391; PubMed=11747435; Wlodawer A., Li M., Gustchina A., Dauter Z., Uchida K., Oyama H., Goldfarb N.E., Dunn B.M., Oda K.; "Inhibitor complexes of the Pseudomonas serine-carboxyl proteinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Carboxyl proteinase from Pseudomonas defines a novel family of subtilisin-like enzymes.";
Subtilisin-like enzymes.";
Nat. Struct. Biol. 8:442-46(2001)
-!- CATALYTIC ACTIVITY: Hydrolysis of the B chain of insulin at 13-014, 15-14-14, 15-14-14, 15-15-14, 15-15-15. A good synthetic substrate is Lys-Pro-Ile-Glu-Phe-l-Phe(NO(2))-Arg-Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oyama H., Abe S.-I., Ushiyama S., Takahashi S., Oda K.;
"Identification of catalytic residues of pepstatin-insensitive
carboxyl proteinases from prokaryotes by site-directed mutagenesis.";
J. Biol. Chem. 274:27815-27822(1999).
                                                                                                                                                                                                                                                                                                                                                          "The primary structure of pepstatin-insensitive carboxyl proteinase produced by Pseudomonas sp. No. 101.";
J. Biochem. 118:738-744(1995).
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                                                                                                                                                                                                                 sb.
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                                                                                                                                              MEDLINE=95014496; PubMed=7929375; Oda K., Takahashi S.; Oda K., Takahashi S.; Cloning, mucleotide sequence, and expression of an isovaleryl pepstatin-insensitive carboxyl proteinase gene from Pseudomonas
                                                                                                                                                                                                                                                                             SEQUENCE OF 216-585.
MEDLINE-96157710; PubMed-8576087;
Hayashi K., Izu H., Oda K., Fukuhara K.-I., Matsuo M., Takano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21223584; PubMed-11323721;
Wlodawer A., Li M., Dauter Z., Gustchina A., Uchida K., Oyama
                                                    Pseudomonas sp. (strain 101) (Achromobacter parvulus T1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS) OF 216-585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS) OF 216-587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- COFACTOR: Binds 1 calcium ion per subunit.
-!- SUBCELLULAR LOCATION: Periplasmic.
-!- PTM: Autocatalytically processed.
-!- SIMILARITY: Belongs to peptidase family S53.
                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 216-224.
                   carboxyl proteinase) (Pseudomonapepsin)
                                                                                                                                                                                                                                            Biol. Chem. 269:26518-26524(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99419069; PubMed=10488127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 40:15602-15611(2001).
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                                                                        Bacteria; Proteobacteria.
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1KE2; 11-FEB-03.
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MEROPS; S53.001;
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Query Match
Best Local Similarity 23.5%; Pred. No. 1.6;
Matches 78; Conservative 33; Mismatches 108; Indels 113; Gaps 16;
                                                                                                                                                                                                                                                                                                     103 TIPAGL---YDPFEYKVPVNADASFSPTNFVLDGTASADIFAGTYDYVIINPNPGIIYIV 159
                                                                                                                                                                                                                                                                                                                          160 G------EGVSKGNDYVVEAGKT---YHFTVQRQGPGDAASVVVTGEGGNEF 202
                                                                                                                                                                                                                                                                                                                                                                                   252 GVSQTLQDLQQFTSANGLASVNTQTIQTGSSNGDYSDDQQQGEWDLDSQSIVGSAG--- 308
                                                                                                                                                                                                                                                                                                                                                                                                                       203 APVQNLQW----SVSGQT-VTLTWQAPASDKRTYVLNESFDTQTLPNGWTMIDADGDGH 256
                                                                                                                                                                                                                                                                                                                                                                                                                                         309 GAVQQLLFYMADQSASGNTGLTQAFNQAVSDNVAKVINVSL-----GWCEADANADG- 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 NWLSTINVYNTATHTG-----------DGAMFSKSWTASGGAKIDLSPDN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : :: || || || || 361 TLQAEDRIFATAAAQGQTFSVSSGDEGVYECNNRGYPDGSTYSVSWPAS-----SPNV 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 IAV-------GGTTLYTTSAGAYSNE-----TVWNEGLDSNGKLWATGGGGYSVYES 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 YLVIPKVIVPENGKLSYWVSSQVPWINEHYGVFLSTIGNEAANFIIKLLEETLG----SD 351
Hydrolase, Protease, Serine protease, Zymogen, Periplasmic, Signal,
                                                                                                                                           CALCIUM.

CALCIUM (VIA CARBONYL OXYGEN).

CALCIUM (VIA CARBONYL OXYGEN).

CALCIUM (VIA CARBONYL OXYGEN).

CALCIUM.
                                                                                   295 CHARGE RELAY SYSTEM.
299 CHARGE RELAY SYSTEM.
502 CHARGE RELAY SYSTEM.
391 CHARGE RELAY SYSTEM.
543 CALCIUM.
554 CALCIUM (VIA CARBONYL OXYGEN CALCIUM (VIA CARBONYL OXYGEN CALCIUM (VIA CARBONYL OXYGEN CALCIUM.
563 CALCIUM.
7 61072 MW; E193D8B2C225829A CRC64;
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PSEUDOMONALISIN.
REMOVED IN MATURE FORM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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Search completed: May 18, 2004, 11:43:30 Job time: 10.2836 secs

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STRAIN=W50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q51839; Q51840;
STRAIN=W50;
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                                                                                                                                               1 MRKLNSLFSLAVLLSLLCWG.....QNLTGSAVGQKVTLKWDAPN
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 GenCore version 5.1.6
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Maximum Match 1008
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0977y4 clostridium Q97jy4 clostridium Q9Cj55 lactococcus Q8thC9 methanosarc Q982g1 streptomyce Q869w3 shewanella Q912m3 pseudomonas Q7udus rhokopirell Q92qw9 rickettsia Q82xt8 nitrosomona Q82xt8 nitrosomona Q82xt8 nitrosomona Q82xt8 nitrosomona Q8167 pseudomonas Q815 streptomyce Q93j50 streptomyce Q93j50 streptomyce Q93j50 streptomyce Q93j50 streptomyce Q93j50 streptomyce Q93j50 streptomyce Q93j50 streptomyce Q93j50 streptomyce Q94h5 trickettsia Q8kbu rickettsia Q8kbu rickettsia Q9kkb rickettsia Q9kkb rickettsia Q9kkb rickettsia Q9kkb rickettsia Q9kkb rickettsia Q9kkb rickettsia Q9kkb rickettsia Q9kkb rickettsia Q9kkb rickettsia
                  Q60046 thermoanaer
                                                                    0912M3
Q7UDU8
Q92EK2
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Q8G7K7
Q8T167
                                Q9CJ55
Q8THC9
Q9S2G1
Q8E9W3
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Q93J50
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Q9KKB4
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Q8E9G6
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Q8TP72
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706
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11379
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2009
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## ALIGNMENTS

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RESULT 1

O51839

AC 021839

D1 10-NOV-1996 (TrEMBLIAE). 01, Created)
DT 01-NOV-1996 (TrEMBLIAE). 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLIAE). 25, Last amnotation update)
DE Arginine-specific thiol protease precursor.
GN POTPHYTOMONAS GINGIVALIS (Bacteroides gingivalis).
CC Bacteria; Bacteroidetes; Bacteroides Glass); Bacteroidales;
CC Porphytomonadaces; Porphytomonas.
CC Bacteria; Bacteroidetes; Bacteroides (Lass); Bacteroidales;
CC Bacteria; Bacteroidetes; Bacteroides (Lass); Bacteroidales;
CC Bacteria; Bacteroidetes; Bacteroides (Lass); Bacteroidales;
CC Bacteria; Bacteroidetes; Bacteroides (Lass); Bacteroidales;
CC Bacteria; Bacteroidetes; Bacteroides (Lass); Bacteroidales;
CC Bacteria; Bacteroidetes; Bacteroides (Lass); Bacteroidales;
CC Bacteria; Bacteroides Gondain and a haemaggiutinin domain:
CS TRAINS-SOUBMCE FROM N.A.
CC STRAINS-SOUBMCE FROM N.A.
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PRT; 1706
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                                                     1382 PVKNLKAQPDGGDVVLKWEAPS 1403
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                              476 HVQNLIGSAVGQKVTLKWDAPN 497
                                                                                                                                                                                                                                                                              MEDLINE=96071894; PubMed=7591131;
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(TrEMBLrel. 03, I
(TrEMBLrel. 25, I
                                                                                                               PRELIMINARY:
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1262
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720 126
1706 AA;
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PRPR1.
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                                                                                                                                                                                                                                 NCBI TaxID=837;
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01-MAY-1997 (
01-OCT-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1146 ESSTHGEAPAEWITIDADGDGQGWLCLSSGQLDWLTAHGGINVVSSFSWNGMALNPDNYL 1205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 SFDTQTLPNGWIMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 YLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETL---GSD 351
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                                                                                                                                                                                                                                                                                                                                         671 TATTOGOKVTLKWDAPSTKTNATINTARSVDGIRELVLLSVSDAPELLRSGQAEIVLEAH
                                                                                                                                                                                                                                                                                                                                                                   DVWEDGTGYQMLWDADHNQYGASIPEE--SFWFANGTIPAGLYDPFEYKVPVNADASFSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --DKRTYVLNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 ----EGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDV--AVSGEGSSND
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                       36.0%; Score 951.5; DB 2; Length 1706; 31.9%; Pred. No. 2.7e-50; ive 74; Mismatches 156; Indels 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 1706 ARGININE-SPECIFIC THIOL PROTEASE 1706 AA; 185626 MW; E8EDF07C9813B844 CRC64;
                                        A GO; GO: 0005524; F:ATP binding; IEA.

GO; GO: 0005234; F:ATP binding; IEA.

GO; GO: 0008234; F:Cysteine-type peptidase activity; IEA.

R GO; GO: 0006310; F:DNA ligase (ATP) activity; IEA.

GO; GO: 0006281; P:DNA recombination; IEA.

R GO; GO: 0006281; P:DNA repair; IEA.

GO; GO: 0006508; P:DNA replication; IEA.

R GO; GO: 0006508; P:DNA replication; IEA.

R GO; GO: 0006508; P:DNA replication; IEA.

R InterPro; IPR0077110; IG-like.

R InterPro; IPR007710; Ig-like.

R InterPro; IPR007769; Peptidase.

R Pfam; PF01364; Peptidase.

R Pfam; PF01365; Peptidase.

R Pfam; PF03785; Peptidase.

R Pfam; PF03785; Deptidase.

R PF0271E; RS00697; DNA_LIGASE_A1; 1.
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              to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VIGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS---
                                                                                                                                                                                                                            POTENTIAL
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Slakeski N.;
Submitted (NOV-1995) to th
EMBL; L26341; AAC18876.1;
HSSP; P95493; LCVR.
                                                                                                                                                                                                                                                                                  Best Local Similarity 31.9
Matches 237; Conservative
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1706
                                                                                                                                                                                                               Protease; Signal
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1323 YTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKKCVNVTV-NSTQFN 1381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aduse Opoku J., Muir J., Slaney J.M., Rangarajan M., Curtis M.A., "Characterization, genetic analysis, and expression of a protease antigen (PrpRI) of Porphyromonas gingivalis W50."; Infect. Immun. 63:4744-4754 (1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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R HSSP; P95439; LVA.

R HSSP; P95439; LVA.

R RFSP; P95439; LVA.

R RFSP; P95439; LVA.

R GO; GO:000524; F:APP binding; IEA.

GO; GO:000524; F:Cysteine-type peptidase activity; IEA.

GO; GO:0006210; F:DNA repair; IEA.

GO; GO:0006210; F:DNA repair; IEA.

GO; GO:0006210; P:DNA repair; IEA.

GO; GO:0006281; P:DNA repair; IEA.

R GO; GO:0006281; P:DNA repair; IEA.

R GO; GO:0006281; P:DNA replication; IEA.

R GO; GO:0006281; P:DNA replication; IEA.

R GO; GO:0006281; P:DNA replication; IEA.

R InterPro; IPR001769; Peptidase.

R InterPro; IPR001769; Peptidase.

R InterPro; IPR001769; Peptidase.

R Pfam; PF01364; Peptidase.

R Pfam; PF01365; Peptidase.

R Pfam; PF01365; Peptidase.

R Pfam; PF01365; Deptidase.

R Pfam; PF01785; Peptidase.

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62 BETA-ADHESIN.
185705 MW; 0E56DCD8?FDA8CDD CRC64;
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Last annotation update)
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| 90;                                                                  | GO; GO:00<br>InterPro; |                                                                      | InterPro;<br>Pfam; PF0 |                                                                          | FT CHAIN<br>FT SQ SEQUENCE 1                                         | Query Match<br>Best Local Simi                                   | Matc                                                                   | 22      | 671                                                                    | 69 ( | 731                                                                    | 127     | MNI 067 da                                                             | Qy 186 PGD | DP 850 SCD | Oy 194 | Db 910 PKV                                                        | QY 238 DTQ                     | Db 970 E-N                              | QY 298 VTP | Db 1026 ITP    | Qy 351 | Db 1086 EAI                                             | 73£ YQ                                                                  | Db 1146 STH | Qy 386                                                | Db 1206 KDV | Qy 386 | Db 1266 EAN                                                                 | Qy 421 YRDI                                                                                             | Db 1326 YRD | Qy 481 TGSJ | Db 1385 KAQ                       | RESULT 4<br>Q9R9B7<br>ID Q9R9B7                                                                                                                                                                   |
|----------------------------------------------------------------------|------------------------|----------------------------------------------------------------------|------------------------|--------------------------------------------------------------------------|----------------------------------------------------------------------|------------------------------------------------------------------|------------------------------------------------------------------------|---------|------------------------------------------------------------------------|------|------------------------------------------------------------------------|---------|------------------------------------------------------------------------|------------|------------|--------|-------------------------------------------------------------------|--------------------------------|-----------------------------------------|------------|----------------|--------|---------------------------------------------------------|-------------------------------------------------------------------------|-------------|-------------------------------------------------------|-------------|--------|-----------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------|-------------|-------------|-----------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 790 TNMIMDGTASVNIPACTYDFAIAAPQANAKIWIAGQGFTKEDDYVFEAGKKYHFLMKKMG 849 | / 186 PGDAASVV 193     | 850 SGDGTELTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVAAGNHEYCVEVKYTAGVS 909 | 194DKRTYVL             | 910 PKVCKDVTVEGSNEFAPVQNLTGSAVGQKVTLKWDAPNGTPNPNPNPNPNPNPNPNPNFLTLSE 969 | 236 SFDTQTLPNGWTWIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN 295 | 296 YLVTPKVTVPBNGKLSYWVSSQ-VPWTNBHYGVFLSTTGNBAANFTIKLLEETLGS 350 | 1026 YLITPALDLPNGGKLTFWYCAQDANYASEHYAVYASSTGNDASNFTNALLEETITAKGVR 1085 | 351 354 | 1086 SPEAIRGRIQSTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETF 1145 | 355  | 1146 ESSTHGEATAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVSSFSWNGMALNPDNYL 1205 | 360 359 | 1206 ISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGL 1265 | 360        | 1266       | 416    | 1323 YTYTVYRDGTKIKEGLIETTFEEDGVATGNHEYCVEVKYTAGVSPKKCVNVTV-NSTQFN | 476 HYQNLTGSAVGQKVTLKWDAPN 497 | :  <br> 382 PVKNLKAQPDGGDVVLKWEAPS 1403 |            | SULT 3<br>1816 | 1816   | 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, | 01-OCT-2003 (TrEMBLrel. 25, Last annotation Arg-gingipain-1 proteinase. |             | Porphyromonadaceae; Porphyromonas.<br>NCBI_TaxID=837; |             |        | Travis J., Barr P.J.;<br>"Molecular cloning and structural characterization | <pre>gingipain proteinase of Porphyromonas gingivalis. Bior<br/>proteinase-adhesin polyprotein.";</pre> |             |             | MEROPS, C25.003<br>GO, GO:0005524 | GO; GO:0008234; F:cysteine-type peptidase activity; IEA.<br>GO; GO:0003910; F:DNA ligase (ATP) activity; IEA.<br>GO; GO:00062310; P:DNA recombination; IEA.<br>GO; GO:0006281; P:DNA repair; IEA. |
| qq                                                                   | à                      | Д                                                                    | δλ                     | Ωp                                                                       | S<br>P                                                               | δλ                                                               | d                                                                      | ò       | qq                                                                     | ò    | DP                                                                     | ò       | 업                                                                      | à          | ΩD         | Š      | qq                                                                | δ                              | qq                                      | ì          | 2 ö            | A D    | 55                                                      | 2 2                                                                     | őő          | ŏõi                                                   | Z Z 1       | 2 2 2  | 3 2                                                                         | 22                                                                                                      | 로           |             | ដីដី                              | DA RO                                                                                                                                                                                             |

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IRGRIQGTWRQKTVDLPAGTKXVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETFES 1145
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                                                                                                                                                                                                                                                                                                                                                                                                          TTQGQKVTLKWDAPSTKTNATTNTARSVDGIRELVLLSVSDAPELLRSGQAEIVLEAH 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEDGTGYOMLWDADHNOYGASIPEE -- SFWFANGTIPAGLYDPFEYKVPVNADASFSP 126
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|DGTELTISEGGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVATGNHEYCVEVKYTAGVS 909
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0006560; P:DNA replication; IEA.
0006508; P:proteolysis and peptidolysis; IEA.
0; IPR0017; DNA ligase.
0; IPR007110; IG-like.
0; IPR001769; Peptidase C25.
0; IPR005536; Peptidase C25.
1; PS0164; Peptidase C25.
1; PS01669; DNA LIGASE Al; 1.
1; PS0169; DNA LIGASE Al; 1.
228 719 MATURE 50-KDA CYSTEINE PROTEINASE GINGIPAIN.
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                                                                                                                                                                                                                                                                                       35.8%; Score 944.5; DB 2; Length 1704;
nilarity 31.9%; Pred. No. 7.4e-50;
Conservative 75; Mismatches 160; Indels 267;
                                                                                                                                                                                                                                               1704 AA; 185436 MW; 6A34B40131C2A676 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS---
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|PDGGDVVLKWEAPS 1401
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PRT; 1687 AA.

PRELIMINARY;

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ACCOUNT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE

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1127 ESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLDWLTAHGGTNVVASFSWNGMALNPDNYL 1186
                                                                                                                                                                                                                                                                                                                                                            419 TVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQ 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okamoto K., Kadowaki T., Nakayama K., Yamamoto K.,
"Cloning and sequencing of the gene encoding a novel lysine-specific
cysteine proteinase (Lys-gingipain) in Porphyromonas gingivalis:
structural relationship with the arginine-specific cysteine proteinase
                                                                                                                                                   1187 ISKDVIGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGL
                                                                                                                                                                                                                           ----YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD-------PIPAGMARIILEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 HDVWEDGIGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP
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Pred. No. 2.3e-42;
5; Mismatches 170; Indels 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97044756; PubMed=8889827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  479 NLTGSAVGQKVTLKWDAPN 497
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29.8%; Pre
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J. Biochem. 120:398-406(1996).
EMBL; D83258; BAA11870.1; -.
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02,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KSEGVKL-----
                                                                                                                                                                                                                                                                                                                                                                                                           Han N., Dong H., Progulske-Fox A.; "Cloning and characterization of hagE from P. gingivalis 381."; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AF026946; AAD01810.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.7%; Score 943.5; DB 2; Length 1687; 31.8%; Pred. No. 8.4e-50; .ive 75; Mismatches 160; Indels 269;
                                                                                                                                                                     Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MERCOFS: C25.001; ---

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000524; F:ATP binding; IEA.

GO; GO:0005314; F:Cysteine-type peptidase activity; IEA.

GO; GO:0005310; F:DNA ligase (ATP) activity; IEA.

GO; GO:0006281; P:DNA recombination; IEA.

GO; GO:0006281; P:DNA repair; IEA.

GO; GO:0006281; P:DNA replication; IEA.

GO; GO:0006589; P:DNA replication; IEA.

R InterPro; IPR000170; Deptidase.

R InterPro; IPR001769; Peptidase.

R InterPro; IPR001769; Peptidase.

R InterPro; IPR005536; Peptidase.

R Pfam; PF01364; Peptidase.

R Pfam; PF01364; Peptidase.

R Pfam; PF01365; Peptidase.

R Pfam; PF01365; Peptidase.

R Pfam; PF01365; Peptidase.

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R Pfam; PF01365; Peptidase.

R Pfam; PF01365; Peptidase.
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(TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last Sequence update)
(TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF03785; Peptidase_C25_C; 1.
PROSITE; PS00697; DNA_LIGASE_A1; 1.
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235; Conservative
                                                                                                 Hemagglutinin/protease.
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      NCBI_TaxID=837;
01-MAY-2000
01-MAY-2000
                                                                01-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                              STRAIN=381;
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1163 ESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASFSWNGMALNPDNYL 1222
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                                                                                                                                                                                                                     693 TATTÓGOKVTLKWDAPS----AKKAEGSREVKRIGÖGLFVTIEPANDVRANEAKVVLAA 747
                                                                                                                                                                                                                                                                               DNVWGDNTGYQFLLDADHNTFGSVIPATGPLF-TGTASSNLYSANFEYLLPANADPVVTT 806
                                                                                                                                                                                                                                                                                                                              807 QNIIVTGQGEVVIPGGVYDYCITNPEPASGROWIAGDGGNQPARYDDFTFEAGKKYTFTM 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS---- 350
                                                                                                                                                                                                                                                                                                             127 INFVLDGTASADIPAGTYDYVIINPNP--GIIYIVGEG---VSKGNDYVVEAGKTYHFTV 181
                                                                                                                                                                                            -----PIPAGMARILLEA
                                                                                                                                                                                                                                                 68 HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYXVPVNADASFSP
                                                                                                                                                                                                                                                                                                                                                                                                    867 RRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEEDGVAAGNHEYCVEVKYT
                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VIGEGGNEFAPVONLQWSVSGQTVTLTWQAPAS-----DKRTYVLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              927 AGVSPKVCKDVTVEGSNEFAPVQNLTGSAVGQKVTLKWDAPNGTPNPNPNPNPGTTTLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1103 SPEAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416 YTYTVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFA
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 --KSEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDV--AVSGEGSSND
                                                                                                                             31.0%; Score 818; DB 2; Length 1723; 29.4%; Pred. No. 5.4e-42; ive 78; Mismatches 166; Indels 280;
       InterPro; IPR000977; DNA_ligase.
InterPro; IPR01769; Peptidase_C25.
InterPro; IPR005536; Peptidase_C25.
Pfam; PF01364; Peptidase_C25; I.
Pfam; PF03785; Peptidase_C25; I.
PROSITE; PS00697; DNA_LIGASE_A1; I.
SEQUENCE 1723 AA; 186931 MW; 4508A7E50197CEBD CRC64;
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Last annotation update)
                                                                                                                                                                                         TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD-
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P96967;
01-MAY-1997 (TEMBLEEL: 03,
01-MAY-1997 (TEMBLEEL: 03,
01-OCT_2003 (TEMBLEEL: 25,
                                                                                                                            Query Match
Best Local Similarity 29.4%
Matches 218; Conservative
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|343 TVYRDGTKIKBGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKVCVNVTI-NPTQFNPVK 1401
-----VTGEGGNEFAPVQNLQMSVSGQTVTLTWQAPAS-----DKRTYVLNE 235
                                                                                                                                   927 AGVSPKVCKDVTVEGSNEFAPVQNLTGSAVGQKVTLKWDAPNGTPNPNPNPNPNFTTLSE 986
                                                                                                                                                                 SPDIQILPNGWIMIDADGDGHNWLSIINVYNIATHIGDGAMFSKSWIASGGAKIDLSPDN 295
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                                                                           367 RRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIQEGLTATTFEEDGVAAGNHEYCVEVKYT
                                                                                                                                                                                                                                                                                                                                                                   -----KSEGVKL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lys-gingipain.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
EMBL; U54691; AAA99810.1; -.
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Last annotation update)
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                                               QRQGPGDAASVV----
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                       -YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYTY
                                                   918 STEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTWGGSPTPTDYTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96213011; PubMed=8631659;
Barkocy-Gallagher G.A., Han N., Patti J.M., Whitlock J.,
Progulske-Fox A., Lantz M.S.;
"Anglysis of the prtP gene encoding porphypain, a cysteine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     593 TATTQGQXVTLKWEAPS-----AKKAEGSREVKRIGDGLFVTIEPANDVRANEAKVVLAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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U. Bacteriol. 178:734-2741(1996).

E. Batteriol. 178:734-2741(1996).

E. Batteriol. 178:734-2741(1996).

E. Batteriol. 178:734-2741(1996).

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E. Batteriol. 178:734-2741(1996).

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E. Batteriol. 178:734-2741(1996).

E. Batteriol. 178:735-2741(1996).

E. Batteriol. 178:745-178.

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E. Bat
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
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222; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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PRTP.
              386
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 858 ISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGL 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                502 RRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEEDGVAAGNHEYCVEVKYT 561
                                                                                                                                                                         A Han N. Lepine G., Whitlock J., Wojciechowski L., Progulske-Fox A.;

A Han N. Lepine G., Whitlock J., Wojciechowski L., Progulske-Fox A.;

A Harep mantigene family in Porphyromonas gingivalis.";

B. Mantigene family in Porphyromonas gingivalis.";

Submitted (AuG-1996) to the EMBL/GenBank/DDBJ databases.

B. MEL, 168468; AAB49691.1;

B. GO; GO:0005214; F:ATP binding; IEA.

GO; GO:0005214; F:ATP binding; IEA.

R. GO; GO:0005214; F:DNA ligase (ATP) activity; IEA.

R. GO; GO:0006219; P:DNA recombination; IEA.

R. GO; GO:0006281; P:DNA replication; IEA.

R. GO; GO:0006281; P:DNA replication; IEA.

R. GO; GO:0006281; P:DNA replication; IEA.

R. GO; GO:0006281; P:DNA replication; IEA.

R. InterPro; IPR00097; DNA ligase.

R. InterPro; IPR001769; Peptidase C25.

R. InterPro; IPR001769; Peptidase C25.

R. InterPro; IPR001861; Peptidase C25.

R. InterPro; IPR001861; Peptidase C25.

R. InterPro; IPR001861; Peptidase C25.

R. InterPro; IPR001861; Peptidase C25.

R. InterPro; IPR001861; Peptidase C25.

R. Ram; PP01364; Peptidase C25.

R. Ram; PR01364; Peptidase C25.

R. RAMXT; SM00060; PN3; 1.

RAMXT; SM00060; PN3; 1.

ROSITE; PS00697; DNA LIGASE A1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             738 SPEAIRGRIQGTWROKTVDLPÅGTKYVAFRHFOSTDMFYIDLDEVBIKANGKRADFTETF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---DKRTYVLNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFE-NGIPASWKTIDADGDGHGW-KPGNAPGIAGYNSNGCVYSESF-GLGGIGV-LTPDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD-------PIPAGMARIILEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.9%; Score 816; DB 2; Length 1358;
29.6%; Pred. No. 5.1e-42;
.ive 75; Mismatches 171; Indels 274; Gaps
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 219; Conserv
                                                                                                                                 SEQUENCE FROM N.A.
                                                                             NCBI_TaxID=837;
                                                                                                                                                           STRAIN=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
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1223 LISKDVIGAIKVKYYYAVNDGFPGDHYAVMISKIGTNAGDFTVVFEETPNGINKGGARFG 1282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         807 QNIIVTGQGEVVIPGGVYDYCIINPEPASGROWIAGDGGROOPARYDDFTFEAGKKYTFTM 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             867 RRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEEDGVAAGNHEYCVEVKYT 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 INFVLDGTASADIPAGTYDYVIINPNP--GIIYIVGEG---VSKGNDYVVEAGKTYHFTV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAP-----ASDKRTYVLN 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 927 AGVSPKVCKDVTVEGSNEFAPVQNLTGSSVGQKVTLKWDAPNGTPNPNPNPNPNPGTTLS 986
                                                                                                                                                                                                                                                                                                                                                                                                         :|| || || || || || :| || || || :| 1 || || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 || 1 ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 ESFDIQILPNGWIMIDADGDGHNWLSTINVYNTATHIGDGAMFSKSWIASGGAKIDLSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 NYLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1103 RSPKAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTET
                                                                                                                                                                                                                                TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD------PIPAGMARIILEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 418 YTVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHV
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 ------KSEGVKL--
                                                                                                                               30.0%; Pred. No. 2.4e-41;
.ive 69; Mismatches 173; Indels 277;
                                                                                                              Length 1732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
                                  187931 MW; B2337463D5CB5EA5 CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                30.6%; Score 807.5; DB 2; 30.0%; Pred. No. 2.4e-41;
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                                                                                                                               Local Similaricy ... hes 222; Conservative
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                                                                                                                                                                                                                                                                                                               1103 RSPKAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTET 1162
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|163 FESSTHGEAPAEWITIDADGDGQGWLCLSSGQLDWLTAHGGSNVVSSFSWNGMALNPDNY 1222
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                                                                     927 AGVSPKVCKDVTVEGSNEFAPVQNLIGSSVGQKVTLKWDAPNGTPNPNPNPNPNPGTTLS 986
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11-Spine specific oysteine protease protess.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales,
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Infect. Immun. 66:3035-3042(1998).

REALL, ARCIPTOROSON SINGIALIS.";

REALL, ARCHOTOSO, AACZ6523.1;

ROJ, GO:0005224; F:ATP binding; IEA.

GO; GO:0005234; F:ATP binding; IEA.

GO; GO:0005234; F:ATP binding; IEA.

GO; GO:0005214; F:ATP binding; IEA.

GO; GO:0005219; F:DNA repair; IEA.

ROJ, GO:0006210; F:DNA repair; IEA.

GO; GO:0006281; P:DNA repair; IEA.

ROJ, GO:0006280; P:DNA repair; IEA.

ROJ, GO:0006280; P:DNA repair; IEA.

ROJ, GO:0006280; P:DNA repair; IEA.

InterPro; IPR000977; DNA ligase.

InterPro; IPR001769; Peptidase C25.

RITCETPO; IPR00558; Peptidase C25.

REAM: PF03184; Peptidase C25.

REAM: PF03185; Peptidase C25.

REAM: PR03185; Peptidase C25.

REAM: PR03185; Peptidase C25.

REAM: PR03185; Peptidase C25.

REAM: PROSITE; PS00697; DNA_LIGASE_A1; 1.
                    ------VIGEGGNEFAPVONLOWSVSGQIVTLIWQAP--
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MEDLINE=98298016; PubMed=9632563;
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418 YTVYRDNVVIAQNLAATTENQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHV 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 277;
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | Droducts.n; | 
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                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Last Sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.5%; Score 805.5; DB 2; 29.6%; Pred. No. 2e-41; live 73; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD-
                                                                                                                                                                                                                                                                   PRT; 1223 AA.
                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 10, Created)
                                                                                                                                                        1402 ÓNLTAEQAPNSMDAILKWNAP 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00697; DNA_LIGASE_A1; 1.
                                                                                                                 478 QNLTGSAV--GQKVTLKWDAP 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99143166; PubMed=9988746;
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nes 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                  130k-HMGD (Fragment)
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01-MAY-1999
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1043 NYLITPALDLPNGGKLIFWVCAQDANYASEHYAVYASSTGNDASNFTNALLEETITAKGV 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1103 RSPKAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTET 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1283 LSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNČSDLNYILLDDIQFTMGGSPTPTDYT 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1163 FESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGSNVVSSFSWNGMALNPDNY 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .223 LISKDVTGATKVKYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFG 1282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 NYLVTPKVTVPENGKLSYMVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS--- 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=92235907; PubMed=10219167;
Slakeski N., Cleal S.M., Bhogal P.S., Reynolds E.C.;
"Chazacterization of a Porphyromonas gingivalis gene prtK that encodes a lysine-specific cysteine proteinase and three sequence-related adhesins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNFVLDGTASADIPAGTYDYVIINPNP--GIIYIVGEG---VSKGNDYVVEAGKTYHFTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        807 QNIIVTGGGEVVIPGGVYDYCITNPEPASGKWWIAGDGGNQPARYDDFTFEAGKKYTFTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PIPAGMARIILEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 DNVWGDNTGYQFLLDADHNTFGSVIPATGFLF-TGTASSNLYSANFEYLIPANADPVVTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----VIGEGGNEFAPVONLOWSVSGQTVTLTWQAP-----ASDKRTYVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               693 TATTÓGOKVTLKWEAPS----AKKAEGSREVKRIGDGLFVTIBPANDVRANEAKVVLAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1732;
                                                                                                                                                             --LSAYAGOOV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.5%; Score 806.5; DB 2; 29.7%; Pred. No. 2.8e-41; ive 72; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD---
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Matches 220; Conservative
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Best Local
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357

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165 KGNDYVVEAGKT---YHFT----VQRQGPGDAASVVVTGEGGNEFAPVQNLQWSVSG
                                                             Indels 207;
        Length 1097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------PAPYQERTID-
     21.3%; Score 561.5; DB 2;
29.8%; Pred. No. 2.4e-26;
tive 48; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                         325 YGVFLSTTGNEAANFTIKLLEETLGS-----
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                                Best Local Similarity 29,8
Matches 158, Conservative
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Matches 94; Conserv
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SEQUENCE FROM N.A.
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295 NYLVIPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS--- 350
                                                                                                        |||:|| : | ||||: || 534 NYLITPALDLPNGGKLIFFWVCAQDANYASEHYAVYASSTGNDASNFTNALLEETITAKGY 593
                                                                                                                                                                                    ----XSEGVKL---- 366
                                                                                                                                                                                                                                                                                                                                           713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             714 LISKDVIGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFG 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The tla gene of Porphyromonas gingivalis W50: a homologue of the arginine-specific protease precursor (PrpRI) which shares sequence of animinatity to TonB-linked receptors.";

J. Bacteriol. 179:4778-4788(1997).

--- SUBCELLUIAR LOCATION: OUTER MEMBRANE (BY SIMILARITY).

EWBL; V07618; CAA68897.1;

GO; GO:0019867; C:Outer membrane, IEA.

R GO; GO:000524; F:ATP binding; IEA.

R GO; GO:000524; F:ATP binding; IEA.

R GO; GO:0006216; F:Tensporter activity; IEA.

R GO; GO:0006216; F:Tensporter activity; IEA.

R GO; GO:0006211; P:INA ligase (ATP) activity; IEA.

R GO; GO:0006211; P:INA recombination; IEA.

R GO; GO:0006281; P:DNA recombination; IEA.

R GO; GO:0006281; P:DNA repair; IEA.

R GO; GO:0006281; P:DNA repair; IEA.

R GO; GO:0006281; P:DNA repair; IEA.

R GO; GO:0006281; P:DNA repair; IEA.

R GO; GO:0006281; P:DNA repair; IEA.

R GO; GO:0006281; P:DNA repair; IEA.
                                                                                                                                                                                                                                                                                                                        YTVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHV
                                                                                                                                                                                                                                  594 RSPEAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97386416; PubMed=9244265;
Aduse-Opoku J., Slaney J.M., Young K.A., Muir J., Rangarajan M.,
                                                                                                                                                                                                                                                                                     367 -----PAPYQERTID--------LSAYAGQQV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 02, Created)
(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1097 AA.
                                                                                                                                                                                    ---DKPAPMNLV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
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InterPro; IPR000531; TonB boxC.
Pfam; PF00593; TonB dep Rec;
PROSITE; PS00697; DNA LIGASE_A1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 QNLTGSAV--GQKVTLKWDAP 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      893 ONLTAEQAPNSMDAILKWNAP 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0006810; P:transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TonB-linked adhesin precursor.
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                                                                                                                                                                                                                                                                                                                                                                     ---- DKPAPMNLV--- 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :|: | | | SERINGMALNPDNYLISKDVTGATKVKYYAVNDGFPGDHYAVMI 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     619 SKTGTNAGDFTVVFEETPNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFR 678
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"Genomic analysis of Porphyromonas gingivalis for vaccine discovery.";
"Genomic despectation to the EMBL/GenBank/DDBJ databases.
EMBL; AF237555; AAF81413.1; -.
SEQUENCE 312 AA; 34592 MW; 0D5792C9643A25F5 CRC64;
                                                                                                                                                                                                                                                                381 GIAGYNSNGCVYSESF-GLGGIGV-LTPDNYLITPALDLPNGGKLTFWVCAQDANYASEH
                                                                                                                                                                                                                                                                                                                                                                                                          267 KGSDYTVATGRLRFGIDFTPEWSLNLYQNVFLGDAIPV----GGSNEFAPVQNLTGSSVG
                                                                                                                                      323 QKVTLKWDAPNGTPNPNPNPNPNPGTTLSESFE-NGIPASWKTIDADGDGHGW-KPGNAP
                                                                                                                                                                                                                    266 NTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTPRVTVPENGKLSYWVSSQ-VPWTNEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              499 HFQSTDMFYIDLDEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            391 HFNSTGIFRLYLDDV--AVSGEGSSNDYTYTVYRDNVVIAQNLAATTFNQENVAPGQYNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   739 CVEVKYTAGVSPKKCVNVTV-NSTQFNPVQNLTAEQAPNSMDAILKWNAP 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449 CVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNLTGSAV--GQKVTLKWDAP 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical outer membrane protein PG27.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria, Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.4%; Score 379; DB 2; Length 312; 37.2%; Pred. No. 8.6e-16; Live 44; Mismatches 85; Indels
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--VSGQTVTLTWQAPASDK-
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                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.1%; Score 213.5; DB 2
38.8%; Pred. No. 1.5e-05;
tive 19; Mismatches 42.
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    GGNEFAPVONLOWS --
                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Job time : 41.3342 secs
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                                                                                                                                                                                                                                                                                                           488 GRIKWN-
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Best Local
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                                                        349
                                                                   V-----SGEGSSNDYTYTVYRDNVVIAQNIAATTFNQENVAPGQYNYCVEVKYTAGV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
                                                                                                          SDKPAPMNLV---KSEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVA 406
                                                                                                                             168 ILYTPLPRRAPCPHPGGYTYSVFRDGQKIASGLSALAYIDTDVPYGTQDYCVQVNYLQGD 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRDPIPAGMARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGT----IPA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 GLYDPFEYKVPVNADA-----SFSPTNFVL----DGTASADIPAGTYDYVIIN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GISTAGNYLITPNIEGAKRVKYWVCNQYSTNPEHYAVMVSTTGTAIEDFVLLFDDSITGK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNPGI----IYIVGEGUS-----KGNDYVVEAGKIYHFIVQR---QGPGDAASVVVTGE 197
                            55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---PVPNGWLEIDADA----DGA---TWGSPSGSF--SVP----YGHNGLCTYSHIRS 98
                  LSESFES-GIPAIMKTIDADGDGYNWMHLTN-----FTGQSGLCVSSASYIGGVGA-LT
LNESFDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLS
                                                     PDNYLVTPKVTVPENG--KLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLG
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25.4%; Pred. No. 1.6e-12;
.ive 62; Mismatches 191; Indels 194; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ross B.C., Czajkowski L., Hocking D., Margetts M., Webb E., Rothel Patterson M., Agius C., Camuglia S., Reynolds E., Barr I.G.; "Identification of vaccine candidates from genomic analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ross B.C., Barr I., Patterson M., Agius C., Rothel L., Margetts Hocking D., Webb E.;
"P. gingivalis polypeptides and nucleic acids.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative outer membrane protein PG57.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porphyromonas gingivalis.", Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AY007522, AAG24228.1; ... InterPro; IPR003961; FN III. SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103632 MW; SFF2198D6914DAE8 CRC64;
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                                                                                                                                                                                                                     SPKVCKDVTVEGS 471
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SEQUENCE FROM N.A.
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Matches 152; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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-VLNESFDTQTLPNGWTMIDADGDGH 256
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                                                                                                                                                                                                                                                                                                                                   315 SSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDKPAPMNLVKSEGVKLPAPYQER 373
                                                                                                                                                                                                                                                                                                                                                                                            STQDANWAABHYAVMASTTGTAVGDFVI-LFBBTM-TAKPT------GAWYER 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420
                                                                                                             275 LRDNPLQVEYCVTAVYDESIESSTVCGTLHYATDALLYENFENGPVPNGMLVIDADGDGF 334
                                                                                                                                                                                                 257 NWLSTINVYNT-ATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTPKVTVPENGK-LSYWV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 TIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTVYRDNVV--IAQNL 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 YRDGVKIASGLTEPTFLDEDVPAGEHTYCVEVQYQGGVSDKVCVDVEVK---DFKPVTNL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           432 AATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKD----VTVEGSNEFA-----HVQNLT 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81
219 GQN----VGRLTWNYPEDYQPEGKGNEELQLSGYNIYANGTLLAQIKDVSILEYVDSTYS
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"P. gingivalis polypeptides and nucleic acids.";
Submitted (UNN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF155351; AAD38410.1;
-. SEQUENCE 293 AA; 32272 MW; CC03EAC241F7F6F1 CRC64;
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Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria, Bacteroidetes, Bacteroides (class); Bacteroidales, Porphyromonadaceae; Porphyromonae.
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5434, Ap
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Copyright (c) 1993 - 2004 Compugen Ltd.
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| 8811<br>8811<br>8811<br>8811<br>8811<br>8710<br>2710<br>2710<br>2710<br>2710<br>2710<br>2710<br>2710<br>2                                                                                                                                                                                                                                                                                                                                                                   | ALIUT 1  SULT 1  SULT 1  SEQUENCE 2, Application US/08570311  Patent No. 5824791  GENERAL INFORMATION:  APPLICANT: Progulske-Fox, Ann  APPLICANT: Lepine, Guylaine  APPLICANT: Han, Naiming  APPLICANT: Han, Naiming  APPLICANT: Han, Naiming  APPLICANT: Han, Naiming  APPLICANT: Lantz, Marilyn  APPLICANT: Lantz, Marilyn  APPLICANT: Aptit, Joseph  TITLE OF INVENTION: Cloned Porphy  TITLE OF INVENTION: Cloned Porphy  TITLE OF INVENTION: Cloned Porphy  TITLE OF INVENTION: Cloned Porphy  TITLE OF INVENTION: Cloned Porphy  TITLE OF INVENTION: A 1st Street, STREET: 2421 N.W. 41st Street, STREET: 2421 N.W. 41st Street, STREET: 2421 N.W. 41st Street, STREET: 2421 N.W. 41st Street, STREET: 35606  CORPUTER: READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER: IBW PC COMPatible  OCURRENT APPLICATION DATA:  APPLICATION NUMBER: US/08/570,3  FILING DATE: 09-DEC-1994  CLASSIFICATION: 424  PRIOR APPLICATION NUMBER: US 08/353,4  FILING DATE: 25-JAN-1991  CLASSIFICATION: 424  PRIOR APPLICATION NUMBER: US 07/647,1  FILING DATE: 25-JAN-1991  CLASSIFICATION NUMBER: US 07/647,1  FILING DATE: 25-JAN-1991  CLASSIFICATION NUMBER: US 07/647,1  FILING DATE: 25-JAN-1991  CLASSIFICATION NUMBER: US 07/647,1  FILING DATE: 25-JAN-1991  CLASSIFICATION NUMBER: US 07/647,1  RECLEMENT NUMBER: US 05-05-05-05-05-05-05-05-05-05-05-05-05-0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
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100.0%; Score 2641; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.4e-205;
Matches 497; Conservative 0; Mismatches 0;
                          PRICATION NUMBER: US/08/353,485
CLASSIPICATION NUMBER: US/08/353,485
FILING DATE: 09-DEC-1994
CLASSIPICATION ATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION: Q24
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1968
ATTORNEY AGENT INFORMATION:
NAME: Whitlock Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.CZ
TELECOMMUNICATION INFORMATION:
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US-08-570-311-14
; Sequence 14, Application US/08570311
; Patent No. 5824791
; GENERAL INPORMATION:
; APPLICANT: Progulske-Fox, Ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 SEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTV 420
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Patent No. 5830710
GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Hann, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCE: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 TLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTP
                                                                                                                                                                                                                                                                                                                1 MRKLNSLFSLAVLLSLLCWGQTAAAQGGPKTAFSVTHQAVQKGIRTSKVKDLRDPIPAGM
                                                                                                                                                                                                                                                                                                                                                                           1 MRKINSLFSLAVILSILCWGQTAAAQGGPKTAPSVTHQAVQKGIRTSKVKDLRDPIPAGM
                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDPFEYKVPVNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DASFSPTNFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEGVSKGNDYVVEAGKTYHFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 SEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTV
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                            Length 497;
                                                                                                                                                                                                                                                       Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                         ; Score 2641; DB 2;
; Pred. No. 1.4e-205;
0; Mismatches 0;
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: 2421 N.W. 41st Street, Suite A-1
Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 TGSAVGOKVTLKWDAPN 497
                                                                                                                                                                                         100.0%;
497 amino acids
                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 497; Conservative
                             ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-570-311-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FL
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US-08-353-485-2
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1026 YLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASNFTNALLEETITAKGVR 1085
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                                                                                                                                                 361 SEGVKLPAPYQERTIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTV 420
                                                                                                                                                                                              421 YRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 910 PKVCKDVIVEGSNEFARVQNLIGSAVGQKVTLKWDARNGTRNRNRNRNRNRNRGTITLSE 969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 YLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETL---GSD 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Reynolds, Eric C.
APPLICANT: Reynolds, Eric C.
APPLICANT: Bhogal, Peter S.
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
TITLE REFERENCE: Reynolds
CURRENT APPLICATION NUMBER: US/09/066,330A
CURRENT APPLICATION NUMBER: PN 6275
EARLIER FILING DATE: 1998-10-30
EARLIER FILING DATE: 1995-10-30
EARLIER FILING DATE: 1996-10-30
EARLIER FILING DATE: 1996-10-30
EARLIER FILING DATE: 1996-10-30
EARLIER FILING DATE: 1996-10-30
NUMBER OF SEQ ID NOS: 15
                                                 301 KVTVPENGKLSYWVSGQVPWINEHYGVFLSTIGNEAANFTIKLLEETLGSDKPAPMNLVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    671 TATTQGQKVTLKWDAPSTKTNATTNTARSVDGIRELVLLSVSDAPELLRSGQAELVLRAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 TAAAQG------GPKTAPSVTHQAVQK--GIR----TSKVKDLRDPIPAGMARIILEAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
36.0%; Score 951.5; DB 4;
Best Local Similarity 31.9%; Pred. No. 5.6e-68;
Matches 237; Conservative 74; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                           US-09-066-330-10; Sequence 10, Application US/09066330A; Patent No. 6511666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Porphyromonas gingivalis US-09-066-330-10
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LENGTH: 1706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 TLPNGWIMIDADGDGHNWLSTINVYNTAIHTGDGAMFSKSWTASGGAKIDLSPDNYLVTP 300
             APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Han, Maiming
APPLICANT: Datt, Mattiyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF SEQUENCES: 29
CORRESPONDENCES ADDRESS:
ADDRESSEE TEG W. Whitlock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 TLPNGWTWIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2641; DB 2;
100.0%; Pred. No. 1.7e-204;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                                     E: Ted W. Whitlock
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Whitlock, Ted W.
REGIETRATION UNDRER: 36,965
REFRENCE/DOCKET NUMBER: UP15
TELECOMMUNICATION INFORMATION:
TELEPAX: (904) 375-8100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
Tumwasorn, Somying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 497; Conservative
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                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                Gainesville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 09
                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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CITY: Ga
STATE: E
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| Db 743 E-NGIPASWKTIDADGDGHGW-KPGNAPGIAGYNSNGCVYSESF-GLGGIGV-LTPDNYL 798  Cy 298 VTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVPLSTTGNEAANFTIKLLEETLGS 350 | 979 KDVTGATKVKYYYANNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLST 10 386                                                                                                                                                                                                                                                | RESULT 6 US-08-336-10  ; Sequence 10, Application US/08336308A ; Patent No. 6017332 ; Patent No. 6017322 ; APPLICANT: Travis, James ; APPLICANT: Potempa, Jan S. APPLICANT: Partoff, Nadia J. ; APPLICANT: Partoff, Nadia J. ; TITLE OF INVENTION: Porphyromonas gingivalis ; TITLE OF INVENTION: Arginine-specific Proteinase Coding Sequences ; NUMBER OF SEQUENCES: 16 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE Greenlee, Winner and Sullivan, P.C. ; STREET: 5370 Manhattan Circle, Suite 201                           | CULTY: Boulder  STATE: Colorado  COUNTRY: US  ZIP: 80303  COMPUTER READABLE FORM:  MEDIUM TYPE: FLOPPY disk  COMPUTER: IBM FC compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: Patentin Release #1.0, Version #1.30  CURRENT APPLICATION DATA:  APPLICATION NUMBER: US/08/336,308A  FILING DATE: 08-NOV-1994  CLASSIFICATION DATA:  APPLICATION NUMBER: US 08/119,361  FILING DATE: 10-SEP-1993  FILING DATE: 10-SEP-1993  RICH APPLICATION DATA:  APPLICATION NUMBER: US 08/265,441  FILING DATE: 24-JUN-1994  ATTORNEY/AGENT INFORMATION:  NAME: FEATENT INFORMATION:  NAME: FEATENT INFORMATION:  REFERENCE/DOCKET NUMBER: 33,878  REFERENCE/DOCKET NUMBER: 21-93C  TELECOMMUNICATION INFORMATION:  TELEPHONE: (303) 499-8089 |
|--------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Qy         352 KPAPM                                                                                                                       | Cy 416 YITTUVEDNUVIAQULAATTENQENVAPGQVNYCUEVKYTAGVSPKVCKDVTVEGSNEFA 475  Db 1323 YITYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKKCVNVTV-NSTQFN 1381  Qy 476 HVQNLTGSAVGQKVTLKWDAPN 497  Db 1382 PVKNLKAQPDGGDVVLKWEAPS 1403  RESULT 5  US-09-482-500A-1  ; Sequence 1, Application US/09482500A ; GENERAL INFORMATION: | ## APPLICANT: Travis, James ### APPLICANT: Imamura, Takahisa ### APPLICANT: Imamura, Takahisa #### APPLICANT: Imamura, Takahisa #### APPLICANT: Detempa, Jam ### TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION ### TITLE OF INVENTION: MYMBER: US/09/482,500A ### CURRENT APPLICATION NUMBER: US/09/482,500A ### PRIOR PRILING DATE: 2001-12-17 ### PRIOR PRILING DATE: 1999-01-13 ### NUMBER OF SEQ ID NOS: 4 ### SEQ ID NO 1 ### SEQ ID NO 1 ### ILENGTH: 1477 ### TITLE OF TAKE: PRIL | Query Match   35.84;   Score 944.5;   DB 4;   Length 1477;     Best Local Similarity   31.94;   Pred. No. 1.7e-67;   Indels 267;   Gaps   20;     A44 TATTGGGKVTLKWDAPSTRINATINIARSVERICLES/SAPELLES/GOABIVLEAH 68                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |

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INMUNOCENIC COMPOSITIONS COMPRISING
PORPHYROMONAS GINGIVALLS PROTEINS AND/OR PEPTIDES AND
METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1704;
                                                                                                                                                                                                                                                       Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.8%; Score 944.5; DB 3; 31.9%; Pred. No. 2.1e-67; tive 75; Mismatches 160;
                                                                                  3: Greenlee, Winner and Sullivan, 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,324
FILING DATE: 21-MAR-1997
CLASSIFICATION: 536
PRIOR APDITON: 536
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,945
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 103-95
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TELEPHONE: (303) 486-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1704 amino acids
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Matches 235; Conservative
TITLE OF INVENTION: DORE
TITLE OF INVENTION: PORE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, W
STREET: 8370 Manhatea
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                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                  CITY: Bor
STATE: CC
COUNTRY:
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                                                                                                                                35.8%; Score 944.5; DB 3;
31.9%; Pred. No. 2.1e-67;
tive 75; Mismatches 160;
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Travis, James
Genco, Caroline A.
                                                                                                                                                Local Similarity 31.9%
hes 235; Conservative
                                 LENGTH: 1704 amino acids
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                             ; TYPE: amino acid
; TOPOLOGY: linear
; MOLEGULE TYPE: protein
US-08-336-308A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FAPPLICANT: 7
APPLICANT: 7
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                                                                                                                           ---YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYTYTV
                                                                                                                                                                                   YRDNIVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                Porphyromonas gingivalis
Arginine-specific Proteinase Coding Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle, Suite 201 CITY: Boulder STATE: Colorado COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/336,308
APPLICATION NUMBER: 08/336,308
FILING DATE:
APPLICATION NUMBER: US 08/265,441
FILING DATE: 24-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ferber: Donna M.
REGISTATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 21-93C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Floppy disk
IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09490931
Patent No. 6274718
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      1385 KAQPDGGDVVLKWEAPS 1401
                                                                                                                                                                                                                                           481 TGSAVGOKVTLKWDAPN 497
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tradis, James APPLICANT: Potempa, Jan S. APPLICANT: Potempa, Jan S. APPLICANT: Pavloff, Nadine TITLE OF INVENTION: Porphyro IIILE OF INVENTION: Arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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             ----PAPYOERTID
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80303
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Score 944.5; DB 3; Length 1704; Pred. No. 2.1e-67;

35.8%; 31.9%;

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1086 BAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETFES 1145
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                                                                                                                                                                                                 731 DVWNDGSGYQILLDADHDQYGQVIPSDTHTLW-PNCSVPANLFAPFEYTVPENADPSCSP
                                                         --GPKTAPSVTHQAVQK--GIR----TSKVKDLRDPIPAGMARIILEAH
                                                                                                         671 TATTOGOKVTLKWDAPSTKTNATTNTARSVDGIRELVLLSVSDAPELLRSGQAEIVLEAH
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  Gaps
  Mismatches 160; Indels 267;
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: 2421 N.W. 41st Street, Suite A-1
Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DKPAPMNLV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Progulske-Fox, Ann APPLICANT: Tumwasorn, Somying APPLICANT: Lepine, Guylaine APPLICANT: Han, Naiming APPLICANT: Lantz, Marilyn APPLICANT: Patti, Joseph
75;
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  Conservative
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                                                         22 TAAAQG--
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STREET: 242
CITY: Gaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-570-311-29
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1187 ISKDVTGATKVKYYXAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGL 1246
                             1127 ESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASFSWNGMALNPDNYL 1186
                                                                                                                                                                                                 ---YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYTY 418
                                                                                                                                                                                                                                                      419 TVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQ 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tumwasorn, Somying
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Ted W. Whitlool
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: Ted W. Whitlock
: 2421 N.W. 41st Street, Suite A-1
Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION: 424
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APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UF15.C3
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Patent No. 5824791
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REGISTRATION NUMBER: 36,965
REFRENCE/DOCKET NUMBER: UF15.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 1358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATTQGQKVTLKWDAPSTKTNATTNTARSVDGIRELVLLSVSDAPELLRSGQAEIVLEAH 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 891 PKVCKDVTVEGSNEFAPVQNLTGSAVGQKVTLKWDAPNGTPNPNPNPNPNPNPNPNPGTTTLSE 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 TAAAQG-----GPKTAPSVTHQAVQK--GIR---TSKVKDLRDPIPAGMARIILEAH 68
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                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                 FILING DATE:
CLASSIPICATION: 424
PRIORATION: 424
PRIORAPPLICATION: 424
PRIORA APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIPICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-UAN-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 08-SEP-1981
PRIOR APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INPORMATION:
NUMBER: US 07/241,640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --DKPAPMNLV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1687 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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32606
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424

PRIOR APPLICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485

FILING DATE: 09-DEC.1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119

FILING DATE: 25-JAN-1991

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640

FILING DATE: 08-SEP-1988

ATTORNEY APAGENT INFORMATION:
NAME: WAITLOCK, Ted W.
REGISTRATION NUMBER: 36,965

REFERENCE DOCKET NUMBER: 36,965

REFERENCE DOCKET NUMBER: 36,965

FELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERRISTICS:
FUNCTH: 1732 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 222; Conservative
                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                       Gainesville
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             798 ESSTHGEAPAEWTTIDADGDGDDWLCLSSGQLDWLTAHGGTNVVASFSWNGMALNPDNYL 857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             738 SPEAIRGRIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETF 797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          918 STEANGAKPQSVWIERTVDLPAGTKXVAFRHYNCSDLDYILLDDIQFTMGGSPTPTDYTY 977
                                                                               30.9%; Score 816; DB 2; Length 1358;
29.6%; Pred. No. 3.7e-57;
Live 75; Mismatches 171; Indels 274; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------PIPAGMARIILEA
                                                                                                                                                                                                                         HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP
                                                                                                                                                                                                                                                                                           TNEVLDGTASADIPAGTYDYVIINPNP--GIIYIVGEG---VSKGNDYVVEAGKTYHFTV
                                                                                                                                                                                                                                                                                                                                                                                                 RRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFREDGVAAGNHEYCVEVKYT
                                                                                                                                                                                                                                                                                                                                                                                                                                   -----VTGEGGNEFAPVONLOWSVSGQTVTLTWQAPAS------DKRTYVLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    562 AGVSPKVCKDVTVEGSNEFAPVONLTGSAVGOKVTLKWDAPNGTPNPNPNPNPGTTTLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDN
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                                                                                                                                                    22 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD--
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Patent No. 5824791
GENERAL INFORMATION:
APPLICANT: Tumwasorn, Somying, APPLICANT: Lepine, Guylaine, APPLICANT: Han, Naiming, APPLICANT: Lepine, Marilyn, APPLICANT: Lantz, Marilyn, APPLICANT: Lantz, Marilyn, APPLICANT: Lantz, Marilyn, APPLICANT: Patti, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1037 NLKAQPDGGDVVLKWEAPS 1055
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                                                                                                                Matches 219; Conservative
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          TOPOLOGY: linear MOLECULE TYPE: protein
amino acid
                                                                               Query Match
Best Local Similarity
                                  ; MOLECULE TY!
US-08-570-311-27
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US-08-570-311-10
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693 TATTQGQKVTLKWEAPS----AKKAEGSREVKRIGDGLFVTIEPANDVRANEAKVVLAA 747
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Cloned Porphyromonas gingivalis Genes and Probes for the Detection of Periodontal Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESFDTQTLPNGWTM1DADGDGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327 AGVSPKVCKDVTVEGSNEFAPVQNLTGSSVGQKVTLKWDAPNGTPNPNPNPNPNPGTTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 277;
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                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/03/570,311
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30.0%; Pred. No. 1e-56;
tive 70; Mismatches 172;
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22 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD-
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|1402 QNLTAEQAPNSMDAILKWNAP 1422
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      10:
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                                   LENGTH: 1732 amino acids TYPE: amino acid
                                                                                                                                                              Matches 222; Conservative
     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                          OROGPGDAASVV--
                                                                    linear
                                                                                                                                               Best Local Similarity
                                                                  TOPOLOGY:
                                                                                               US-08-353-485-10
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US-08-570-311-8
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                  1103 RSPKAIRGRIQGTWRQKTVDLPÅGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTET 1162
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                                                                                                                                                                                                                       1223 LISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFG 1282
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NYLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS--- 350
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APPLICANT: Tumwasorn, Somying
APPLICANT: Lepline, Guylaine
APPLICANT: Lepline, Guylaine
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
STREET: A11 N.W. 41st Street, Suite A-1
                                                                                                                                                 418 YTVYRDNVVIAQNLAATTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHV
                                                                 ---KSEGVKL----
                                                                                                                                                                                                                                                         ----YLAFRHFNSTGIFRLYLDDV--AVSGEGSSNDYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPRIATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                               ---DKPAPMNLV--
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APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION 424
PRICE APPLICATION UNMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 09-DEC-1994
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RRFERENCS/DOCKET NUMBER: UF15.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 372-8100
TELEFAX: (904) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                 1402 ONLTAEQAPNSMDAILKWNAP 1422
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Patent No. 5830710
GENERAL INFORMATION:
                                                                                                                           --PAPYQERTID
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                                                                                                                                                                                                      68 HDVWEDGIGYOMLWDADHNOYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP 126
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                                                                                                                                                                                                                                                                                                                                               927 AGVSPKVCKDVTVEGSNEFAPVONLTGSSVGOKVTLKWDAPNGTPNPNPNPNPGTTLS
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                                                                                                        ---PIPAGMARIILEA
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30.8%; Score 812.5; DB 2; Length 1732; 30.0%; Pred. No. 1e-56; tive 70; Mismatches 172; Indels 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAP----
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Patent No. 5824791
GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
APPLICANT: Lumwasorn, Somying
APPLICANT: Lepine, Guylaine
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385
371 GW-KPGNAPGIAGYNSNGCVYSESF-GLGGIGV-LTPDNYLITPALDLANGGKLTFWVCA 427
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APPLICANT: Progulske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENITON: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENITON: and Probes for the Detection of Periodontal Disease
CORRESPONDENCE: ADDRESS:
                                                                                                                         487
                                                                                                                                                                                                                      488 AGTKYVAFRHFQSTDMFYIDLDEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDG 547
                                                                                                                                                                                                                                                                                                                        548 QDWLCLSSGQLDWLTAHGGTNVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGF 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 NVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNLTGSAVGQKVTLKWDAPN 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    728 GVATGNHEYCVEVKYTAGVSPKVCVNVII-NPIQFNPVKNLKAQPDGGDVVLKWEAPS 784
                                                                                                       -PAPYOERTID----
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,485
FILING DATE: 09-DEC-1994
PRIOR APPLICATION 424
PRIOR APPLICATION WORRER: US/08/353,485
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
                                                                                                                                                                          ---KSEGVKL
                                                                        317 Q-VPWTNEHYGVFLSTTGNEAANFTIKLLEETLGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEE: Ted W. Whitlock
: 2421 N.W. 41st Street, Suite A-1
Gainesville
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08353485
Patent No. 5830710
                                                                                                                                                                       354 APMNLV-----
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REFERENCE/DOCKET NUMBER: UFI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                         377 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSVIPATGPLF-TGTASSNLYSANFEYLIPANADPVVTTQNIIVTGQGEVVIPGGVYDYC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 IINPNP--GIIYIVGEG---VSKGNDYVVEAGKTYHFTVQRQGPGDAASVV----- 193
                  APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VTGEGGNEFAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1087;
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.5%; Score 806.5; DB 2; 29.4%; Pred. No. 1.6e-56; tive 76; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRICR APPLICATION DATA.
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-DAN-1991
CLASSIFICATION 424
PRICR APPLICATION DATA.
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DBC-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 8
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Best Local Similarity 29.4%
Matches 211; Conservative
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LENGTH: 1087 amino acid
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     Han, Naiming
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                                                                                                                                    39 AVQKGIRTSKVKDLRD------PIPAGMARIILEAHDVWEDGTGYQMLWDADHNQY
                                                                                                                                                    488 AGTKXVAFRHFQSTDMFYIDLDEVBIKANGKRADFTBTFESSTHGEAPAEWTTIDADGDG
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Patent No. 651166
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric C.
APPLICANT: Bhogal, Peter S.
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
FILE REFERENCE: Reynolds
CURRENT APPLICATION NUMBER: US/09/066,330A
CURRENT FILING DATE: 1998-09-15
EARLIER APPLICATION NUMBER: PN 6275
                                                                                                               265;
                                                                                      DB 2; Length 1087;
                                                                                                               Indels
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                                                                                    30.5%; Score 806.5; DB 2; 29.4%; Pred. No. 1.6e-56; tive 76; Mismatches 166;
          : 1087 amino acids amino acids
                                                                                                            Conservative
SEQUENCE CHARACTERISTICS
                                               ; MOLECULE TYPE: protein US-08-353-485-8
                                    linear
                                                                                 Query Match
Best Local Similarity
Matches 211; Conserv
         LENGTH: 10
TYPE: amir
TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     867 RRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEEDGVAAGNHEYCVEVKYT 926
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                                                                                                                                                                                                                                                                                                                                                                 748 DNVWGDNTGYQFLLDADHNTFGSVIPATGPLF-TGTASSNLYSANFEYLIPANADPVVTT
                                                                                                                                                                                                                                                                                                                                                                                                                     68 HDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKVPVNADASFSP
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                                                                                                                                                                                                                                                                                           Indels 277;
                                                                                                                                                                                                                                                  Length 1732;
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                                                                                                                                                                                                                                             30.5%; Score 806.5; DB 4; 29.7%; Pred. No. 3.2e-56; iive 72; Mismatches 172;
                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                               22 TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --DKPAPMNLV------
EARLIER FILING DATE: 1995-10-30
EARLIER APPLICATION NUMBER: PCT/AU96/00673
EARLIER FILING DATE: 1996-10-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
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Job time : 21.3555 secs
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                                                                                                                                                                       ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                             Query Match 30.5
Best Local Similarity 29.7
Matches 220; Conservative
                                                                                                          SEQ ID NO 11
LENGTH: 1732
                                                                                                                                                                                                  US-09-066-330-11
                                                                                                                                                         TYPE: PRT
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May 18, 2004, 11:42:50 ; Search time 38.497 Seconds (without alignments) 3592.387 Million cell updates/sec
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1 MRKLNSLFSLAVLLSLLCWG......QNLTGSAVGQKVTLKWDAPN
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| Cgn2 6/ptcdata/1/pubpaa/0809B_PUBCOMB.pep:
| Cgn2 6/ptcdata/1/pubpaa/0809C_PUBCOMB.pep:
| Cgn2 6/ptcdata/1/pubpaa/0810B_PUBCOMB.pep:
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| Cgn2 6/ptcdata/1/pubpaa/0810C_PUBCOMB.pep:
| Cgn2 6/ptcdata/1/pubpaa/0810C_MBW_PUB.pep:
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Cgn2_6/ptcdata/1/pubpaa/US06_NEW_PUB.ppp:*

Cgn2_6/ptcdata/1/pubpaa/US07_NEW_PUB.ppp:*

Cgn2_6/ptcdata/1/pubpaa/US07_NEW_PUB.ppp:*

Cgn2_6/ptcdata/1/pubpaa/US08_NEW_PUB.ppp:*

Cgn2_6/ptcdata/1/pubpaa/US08_PUBCOMB.ppp:*

Cgn2_6/ptcdata/1/pubpaa/US08_PUBCOMB.ppp:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications AA:*
: /cgn2_6/ptodata/1/pubpaa/USO7.
: /cgn2_6/ptodata/1/pubpaa/PCT N
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |         | Description     | Sequence 10, Appl | Sequence 11, Appl | Sequence 3, Appli | Sequence 5, Appli | Sequence 6, Appli | Sequence 4, Appli | Sequence 27, Appl | Seguence 51483, A    | Sequence 3, Appli | Sequence 101, App | Sequence 6, Appli | Sequence 62947, A    | Sequence 9, Appli | Sequence 15, Appl | Sequence 66335, A    |
|-----------|---------|-----------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|----------------------|-------------------|-------------------|-------------------|----------------------|-------------------|-------------------|----------------------|
| SUMMAKIES |         | QI              | US-10-229-066-10  | US-10-229-066-11  | US-10-174-695-3   | US-10-174-695-5   | US-10-174-695-6   | US-10-174-695-4   | US-10-387-977-27  | US-10-282-122A-51483 | US-10-229-066-3   | US-10-387-977-101 | US-10-387-977-6   | US-10-282-122A-62947 | US-10-387-977-9   | US-10-387-977-15  | US-10-282-122A-66335 |
|           |         |                 | 14                | 14                | 15                | 15                | 15                | 15                | 15                | 12                   | 14                | 15                | 15                | 12                   | 15                | 15                | 12                   |
|           |         | Match Length DB | 1706              | 1732              | 419               | 419               | 231               | 196               | 29                | 1483                 | 42                | 509               | 31                | 1946                 | 31                | 26                | 2468                 |
|           | * 5     | Match           | 36.0              | 30.5              | 30.0              | 25.1              | 17.3              | 7.1               | 5.7               | 5.7                  | 5.6               | 5.5               | 5.5               | 5.4                  | 5.3               | 5.3               | 5.2                  |
|           |         | Score           | 951.5             | 806.5             | 791.5             | 662.5             | 457.5             | 188.5             | 150               | 150                  | 148               | 145               | 144               | 143                  | 141               | 139               | 138.5                |
|           | קן ונספ | No.             | 1                 | 7                 | М                 | 4                 | ហ                 | 9                 | 7                 | 60                   | σ                 | 10                | 11                | 12                   | 13                | 14                | 15                   |

| Sequence 4, Appli<br>Sequence 82, Appl<br>Sequence 47453, Ap<br>Sequence 11953, A<br>Sequence 1394, Ap<br>Sequence 13, Appli<br>Sequence 7, Appli<br>Sequence 7, Appli<br>Sequence 7, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 12, Appli<br>Sequence 12, Appli<br>Sequence 2, Appli<br>Sequence 45627, A<br>Sequence 45627, A<br>Sequence 15, Appli<br>Sequence 15, Appli<br>Sequence 15, Appli<br>Sequence 15, Appli<br>Sequence 16, Appli<br>Sequence 16, Appli<br>Sequence 16, Appli<br>Sequence 16, Appli<br>Sequence 16, Appli<br>Sequence 46, Appli<br>Sequence 46, Appli<br>Sequence 46, Appli<br>Sequence 46, Appli<br>Sequence 46, Appli<br>Sequence 41, Appli<br>Sequence 41, Appli<br>Sequence 41, Appli<br>Sequence 41, Appli<br>Sequence 41, Appli<br>Sequence 41, Appli<br>Sequence 41, Appli<br>Sequence 41, Appli                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Sequence 79, Appl |
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| 10-246-330-4<br>10-387-977-8<br>10-186-7-1922-4-29<br>10-186-761-9<br>10-186-761-9<br>10-186-761-9<br>10-235-771-19<br>10-235-771-19<br>10-235-771-19<br>10-282-1223-19<br>10-282-1223-19<br>10-282-1223-19<br>10-282-1223-19<br>10-282-1223-19<br>10-282-1223-19<br>10-282-1223-19<br>10-282-1223-19<br>10-282-1223-19<br>10-282-1223-19<br>10-282-1223-19<br>10-282-1223-19<br>10-282-1233-19<br>10-282-1233-19<br>10-282-1233-19<br>10-282-1233-19<br>10-282-1233-19<br>10-282-1233-19<br>10-282-1233-19<br>10-282-1233-19<br>10-282-1233-19<br>10-282-1233-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19<br>10-372-074-19                                                                                                                                                                                                  | US-10-38/-37/-/9  |
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#### ALIGNMENTS

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RESULT 1
US-10-229-066-10

1 (Sequence 10, Application US/10229066

2 (Publication No. US20030157637A1

2 (Sequence 10, Application No. US20030157637A1

3 (Sequence 10, Application No. US20030157637A1

3 (Sequence 10, Application No. US20030157637A1

3 (APPLICANT: Bhogal, Peter S.

3 (APPLICANT: Bhogal, Peter S.

3 (APPLICANT: Bhogal, Peter S.

3 (CHRENT APLICATION NUMBER: US/10/229,066

3 (CHRENT FILING DATE: 1998-09-16

5 (CHRENT FILING DATE: 1998-09-16

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                                                                                                                                                                                                                                                                                                                 296 YLVTPKVTVPENGKLSYWVSSQ-VPWTNEHYGVFLSTTGNEAANFTIKLLEETL---GSD 351
                                                                                                             850 SÓDCTELTISEGGGSDYTYTVYRDGTKIKEGLTATTFEEDGVATGNHEYCVEVKYTAGVS 909
TNFVLDGTASADIPAGTYDYVIINPNPGI-IYIVGEGVSKGNDYVVEAGKTYHFTVQRQG 185
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Publication No. US20030157637A1

GENERAL INFORMATION:
APPLICANT: Reynolds. Eric C.
APPLICANT: Bhogal, Peter S.
APPLICANT: Blogal, Peter S.
APPLICANT: Blogal, Peter S.
APPLICANT: BLAKERI, Nada

TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
CURRENT APPLICATION NUMBER: US/09/066,330
FRIOR FILING DATE: 2002-08-28
FRIOR FILING DATE: 1998-10-30
FRIOR FILING DATE: 1998-10-30
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                        790 TWMIMDGTASVNIPAGTYDFALAAPQANAKIWIAGQGPTKEDDYVFEAGKKYHFLMKKONG
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Pred. No. 3.2e-62;
                                                                                                                                                          ----VTGEGGNEFAPVQNLQWSVSGQTVTLTWQAPAS---
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Best Local Similarity
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LENGTH: 1732
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                                    HDVWEDGTGYQMLWDADHNQYGASIPBESFWFANGTIPAGLYDP-FEYKVPVNADASFSP 126
                                                                                                                                                                                                                                   INFVLDGTASADIPAGTYDYVIINPNP--GIIYIVGEG---VSKGNDYVVEAGKTYHFTV 181
                                                                                                                                                                                                                                                                        867 RRAGMGDGTDMEVEDDSPASYTYTVYRDGTKIKEGLTATTFEEDGVAAGNHEYCVEVKYT 926
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Publication No. US20030232022A1
GENERAL INFORMATION:
APPLICANT: Slakeski, Nada
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
APPLICANT:
TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REFERENCE: 522282000700
   TAAAQGGPKT----APSVTHQAVQKGIRTSKVKDLRD--
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CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: PCT/AUGO/01588
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 IPGGVXDXCIINPEPASGKGMMIAGDGGNQPARYDDFTFEAGKKXTFTWRRAGMGDGTDME 120
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     58 AGMARIILEAHDVWEDGTGYQMLWDADHNQYGASIPEESFWFANGTIPAGLYDP-FEYKV 116
                                                                                                       117 PVNADASFSPTNFVLDGTASADIPAGTYDYVIINPNP--GIIYIVGEG---VSKGNDYVV 171
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                                     1 ANEAKVVLAADDNVWGDNTGYQFILDADHNTFGSVIPATGPLF-TGTASSNLYSANFEYII
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Publication No. US200302202A1

GENERAL INFORMATION:

APPLICANT: Reynolds, Eric Charles

APPLICANT: Slakeski, Nada

APPLICANT: Chen, Chao Guang

APPLICANT: Chen, Chao Guang

APPLICANT: BLE REFERENCE: 529200007007

FILE REFERENCE: 529200007007

CURRENT APPLICATION NUMBER: US/10/174,695

CURRENT FILING DATE: 2002-66-18

PRIOR PILING DATE: 2000-12-21

PRIOR PILING DATE: 2000-12-21

PRIOR FILING DATE: 1999-12-24

NUMBER: OF SEQ IO NOS: 8

SOFTWARE: FRESEQ for Windows Version 4.0
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                                                                                                                                                                                                           172 EAGKTYHFTVQRQGPGDAASVV--
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                                                                                                                                                                                                                                                                                                                                                                                           116 VPVNADASFSPTNFVLDGTASADIPAGTYDYVIINPNPGI-IYIVGEGVSKGNDYVVEAG 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 --DKRTYVLNESFDTQTLPNGWTMIDADGDGHNWLSTINVYNTATHTGDGAMFSKSWTAS 284
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                                                                                                                                                                                Query Match 30.0%; Score 791.5; DB 15; Length 419; Best Local Similarity 39.9%; Pred. No. 8e-62; Matches 174; Conservative 61; Mismatches 100; Indels 101;
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Publication No. US2003023202A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Eric Charles
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
APPLICANT: Barr, Ina George
TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REFERENCE: 529282000700
CURRENT APPLICATION NUMBER: PCT/AU00/01588
PRIOR APPLICATION NUMBER: PCT/AU00/01588
PRIOR PILING DATE: 2000-10-21
PRIOR APPLICATION NUMBER: AU PQ 4859
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 419
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 3
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ORGANISM: Porphyromonas gingivalis
                                                                         TYPE: PRT
ORGANISM: Porphyromonas gingivalis
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                                                   LENGTH:
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TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: PORPHYROWONAS GINGIVALIS
FILE REFERENCE: 52922000301
CURRENT APPLICATION NUMBER: US/10/387,977
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 09/423,056
PRIOR PILING DATE: 2000-03-22
PRIOR PILING DATE: 1998-04-30
PRIOR PILING DATE: 1998-04-30
PRIOR PILING DATE: 1998-04-30
NUMBER: OF SEQ ID NOS: 105
SEQ ID NO 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 51483, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PEDICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-66
PRIOR PELING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/24,578
PRIOR APPLICATION NUMBER: 60/25,65
PRIOR APPLICATION NUMBER: 60/25,65
PRIOR FILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-06
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 51483
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Zyskind, Judith
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Trawick, John
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                                                                                                                                                                                    127
                                                                                                                                                                                                                                                                                        ---SYTYTVYRDGTKIKEGLTA 146
                                                                                                                                                                                                                                 374 IIDLSAYAGQQVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTVYRDNVVIAQNLAA 433
                                                                                                                                                                                                                                                                                                                                       434 TTFNQENVAPGQYNYCVEVKYTAGVSPKVCKDVTVEGSNEFAHVQNLTGSAVGQKVTLKW 493
                                  254 DGHNWLSTINVYNTATHTGDGAMFSKSWTASGGAKIDLSPDNYLVTPKVTVPENGKLSYW 313
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                                                                                                                                                                                          ----DDSPA-----
                                                                                                                                   314 VSSQVPWTNEHYGVFLSTTGNEAANFTIKLLEETLGSDKPAPMNLVKSEGVKLPAPYQER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: STANDARY, ALL CHARLES, APPLICANT: STANDARY, AND CHARLES, Nada APPLICANT: Chen, Chao Guang APPLICANT: Chen, Chao Guang APPLICANT: Barr, Ian George, TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION FILE REFERENCE: 529282000700 CURRENT FILING DATE: 5002-06-18 PRIOR PPLICATION NUMBER: PCT/AU00/01588 PRIOR PLILING DATE: 2000-12-21 PRIOR PLILING DATE: 1999-12-24 NUMBER OF SEQ ID NOS: 8 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4 LENGTH: 196
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APPLICANT: O'Erien-Simpson, Neil Martin
APPLICANT: Slakeski, Nada
IITLE OF INNENTION: SYNTHEFIC PEPTIDE CONSTRUCTS FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 188.5; DB 1
Pred. No. 1.8e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10174695
Publication No. US20030232022A1
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric Charles
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Best Local Similarity 33.5%;
Matches 59; Conservative
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US-10-387-977-27
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DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH PORPHYROWONAS GINGIVALIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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-NPSGFIIADENDKDIQDAASNGKITVTGSTPVAENSVVNTSSVTYDQNAPQDQAVSITL 1030
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                                                                                                                                                                                                                                     577
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APPLICANT: Bhogal, Peter S.
APPLICANT: Bhogal, Peter S.
APPLICANT: Bhogal, Peter S.
TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE; TITLE OF INVENTION NUMBER: US/10/229,066
CURRENT APPLICATION NUMBER: US/09/066,330
PRIOR PILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: P0-15
PRIOR FILING DATE: 1995-10-30
PRIOR FILING DATE: 1995-10-30
PRIOR FILING DATE: 1996-10-30
NUMBER OF SEQ ID NOS: 15
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                                                                                                                                             Indels 208;
                                                                                                   Query Match 5.7%; Score 150; DB 12; Length 1483; Best Local Similarity 20.2%; Pred. No. 0.0011; Matches 127; Conservative 81; Mismatches 213; Indels 208
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                                        ORGANISM: Clostridium acetobutylicum
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                                                               US-10-282-122A-51483
LENGTH: 1483
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APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Eric Charles
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: PORPHYROWONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROWONAS GINGIVALIS
TILE REFERENCE: 529282000301
CURRENT FILING DATE: 2003-07-18
FRIOR APPLICATION NUMBER: US 09/423,056
PRIOR APPLICATION NUMBER: PCT/AU98/00311
PRIOR FILING DATE: 1990-04-30
PRIOR FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 105
SEQ ID NO 101
IENGTH: 509
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                                                                                                                                           5.6%; Score 148; DB 14; Length 42;
64.1%; Pred. No. 7.3e-06;
Live 7; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 101, Application US/10387977
Publication No. US20040005276A1
GENERAL INFORMATION:
                                                              TYPE: PRT ORGANISM: Porphyromonas gingivalis
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SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3
                                                                                                                                                                                          25; Conservative
                                                                                                                                                                      Best Local Similarity
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US-10-387-977-101
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                                                                                                      US-10-229-066-3
                                          LENGTH: 42
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APPLICANT: Reynolds, Exic Charles
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: SYMPHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREAPMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
FILE REFERENCE: 5.5282000301
CURRENT APPLICATION NUMBER: US/10/387,977
CURRENT FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
PRIOR PILING DATE: 1998-04-30
PRIOR PRILING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FARLSEQ for Windows Version 4.0
SEQ ID NO 6
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                                                     384 QVYLAFRHFNSTGIFRLYLDDVAVSGEGSSNDYTYTVYRDNVVIAQNLAATTFNQENVAP 443
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CURRENT APPLICATION TUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-20-20
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Pred. No. 1e-05;
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Best Local Similarity 96.6%;
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 62947
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PRILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-05
PRIOR PELING DATE: 2001-02-05
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103 TIPAGLYDPFEYKVPVNADASFSPTNFVLDGTASADIPAGTYDYVIINPNPGIIYIVGEG 162
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             465 GWWSFTPGSQLPDGTVVNVVARDAAGNSSPATSITVDGVAPNAPVVEPSNGSELSGTAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.2%; Score 138.5; DB 12; Length 2468; 23.7%; Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166; Indels
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                                             Sequence 66335, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PEDILCATION NUMBER: 60/191,078
PRIOR PEDILCATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                              APPLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Carlos
APPLICANT: Maeslbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Yyskind, Judith
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 107; Conservative
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APPLICANT:
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                                                                                                            GENERAL INFORMATION:

APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Eric Charles
APPLICANT: Slakeshi, Nada
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: PORPHYROWONAS GINGIVALIS
FILE REPERENCE: 52928200301
CURRENT PILING DATE: 203-07-18
FRIOR APPLICATION NUMBER: US 09/423,056
PRIOR FILING DATE: 2000-03-22
FRIOR APPLICATION NUMBER: BCT/AU98/00311
PRIOR APPLICATION NUMBER: AU PO 6528
PRIOR PILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-04-30
SPROR FILING DATE: 1997-04-30
SOFTWARE: FASISED for Windows Version 4.0
SEQ ID NO 9
LENGTH: 31
MANNER. PABLICATION NUMBER: AU PO 6528
SOFTWARE: FASISED for Windows Version 4.0
LENGTH: 31
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Fublication No. US20040005276A1

GENERAL INFORMATION:

APPLICANT: Reynolds, Eric Charles

APPLICANT: Reynolds, Eric Charles

APPLICANT: Slakeski, Nada

TITLE OF INVENTION: SYNTHERIC PEPTIDE CONSTRUCTS FOR THE

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

FILE REFERENCE: 529282000301

CURRENT APPLICATION NUMBER: US 09/423,056

FRIOR APPLICATION NUMBER: PCT/AU98/00311

FRIOR FILING DATE: 1998-04-30

PRIOR FILING DATE: 1998-04-30

PRIOR FILING DATE: 1998-04-30

WUMBER OF SEQ ID NOS: 105

SOFTWARE: FastERQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.3%; Score 139; DB 15; Length 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Porphyromonas gingivalis
Sequence 9, Application US/10387977
Publication No. US20040005276A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
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Matches 26; Conserv
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RESULT 14

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Query Match

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RESULT 15

| LYLDDV 405                                                |    | 1631                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
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| PMNLVKSEGV                                                |    | E CARGO CARAMATA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| 6 ETLGSDKPAP                                              |    | TOTAL COLUMNIA CONTRACTOR COLUMNIA COLO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| 346                                                       |    | CCU                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |

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Search completed: May 18, 2004, 11:52:19 Job time : 40.497 secs

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A Geneseq 29Jan04:\*

1: geneseqp1980s:\*

2: geneseqp2000s:\*

4: geneseqp200s:\*

5: geneseqp2001s:\*

6: geneseqp2003s:\*

7: geneseqp2003s:\*

8: geneseqp2003bs:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARTES

|               |        | ολ             |                            |    | SUMMAKIES |                    |
|---------------|--------|----------------|----------------------------|----|-----------|--------------------|
| Result<br>No. | Score  | Query<br>Match | °<br>Query<br>Match Length | DB | ID        | scr                |
| 1             | 2443   | 100.0          | 450                        | 2  | AAR96021  | Aar96021 P. gingiv |
| 2             | 2443   | 100.0          | 450                        | N  | AAW69489  | 9 Hae              |
| ю             | 2443   | 100.0          | 2628                       | N  | AAR96030  |                    |
| 4             | 2443   | 100.0          | 2628                       | 7  | AAW69488  | Aaw69488 Haemaqqlu |
| 2             | 2436   | 7.66           | 456                        | ~  | AAR96023  | Aar96023 P. gingiv |
| 9             | 2436   | 7.66           | 456                        | ~  | AAR96022  | ч                  |
| 7             | 2436   | 7.66           | 456                        | (1 | AAW69491  | Aaw69491 Haemagglu |
| 60            | 2436   | 99.7           | 456                        | 7  | AAW69490  | Aaw69490 Haemagglu |
| Ø             | 2321   | 95.0           | 439                        | ~  | AAR96024  | Aar96024 P. gingiv |
| 10            | 2321   | 95.0           | 439                        | ~  | AAW69492  | Aaw69492 Haemadqlu |
| 11            | 2063   | 84.4           | 1687                       | 7  | AAR96033  | Aar96033 P. gingiv |
| 12            | 2063   | 84.4           | 1687                       | 7  | AAW69495  | Aaw69495 Haemagglu |
| 13            | 2063   | 84.4           | 1704                       | ~  | AAR70188  | Aar70188 Arg-gingi |
| 14            | 2063   | 84.4           | 1704                       | ~  | AAW34843  | Aaw34843 Arg-gingi |
| 15            | 2063   | 84.4           | 1704                       | m  | AAY67396  | Aay67396 Arg-gingi |
| 16            | 2063   | 84.4           | 1704                       | 4, | AAU08938  | Aau08938 P. gingiv |
| 17            | 2051   | 84.0           | 1706                       | 7  | AAW24786  | Aaw24786 PrtR anti |
| 18            | 2036   | 83.3           | 1087                       | N  | AAR96028  | Aar96028 P. gingiv |
| 19            | 2036   | 83.3           | 1087                       | 7  | AAW69486  | Aaw69486 Haemagglu |
| 20            | 2036   | 83.3           | 1358                       | 7  | AAR96032  | Aar96032 P. gingiv |
| 21            | 2036   | 83.3           | 1358                       | 7  | AAW69494  | Aaw69494 Haemagglu |
| 22            | 2011.5 | 82.3           | 1732                       | 7  | AAR96029  | Aar96029 P. gingiv |
| 23            | 2011.5 | 82.3           | 1732                       | 7  | AAW24787  | Aaw24787 PrtK anti |
| 24            |        | 82.3           | 1732                       | ď  | AAW69487  | Aaw69487 Haemagglu |
| 25            | 727    | 29.8           | 135                        | 9  | ABP55081  | Abp55081 Porphyrom |

| Per      | Aau035/2 F. gingiv |          |          |          | Aay34392 Porphorym | Aau03574 P. gingiv |          | Aay34484 Porphorym | Aar96025 P. gingiv |          | Aar72458 Porphyrom | Aau03575 P. gingiv | Aar77313 Porphyrom | Aaw34805 Arg-speci | Aay34483 Porphorym | Aay34358 Porphorym | Aau03573 P. gingiv | Aaw34798 Arg-speci | Aaw83085 Peptide f |
|----------|--------------------|----------|----------|----------|--------------------|--------------------|----------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| AAB49217 | AAUU3572           | AA134522 | AA134521 | AAI34520 | AAY34392           | AAU03574           | AAY34359 | AAY34484           | AAR96025           | AAW69483 | AAR72458           | AAU03575           | AAR77313           | AAW34805           | AAY34483           | AAY34358           | AAU03573           | AAW34798           | AAW83085           |
|          | 4°C                | •        |          | •        |                    | •                  | •        |                    |                    |          |                    | ·                  |                    |                    |                    |                    | Ť                  |                    |                    |
| 134      | 4 - 6              | 127      | 77.0     | 720      | 938                | 419                | 377      | 312                | 497                | 497      | 970                | 231                | 991                | 49                 | 293                | 299                | 196                | 46                 | 29                 |
| 29.1     | 7.00               | 0.0      | 20.00    | 78.0     | 28.0               | 27.9               | 23.1     | 23.0               | 22.4               | 22.4     | 17.0               | 15.8               | 10.9               | 7.6                | 9.5                | 9.5                | 8.5                | 7.7                | 6.3                |
| 711      | 007                | 9 0      | 200      | 000      | 683                | 680.5              | 565      | 561.5              | 546.5              | 546.5    | 415                | 385                | 267                | 236                | 233                | 233                | 206.5              | 189                | 153                |
| 50       | 7 0                | 0 0      | y (      | 0        | 31                 | 32                 | 33       | 34                 | 35                 | 36       | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

### ALIGNMENTS

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| \$888888\$                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | unit products (see also ARR9602-24) can be obtd. from transformed host cells and used see also ARR9602-24) can be obtd. from transformed host cells and used as vaccines to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of live vaccine. HArepl-4 can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field) |
| S                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Sequence 450 AA;                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |

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This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagA haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 MGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSFKECVNV
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                                                                                                                                                                                                            PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASYI
                                                                                                                                                                                                                                         61 NFEGPONPONYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALL
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                                                                                                                                    Length 450;
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                                                                                                                                                            Indels
                                                                                                                                 100.0%; Score 2443; DB 2;
ilarity 100.0%; Pred. No. 1.2e-184;
Conservative 0; Mismatches 0;
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/label= Sig_peptide
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 Score 2443; DB 2;
Pred. No. 1.2e-184;
; Mismatches 0;
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N-PSDB; AAV58876
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Haemagglutinin protein; periodontal disease; vaccine; hagA.
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                                                                                                                                                                      P. gingivalis 381 haemagglutinin hagA (AAR96030) was identified as the product of the hagA gene (AAT30654) isolated as an BCORV fragment of genomic DNA. The haemagglutinin, or portions of it (see also AAR96021-24), can be obtd. from transformed host cells and used as a vaccine to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of a live vaccine. The haemagglutinin can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appin. (Updated on 16-OCT-2003 to standardise OS field)
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                                                                                                           Porphyromonas gingivalis genes and proteins - used in the detection and vaccination against periodontal disease.
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                                                 Lantz M,
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                                                                                                                                                Claim 6; Page 93-101; 153pp; English.
                                                Tumwasorn S,
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 450. Conservative
           UNIV FLORIDA.
UAB RES FOUND
                                                                        1996-287181/29.
                                                                                                                                                                                                                                                                                                   Sequence 2628 AA;
                                                Progulske-Fox A,
                                                                      WPI; 1996-287181
N-PSDB; AAT30654
          (UYFL ) (
(UABR-) (
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Tumwasorn

Han N, Lantz M,

88US-00241640. 91US-00647119. 94US-00353485.

95US-00570311

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NFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALL 120
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                                                                                                                                                                                                                                                                                             This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagh haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
                                                                                                                                                   encoding haemagglutinin and/or
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   Progulske-Fox A,
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   ŝ
                                                                                                                                                gingivalis genes
                                                                                                                                                                                                                                       Claim 1; Col 91-110; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      450; Conservative
                                                                                                                                                                                  protease poly:peptide(s))
                                                                                                                                                Isolated Porphyromonas
                                                           WPI; 1998-582627/49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2628 AA;
                                                                                          N-PSDB; AAV58875
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standard; protein; 2628

AAW69488

AAW69488

AAW69488 ID AAW6 XX AC AAW6 XX XX DT 22-D XX DE Haem

Haemagglutinin protein hagA

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121 EEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIK 180
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                                                                     MGGSPTPTDYTYTVXRDGTKI KEGLTBTTFEEDGVATGNHEYCVEVKYTAGVSPKECVNV
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                                                                                                                                                                                                TVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
                                                                                                                                                             TVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 450
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Best Local Similarity 99.8
Matches 449; Conservative
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(UABR-) UAB RES FOUND
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04-SEP-1996
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Pred. No. 4.2e-184;
0; Mismatches 1;
                                                                                                                                                                                                     P. gingivalis haemagglutinin hagA HArep3 product
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 110-112; 153pp; English.
                                                                                                                                                                                                                                                                                                Porphyromonas gingivalis; strain 381
                                          AAR96023 standard; protein; 456 AA.
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Best Local Similarity 99.8%;
Matches 449; Conservative
                                                                                                                                                          (first entry)
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(UABR-) UAB RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - encoding haemagglutinin and/or
WIGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETP
                                                                                                                 MGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVNV
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                             ANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASFS
                                                                  WNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFBETP
                                                                                                      NGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFT
                                                                                                                                           MGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVNV
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91US-00647119.
94US-00353485.
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25-JAN-1991;
09-DEC-1994;
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99.7%; Score 2436; DB 2; Length 456; 99.8%; Pred. No. 4.2e-184; ive 0; Mismatches 1; Indels

Conservative

Similarity

Best\_Local Sim: Matches 449;

Query Match

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186
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                                                                      67 NFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALL
                                                                                                                                             BEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIK
                                                                                                                                                                                             ANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTNVVASFS
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PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASYI
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91US-00647119.
94US-00353485.
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(UABR-) UAB RES FOUNI
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N-PSDB; AAV58877.
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0;

Gaps

0 439;

Length

9 99 120 126 180 186

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HARPEP4 (AAR96024) is the product of the HARPEP4 repeat unit (AAM30648) of the hagA gene (AAM30654) of P. gingivalis 318. It forms part of the hagA gene (AAM30654) by the hagA gene (AAM30654) by the hagA gene hagA (see also AAM96030). HARPEP4 and other hagA repeat unit products (see also AAM96031-23) can be obtd. from transformed host cells and used as vaccines to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of live vaccine. HARPEP1-4 can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)
                                used in the detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 WNGMALNPDNYLISKDVTGATKVKYYXAVNDGFPGDHYAVMISKTGTNAGDFTVVFEBTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367 MGGSPTPTDYTYTVYRDGTKIKEGLIETTFEEDGVAIGNHEYCVEVKYTAGVSPKVCVNV
                                                                                                                                                                                                                                                                                                                                                                                                                                   67 NFEGPONPONYLVTPELSIPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALL
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Pred. No. 5e-175;
3; Mismatches 4;
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                                Porphyromonas gingivalis genes and proteins vaccination against periodontal disease.
                                                                            4; Page 114-115; 153pp; English.
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98.4%;
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    N-PSDB; AAT30648
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polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
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                                                                                                      Score 2436; DB 2;
Pred. No. 4.2e-184;
0; Mismatches 1;
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Best Local Similarity 99.8
Matches 449; Conservative
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Haemagglutinin; hagE; periodontal disease; vaccine; antibody
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                                                               Porphyromonas gingivalis; strain FDC381
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                       P. gingivalis haemagglutinin hagE
                                                                                                                                                                                                                                                        Porphyromonas gingivalis genes
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                                                                                                                                                                                                     invention. This sequence represents the hagA haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies to organisms associated with identification procedures. The genes and polypeptides are used as vaccines against periodontal disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKVCVNV
                                                                                                         Lepine
                                                                                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                                                                                                                        Score 2321; DB 2; Length 439;
Pred. No. 5e-175;
3; Mismatches 4; Indels
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                                                                                                      Progulske-Fox
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                                                                                                                                                         Porphyromonas gingivalis genes
                                                                                                      Tumwasorn
                                                                                                                                                                                       Claim 1; Col 139-144; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; protein; 1687 AA.
                           88US-00241640.
91US-00647119.
94US-00353485.
         95US-00570311.
                                                                                                                                                                                                                                                                                                        95.0%;
                                                                                                     Patti JM, Han N, Lantz M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |::| ||||||||
TINPTQFNPVQNL 439
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                                                                                                                                                                   poly:peptide(s))
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                      (UYFL ) UNIV FLORIDA.
(UABR-) UAB RES FOUND
                                                                                                                         WPI; 1998-582627/49.
N-PSDB; AAV58879.
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                    Sequence 439 AA,
         11-DEC-1995;
                                        25-JAN-1991;
09-DEC-1994;
                             08-SEP-1988;
                                                                                                                                                                                                                                                                                                                            426;
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                                                                                                                                                         Isolated
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and proteins - used in the

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Patti

Lantz M,

Han N,

Lepine G,

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P. gingivalis 381 haemagglutinin hagE (AAR96033) was identified as the product of a gene (AAT30656) identified in P. gingivalis 318 genomic DNA. The haemagglutinin can be obtd. from transformed host cells and used as a vaccine to protect humans or animals against periodontal disease. Bapression in Salmonella cells allows prodn. of a live vaccine. The mamagglutinin can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYSESFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEEVLTAKTVVTAPEA I RGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                         Length 1687;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                      84.4%; Score 2063; DB 2;
86.3%; Pred. No. 8.9e-154;
ive 17; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420 VTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 450
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 86.3%
tes 389; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360
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(revised)

16-OCT-2003

AAR96033

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1234 PNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQF 1293
                                                                                                             1294 TMGGSPIPIDYIYIVYKDGIKIKEGLIFITFEEDGVAIGNHEYCVEVKYTAGVSPKECVN 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A low mol.wt. arginine-specific gingipain (AG-1) and high mol.wt. AG (AG-2) were isolated from P. gingivalis strains H66 (ATCC 33277) and W50 (ATCC 53973). The sequences of the proteins were used to design PCR primers and probes to isolate AG DNA. Lambda DASH and lambda ZAP libraries were screened with a probe based on amino acids 11-22 of the AG protein to obtain DNA encoding AG-1 (AAQB3484) and AG-2 (AAQB3489). AG-2 is a prepolyprotein incorporating AG-1. (Updated on 25-WAR-2003 to correct PN field.)
                       PNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQF 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding Arg-gingipain proteins - used to develop prods. for detection, treatment and prevention of periodontal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Arg-gingipain-2; gingivalis; periodontal disease; vaccine; arginine-specific protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to Arg-gingipain-1"
                                                                                                                                                                                          1354 VTINPTOFNPVKNLKAOPDGGDVVLKWEAPS 1384
                                                                                                                                                          VIVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barr PJ, Pavloff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      720. .1091
/label= Hemagglutinin
1092. .1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 70-77; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1092. .1429
/label= Hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1430. .1704
/label= Hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Protease
/note= "corresponds
                                                                                                                                                                                                                                                                           AAR70188 standard; protein; 1704 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                Arg-gingipain-2 prepolyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93US-00119361.
93US-00141324.
94US-00265441.
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                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphyromonas gingivalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-123373/16.
N-PSDB; AAQ83489.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-OCT-1993;
24-JUN-1994;
                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
21-SEP-1995
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                                                                                                                                                          420
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ID AAR7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYSESFG 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagE haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated Porphyromonas gingivalis genes - encoding haemagglutinin and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 KANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 LEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYYAFRHFGCTDFFWINLDDVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lepine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Progulske-Fox A,
                                                                                                                                                                                                                                        Haemagglutinin protein; periodontal disease; vaccine; hagE.
||::| |||||:||
VIINPIQENPVKNLKAQPDGGDVVLKWEAPS 1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumwasorn S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Col 167-182; 101pp; English.
                                                                                                    AAW69495 standard; protein; 1687
                                                                                                                                                                                                                                                                                                                                                                                                            88US-00241640.
91US-00647119.
94US-00353485.
                                                                                                                                                                                                                                                                                                                                                                            95US-00570311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lantz M,
                                                                                                                                                                                                        Haemagglutinin protein hagE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protease poly:peptide(s))
                                                                                                                                                                                                                                                                         Porphyromonas gingivalis.
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UAB RES FOUND
                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1998-582627/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-582627/
N-PSDB; AAV58881.
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25-JAN-1991;
09-DEC-1994;
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                   1354
                                                                                                                                    AAW69495
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Best Local
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PNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYSESFG 1012
                                                                                                         1073 LEETITAKG-VRSPEAIRG-RIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEI 1130
                                                                                                                                                                                                      1131 KANGKRADFTETFESSTHGEAFAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF 1190
                                                                                                                                                                                                                                                  SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET 1250
                                                                                                119
                                                                                                                                                                                           239
                                                                                                                                                                                                                                    240 SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET 299
                                                                                                                                                                                                                                                                                  PNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQF 359
                                                                                                                                                                                                                                                                                                                               TMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVN 419
                                                 59
                                                                                              INFEGPONPONYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANAL
                                                                                                                                                                                        KANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF
                                               PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASY-
                                                                                                                                          LEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arg-specific gingipain protease; gingivalis; periodontal disease;
                          ;
    Length 1704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arg-gingipain high molecular weight prepolyprotein sequence.
                          Indels
   ; Score 2063; DB 2;
; Pred. No. 9e-154;
17; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                               VTINPTQFNPVKNLKAQPDGGDVVLKWEAPS 1401
                                                                                                                                                                                                                                                                                                                                                                            VTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .227
/note= "precursor protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW34843 standard; protein; 1704 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNIV GEORGIA RES FOUND INC
MOREHOUSE SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genco C;
  84.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0013945P.
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                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-479993/44.
Query Match
Best Local Similarity
Matches 389; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT93872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9734629-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-1998
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Protein
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(MORE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1251 PNGINKGGARFGLSTEANGAKPQSVAIERTVDLPAGTKYVAPRHYNCSDLNYILLDDIOF 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TWGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVN 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1013 LGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASNFTNAL 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1191 SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419
                                                                                                            The present sequence represents an arginine-specific protease of Porphyromonas gingivalis. The following peptides, derived from Arg- and Lys-specific high molecular weight proteases, offer proteation against infection: YTYTVYRDGK IKEGIATTE INCOVATGHIE YCVEKTRAGS VSFRVC (1); YTPVEEKONG RMIVIVAKKY (11); QLPPIFDVAC VNGDFLESMP CFAEALMRAQ (111); YTPVEEKONG RMIVIVAKKY (11); PRHENCYENK YTAGGSPRVC KODTV (V); RMFENVERSER YTPVEEKONG (V1); TFAGFEDTYK RMFMYEDGR (V11); DYTYTYRDG TKIKEGITAT FEEDGVATG NMEYCVCVK TAGVSPRVC (V111); YTYTVYRDGT KIKEGITATTF EBDG (IX); RDGTKIKEGL TATTFEEDGV ATGN (X); KIKEGITATT FEEDGVATGN HEY (X1); ARGORDATTES (X11); AND APPREKENG RMIVIVAKKY (X111). They are used in vaccines to protect animals, including humans, from gingivitis and/or periodontal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 INFEGPONPONTLYTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANAL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 KANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arginine specific proteinase; Arg-gingipain; gingipain-2; haemagglutinin; immunogenic component; vaccine; inflammatory response; tissue damage; periodontal disease.
Porphyromonas gingivalis Arg-specific gingipain protease peptide(8) - useful for protecting animals and humans from gingivalis and periodontal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFBET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1073 LEETITAKG-VRSPEAIRG-RIOGTWROKTVDLPAGTXYVAFRHFOSTDMFYIDLDEVEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                 84.4%; Score 2063; DB 2; Length 1704; 86.3%; Pred. No. 9e-154; ive 17; Mismatches 39; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||::||||||:||
VIINPIQENPVKNLKAQPDGGDVVLKWEAPS 1401
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                                                                          Disclosure; Page 68-73; 95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arg-gingipain-2 amino acid sequence.
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Best Local Similarity 86.3*
Matches 389; Conservative
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Porphyromonas gingivalis.

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This sequence represents a Porphyromonas gingivalis arginine-specific proteinase known as Arg-gingipain/gingipain-2 amino acid sequence. Gingipain-2 consists or a 50kp protease component non-covalently associated with a 44kD haemagalutinin component. The proteinase is stimulated by glycine containing peptides and glycine analogues. It is inhibited by cysteine protease group specific inhibitors. The protease preparation can be used in immunosenic compositions and vaccines against inflammatory response and tissue damage caused by P. gingivalis in periodontal disease. It can also be used to screen for agents that modulate Arg-gingipain proteinase activity inhibitors
                            229. .719
/nocte= "Amino acids 229-719 are specifically claimed"
720. .1185
/note= "Amino acids 720-1185 are specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFEGPONPONYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PNPNPGTITILSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAICASSASY-
                                                                                                                                                                                                                                                                                                                           New Porphyromonas gingivalis arginine-specific protease preparation useful for preparing vaccines against periodontal disease and for screening for Arg-gingipain inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.4%; Score 2063; DB 3; Length 1704;
86.3%; Pred. No. 9e-154;
ative 17; Mismatches 39; Indels 6,
              Location/Qualifiers
                                                                                                                                                                                                                          (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Col 29-42; 55pp; English
                                                                                                                                                                                93US-00119361.
94US-00265441.
                                                                                                                                                        94US-00336308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                        Travis J;
                                                                                                                                                                                                                                                                                    WPI; 2000-136659/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1704 AA;
                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ60181.
                                                                                                                                                       08-NOV-1994;
                                                                                                                                                                                                 24-JUN-1994;
                                                                                                                                                                                  10-SEP-1993;
                                                                                               US6017532-A.
                                                                                                                                                                                                                                                        Potempa JS,
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              Key
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||::|||||:||: 1371 VIINPIQENPVKNLKAQPDGGDVVLKWEAPS 1401 420 VIVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 450 g ò

Search completed: May 18, 2004, 11:42:40 Job time : 47.4099 secs

12.

us-08-570-311-16.rpr

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

May 18, 2004, 11:37:00 ; Search time 11.7493 Seconds (without alignments) 3684.135 Million cell updates/sec

Title: Perfect score: Sequence:

US-08-570-311-16 2443 1 PNPNPGTTILSESFENGIPA.....QNLTGSAVGQKVTLKWDAPN 450

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283366 Total number of hits satisfying chosen parameters: 283366 seqs, 96191526 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|    | Description   | harana hemadalutinin A | qinqipain R (EC 3. | ginginain R (RC 3. | JVRiTHO-BINDIFIC OF | arginyl endopentid | d hypoth | hypothetical prote | hypothetical prote | 0     | ical prot | _     | l prot | zed   | probable RTX famil | specif | cal prot | S-laver protein - | cellulose 1.4-bera | cal prot | prot | _      | rein p | tical | 1     | 1 prot | ical prot |       | al prot | S-layer |
|----|---------------|------------------------|--------------------|--------------------|---------------------|--------------------|----------|--------------------|--------------------|-------|-----------|-------|--------|-------|--------------------|--------|----------|-------------------|--------------------|----------|------|--------|--------|-------|-------|--------|-----------|-------|---------|---------|
|    | qr            | T2865                  |                    |                    |                     | 140229             |          |                    |                    |       |           |       |        |       |                    |        |          |                   |                    |          | AE2  | H90975 | T30    | T3441 | AD083 | A8668  | ы         | A8554 | D8689   | D9731   |
|    | Length DB     | 2628                   |                    | 526                |                     | 991                | 052      | 341                |                    |       |           |       |        |       |                    |        |          |                   | 1090 2             |          |      |        |        | 783   |       |        | 461       |       | 926 2   |         |
| de |               | 100.                   | •                  | ω,                 | ď,                  | 10.9               | •        | •                  |                    |       | •         |       | •      |       | •                  |        | •        | •                 | •                  |          |      | 4.9    |        | •     | •     |        | 4.9       |       | 4.9     | 4.9     |
|    | Score         | 2443                   | 2063               | 2040               | 2011.5              | 266                | 132.5    | 132.5              | 130.5              | 127.5 | 126       | 125.5 | 124.5  | 124.5 | 124                | 123.5  | 122      | 121.5             | 121                | 121      | 120  | 120    | 120    | 120   | 120   | 119    | 119       | 119   | 118.5   | 118.5   |
|    | Result<br>No. | 1                      | 7                  | m                  | 4                   | Ŋ                  | 9        | 7                  | œ                  | 6     | 10        | 11    | 12     | 13    | 14                 | 15     | 16       | 17                | 18                 | 19       | 20   | 21     | 22     | 23    | 24    | 25     | 56        | 27    | 28      | 29      |

| hypothetical prote | Darasporal Grystal | probable invasin Z | hypothetical prote | alkaline serine or | beta-dalactosidase | protein-tyrosine-p | probable secreted | conserved hypothet | autolysin fimporte | probable outer mem | internalin-like nr | hypothetical prote | MGC1 protein precu | transferrin-like n | cell wall-associat |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| E86719             | T18213             | E85822             | 876109             | JC4908             | T30551             | A49724             | AD1507            | C69503             | C89874             | AF0472             | AF1772             | A64474             | T18346             | T10729             | AF1489             |
| C)                 | ~                  | N                  | N                  | N                  | ~                  | Н                  | ~                 | 7                  | ~                  | 7                  | ~                  | ~                  | ~                  | N                  | 7                  |
| 1180               | 85                 | 2660               | 3029               | 715                | 034                | 1118               | 821               | 607                | 1248               | 875                | 938                | 987                | 1122               | 274                | 2167               |
| 11                 | 13                 | 2                  | ĕ                  |                    | ۲                  | Н                  |                   |                    | _                  |                    |                    |                    | _                  | _                  |                    |
| 4.8 11             |                    | 4.7 26             |                    |                    | 4.7                | 4.7                |                   | 4.7                |                    |                    | 4.6                | 4.6                |                    | 4.6                | 4.6                |
| 4.8                |                    |                    |                    | 4.7                |                    | 4.7                | 4.7               |                    | 4.7                |                    |                    |                    | 4.6                |                    | 111.5 4.6          |

## ALIGNMENTS

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Gaps 9 1074

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C; Species: Porphyromonas gingivalis
C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 17-Nov-2000
C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 17-Nov-2000
C; Accession: 130836; 130837; 130526; A53113
R; Barkcy-Gallagher, G.A.; Han, N.; Patti, J.M.; Whitlock, J.; Progulske-Fox, A.; Lantz
J. Bacteriol. 178, 2734-2741, 1996
A; Title: Analysis of the prtP gene encoding porphypain, a cysteine proteinase of Porphy:
A; Reference number: 220895; MUID:96213011; PMID:8631659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1075 LEETITAKG-VRSPBAIRG-RIQSTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEI 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1253 PNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQF 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1133 KANGKRADFTETFESSTHGEATAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVSSF 1192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQF 359
      C;Accession: S49763
R;Aduse-Opoku, J.; Muir, J.; Slaney, J.M.; Rangarajan, M.; Curtis, M.A. submitted to the EMBL Data Library, November 1994
A;Description: Cloning, sequence analysis and expression in Escherichia coli cA;Recession: S49763
A;Accession: S49763
A;Accession: S49763
A;Accession: Jreliminary
A;Molecule type: DNA
A;Mesidues: L1526 cADU>
A;Cross-references: EMBL:X82680
C;Genetics:
A;Gene: prpR1
C;Keywords: cysteine proteinase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Residues: 1-1732 <BAR>
A; Residues: 1-1732 <BAR>
A; Cross-references: EMBL: U42210; NID: 91314325; PID: 91314326; PIDN: AAB06565.1
R; Slakeski, N.; Cleal, S.M.; Reynolds, B.C.
submitted to the EMBL Data Library, October 1996
A; Reference number: Z20896
A; Reference number: Z20837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               958 PNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYSESFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 INFEGPONPONYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 KANGKRADFIETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVN
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                          Match 83.5%; Score 2040; DB 2; Local Similarity 85.6%; Pred. No. 3.6e-133; les 386; Conservative 17; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Accession: T30836
A, Status: preliminary; translated from GB/EMBL/DDBJA; Molecule type: DNA
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A;Molecule type: DNA
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VTVNSTQFNPVKNLKAQPDGGDVVLKWEAPS 1403
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                                                                                                    ASSECTATION (BC 3.4.22.37) precursor - Porphyromonas gingivalis
NAlternate names: 50K high molecular mass arginine-specific cysteine proteinase; HGP; R
C;Species: Porphyromonas gingivalis
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 08-Oct-1999
C;Accession: A55426; D5313
R;Pavloff, N.; Potempa, J.; Pike, R.N.; Prochazka, V.; Kiefer, M.C.; Travis, J.; Barr, F
Baol. Chem. 270, 1007-1010, 1995
A;Title: Molecular cloning and structural characterization of the Arg-gingipain proteina
A;Reference number: A55426; MUID:95138080; PMID:7836351
A;Retus: preliminary
A;Molecula type: DNA
A;Residues: 1-1704 cPAV>
A;Residues: 1-1704 cPAV>
A;Cross-references: GB:U15282; NID:9557067; PIDN:AAA69539.1; PID:9557068
B;Pike, R.; MGGraw, W.; Potempa, J.; Travis, J.
J. Biol. Chem. 269; 406-411, 1994
A;Title: Lygine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolat
A;Reference number: A53113; MUID:94103245; PMID:8276827
A;Frine: nyeliminary
A;Reference number: A53113; MUID:94103245; PMID:8276827
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C;Species: Porphyromonas gingivalis
C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 31-Mar-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.4%; Score 2063; DB 2;
86.3%; Pred. No. 1.1e-134;
iive 17; Mismatches 39;
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TVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: protein
A;Residues: 228-249 <PIK>
A;Experimental source: H66
A;Note: sequence extracted from NCBI backbc
C;Keywords: cysteine proteinase; hydrolase
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- Porphyromonas gingivalis

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TLTLTV----VGYNKETVIKTINTNGEPNPYQPVSN-----LTATT-----QGQKV 679
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                                                                                                                                                                                                                                                                                                                                84 TLIFWVCAQDANYASEHYAVYASSTG--NDASNFANALLEEVLTAKIVVTAPEAIRGTRV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   738 -GYQILLDADHOQYGQVIPSDTHTLWPNCSVPANLFAPFEYTVPENADPSCSPTNMIM-- 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 TPIDYTYTVYRDGIKIKEGLIEITFEEDGVAIGNHEYCVEVKYTAGVSPKECVNVTVDPV
                              A;Molecule type: DNA
A;Residues: 1-991 <RES>
A;Cross-references: GB:D26470; NID:g927644; PIDN:BAA05484.1; PID:g927645
                                                                                                                                                                                  50; Mismatches 164; Indels 112;
                                                                                                                                         Length 991;
                                                                                                                                                                                                                                                                                SVNVSCDYNGAIATISANGKMF---GSAVVENGTATINLTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.9%; Score 266; DB 2; 25.9%; Pred. No. 1.7e-10;
               A,Status: preliminary; translated from GB/EMBL/DDBJ
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5.4%; Score 132.5; Best Local Similarity 20.7%; Pred. No. 0.32
Matches 122; Conservative 67; Mismatches
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                                                                                                                                 Query Match
Best Local Similarity 25.9[†]
Matches 114[‡], Conservative
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                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-1350, N'. 1352-1363, 'Y', 1365-1447, 'H', 1449-1732 <LEW>
A; Residues: 1-1350, N'. 1352-1363, 'Y', 1365-1447, 'H', 1449-1732 <LEW>
A; Cross-references: EMBL-AF017059; NID:g2738802; PID:g2738803; PIDN:AAC26523.1
B; Pike, R.; McGraw, W.; Potempa, J.; Travis, J.
J. Biol. Chem. 269, 406-411, 1994
A; Title: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolat
A; Reference number: A53113; MUID:94103245; PMID:8276827
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C;Species: Porphyromonas gingivalis
C;Species: Porphyromonas gingivalis
C;Species: Porphyromonas gingivalis
C;Accession: 140229
R;Okamoto, K.; Misumi, Y.; Kadowaki, T.; Yoneda, M.; Yamamoto, K.; Ikehara, Y.
R;Okamoto, K.; Misumi, Y.; Kadowaki, T.; Yoneda, M.; Yamamoto, K.; Ikehara, Y.
A;Title: Structural characterization of argingipain, a novel arginine-specific cysteine
A;Reference number: 140229; MUID:95168884; PMID:7864651
                                                                                                          ä
A;Residues: 1-795,'I',797-1389,'N',1391-1478,'Y',1480-1732 <SLA>
A;Cross-references: RMB.1075366; NID:g2182811; PID:g2182812; PIDN:AAB60809.1
A;Lewis, J.E.; Macrina, F.L.
Infect. Immun. 66, 3035-3042, 1998
A;Title: IS195, an insertion sequence-like element associated with protease genes: A;Reference number: Z20844; MUID:98298016; PMID:9632563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: sequence extracted from NCBI backbone (NCBIP:141690)
                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Keywords: cysteine proteinase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 229-249 <PIK>
A;Experimental source: H66
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Conserved hypothetical protein Atu3276 [imported] - Agrobacterium tumefaciens (strain CC C)Species: Agrobacterium tumefaciens (species: Agrobacterium tumefaciens (c)Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 (c)Accession: AF2959 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I Karge, P.; Romero, P.; Zhang, S. Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Akauthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                          ster, B.W.

Ajtile: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
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Astross references: GB:AE008689; PIDN:AAL44092.1; PID:g17741659; GSPDB:GN00187
Astross references: strain C58 (Dupont)
C;Genetics: Askone.
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| Oy 373 TYYRRGTRIKEGLTETT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | RESULT 8  A981412  Hypothetical protein PA1874 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: A83412 R;Stcver, C.K.; Phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yana, Y.; Boddy, L.L.; Coulter, S.N.; Folger, K.R.; Kas; A.; Larbig, Nature 406, 959-964, 200 A;Itle: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunis A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A83412 A;Accession: A8 | in PAO1)  sc-2000  .; Hickey, M.J.; B:  l.; Larbig, K.; Lim.  opportunistic path  opportunistic path  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; GSPDB:GN00  s263.1; 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                                               | 949 GOVTADGSG-NWSPTPGTPLANGTVVNATASDPTGNTSADAS 989                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      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| <i>장</i> 원                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 287 TNAGDETVVFEETPNGINKGGARFGLSTEADGAKDQSVWIERTVDLPAGTKXVAFRHY 344                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | hypothetical protein yqbK [imported] - Lactococcus lactis subsp. lactis (strain IL1403)<br>C;Species: Lactococcus lactis subsp. lactis<br>C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli<br>Genome Res. 11, 731-753, 2001<br>A;Title: The complete genome sequence of the lactic acid harrarium Lacthonorus lactic as                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| <u>a</u> è                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             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GSDDR: GNO0146                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
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| amylas<br>C;Spec<br>C;Date<br>C;Acces                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | amylase A-180 - alkaliphllic eubacterium 163-26<br>C;Species: alkaliphllic eubacterium 163-26<br>C;Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 15-Oct-1999<br>C;Accession: S10798                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Ouery Match 5.2%; Score 126; DB 2; Length 1649; Best Local Similarity 20.4%; Pred. No. 1.6; Matches 110; Conservative 56; Mismatches 189; Indels 184; Gaps 28;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Eur. J<br>A;Title<br>A;Refer                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Biochem. 191, 177-185, 1990  P. Biochemical and genetic analysis of a maltopentaose-producing amylase from an a rence number: S10789; MUID:90336627; PMID:1696201                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | QY 40 PGGTSFAGHNSAICASSASYINFEG-PQNPDNY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| A;Stati<br>A;Molec<br>A;Resic<br>A;Cross                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | us: preliminary<br>ule type: DNA<br>lues: 1-1684 «CAN»<br>-references: EMBLX53173: NTD-048305. PIDN. Chharanary 1. Pin. 240006                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | QY 82 GGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALLEEVLTAKTVVTAPEA- 135                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Query<br>Best<br>Match                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 684;<br>684;<br>684; 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| Qy<br>Dp                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | PASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICA-SSASYINFEGPONPDNYLVTP 75                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | OY 178 EIKANGKRADFTETFESSTHGEAPABWTTIDADGDGQGW 216  232 TVAASGDNIYAQGNAFATINGSWITGAPNIYGGTDNSDISGNTNLYIGATGSIAGW 287                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              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                                               | ELS.LPNGGTLTEWVCAQD-ANYASEHYAVYASSTGNDASNFANALLEEVLTAKTV-VTAP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | QY 217 LCLSSGQLDWLTAHGGTNVVASFSWNGMALNPDNYLISKDVTGATKV 263  DD 288 -NIYGGNASAATISGNTHVTIAQSSSTINSVTGGSASGTTISGNTNLDISGAIASQI 343                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  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                                               | GTXXVAFRHFGCTDFFWINLDDVEIKANGKRADFTE 19                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Qy 264 KXYXAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLS 313  Db 344 TNIYGAGIGTSNSFVNVNGNVTTYVNSTNGGARYQLYQGGTVYGNISGSIY 394                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     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                                                                                                 | QY 314 TEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYIL 353                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   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| λ<br>20<br>20                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          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:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   : | OY 354 LDDIQFTWGGSPTPTDXTYTVYRDGTKIKEGLIETTFEEDGVATGNHEYCVEVKYTAG 411  Db 449 TGQALFTGGNAGTGASYAQATNSTTAAQGILYANITNYIKSAFTTGTA 496                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               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                                                                                     | QY 412VSPKECVNVTVDPVQFNPVQNLTGSAVGQKVT 443                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        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| λ<br>2<br>2<br>2<br>3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 328 RIVDLPAGIKYVAFRHYNCSDLNYILLDDIQFIMGGSFIFT 368 :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     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| & 43<br>6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              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A. A. A. A. A. A. A. A. A. A. A. A. 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9

23;

157;

Indels

Length 691;

DB 2;

--TTPPPGGTSFAGHNSAICA

302

--- KYVAFRHYN 345

385

24;

Gaps

Indels 161;

Length 2817;

DB 2;

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uncharacterized protein, related to enterotoxins of other Clostridiales [imported] - Clossocies: Clostridium acetobutylicum (); Species: Clostridium acetobutylicum (); Species: Clostridium acetobutylicum (); Species: Clostridium acetobutylicum (); Species: Clostridium acetobutylicum (); Accession: B97033

R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee (); Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4233-4838, 2001

A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl. A; Reference number: A6900; MUID:21359325; PMID:21359325

A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-2817 < KUR>
A; Residues: 1-2817 < KUR>
A; Resperimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                               PNPLPPTGTTTPGTGTG-PVGSGNGPAESTGPAYTGIGSTSGTQPPVVVDASGNQYAYPK 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              591 TSLYGLVLRDPSSNNLGSFSSSNVFGFIKPSSLRATVSGVSGATVLYRTSNLNTWAAQPT 650
                                                                                                                                                                                                                                                                                                                                                ----TYRVVVTYPDTESAAAVAG-----PIRIPVGV 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 926 PNYGYMLLGYNYING-----KYYYFDNDGVIQTGWVTDRSSKYYLDPSGAAVTGFQNING 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----HNSAICASSASYINFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYA 102
                                                                                                                                                                                                                                             389 DGNRDGIVDATVIYNVLLSNLKFGNINGTALGVSDVPVTRIVTQPSVTTAVVFPMDLFND
                                                                                                                                                                                                                                                                                                     ASEHYAVYASSTGNDASNFANALLEEVLTAKTVVTAPEAIRGTRVOGTWYQKTVQLPAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASFSWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   449 GAYDGNYALSGSTPIĞPVKYYAİNPÖTDĞDĞ----VLSPAELAALPAE----IAS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 GMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNG
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                                                                                                                                                                                                                    --QNPD----NYLVTPELS-LPNGGTLTFWVCAQDAN-
                                                                                                                                                                                                                                                                                                                                                                                          --YVAFRHFGCTDFFWINLDDVEIKANGKRADFT-
                                                                                       45; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Mismatches 149;
                                                                                                                               1 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 INKGGARFGLSTEADGAKPQ-SVWIERTVDLPAGT---
                                            5.1%; Score 124.5; DE 22.1%; Pred. No. 0.67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.2;
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651 VDANTTWVEVGVDTNNN 667
                                                                                                                                                                                                                                                                                                                                             346 GNGRPEVTAGPNGGTA---
                                                                                       Conservative
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00; Conservative
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                                                                 Similarity
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    A; Note: plasmid MP1
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A;Gene: CAC1079
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C.; Ma
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A;Experimental source: strain R1
C;Genetics:
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C)Species: Deinococcus radiodurans
C)Species: Deinococcus radiodurans
C)Species: Deinococcus radiodurans
C)Becies: Deinococcus radiodurans
C;Becies: Dainococcus radiodurans
C;Accession: B75622
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, J.W.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A)Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R, Accession: B7562
A,Accession: B7562
A,Status: preliminary
A,Residues: 1-691 <WHI>
                                 A;Status: preliminary
A;Motecule type: DNA
A;Motecule type: DNA
A;Residues: 1-2291 cHAY>
A;Cross-references: GB:BA000007; PIDN:BAB33965.1; PID:g13360000; GSPDB:GN00154
A;Cross-references: strain 0157:H7, substrain RIMD 0509952
A;Genetics: RCs0542
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                                                                                                                                                                                                                                                                                                                                           NPLTISGSSTAEAGQTVTVTLNGVTYS-GSVQADG---SWSVSLPTADL----SNLTA 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ATVOSNLSWSVDVPAADIQALGNGDLTVNASVTNGVGNTGSGSRDITIDANLPG 740
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number: A99629; MUID:21156231; PMID:11258796
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22.2%; Pred. No. 8.1;
*ive 58; Mismatches 165;
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A;Map position: me
A;Genome: plasmid
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| family exoprotein [imported] - Esche cherichia coli b-2001 #sequence_revision 16-Feb-200 #895547   ; Plunkett III, G.; Burland, V.; Mauoteck, E.J.; Davis, N.W.; Lim, A.; 29-533, 2001   me sequence of enterohemorrhagic Escurber: A85480; MUID:21074935; PMID:11minary pe: DNA   -5188 scgro- ences: GB.AE005174; NID:g12513368; Ences: GB.AE005174; NID:g12513368; Elemence: strain 0157:H7, substrain | Appl. Environ A; Title: Seque A; Accession: A; Status: pre A; Molecule: pre A; Molecule: pre A; Cross-refer Query Match Best Local Matches 10  Qy Qy Qy Db A993                                                                                                                                                            | Microbiol, 61, 4089-4098  Hore analysis of the temper umber: 217646; MUID:9606442  Hillianary; translated from 0  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 EDVA  Hold 4 E |
| Query Match         5.1%; Score 124; DB 2; Length 5188;           Best Local         Similarity 20.7%; Pred. No. 10;           Matches 123; Conservative 67; Mismatches 181; Indels 222; Gaps 34;           Qy 6 GTTTLSESFENGIPASWKIIDADGDGNNWTTPPPEGGTSFAGHNSAICASS 56                                                                                                                                   | QY       109         Db       586         QY       166         Db       700         QY       239         Db       738         QY       295         Db       784         QY       349         Db       837         Search complete                                                                                          | 109 GNDASNFANALLEEVLTAKTVVTAPEAIRGTRYQGTWYQKTVQLPAGTK-YVAFRHFG 165                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |

Job time : 13.7493 secs

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Q51845 porphyromon
P59915 porphyromon
P6071 porphyromon
Q62010 mus musculu
Q05044 lactobacill
P50899 cellulomona
Q52081 staphylococ
Q12535 aspergilus
Q45760 bacillus th
Q28847 bacillus th
Q28789 methanococc
Q49379 mycoplasma
G5847 bacillus me
P2465 aspergilus
P25927 salmonella
P25927 salmonella
P6010 candida alb
O76536 strongyloce
Q60106 xanthomonas
Q9443 homo sapien
P6090 sacratia ma
P1459 secretichia
P60108 sacratia ma
P1451 rickettsia
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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PRTH_PORGI
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GUXB_CELFI
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ATL_STAAU
PNE_ASPAC
CSAA_BACUD
YYE2B_ARCFU
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| 1.2 1861 1 APU THETU P77933 oryza sativ<br>435 1 AM3D ORYSA P06874 bacillus st<br>548 1 THER_BACST P06874 bacillus st<br>1. 1044 1 ITAS CHTCK Q45704 bacillus gall<br>2. 157 1 CBAA_BAUNK Q45704 bacillus full<br>2. 2725 1 FLNC_HUMAN Q14315 homo sapien<br>2. 251 1 AMYB THETU P5695 bacillus th<br>2. 2132 1 PGCA_MOUSE Q61282 mus musculu<br>3. 2 1289 1 C5AB BACUD Q61282 mus musculu<br>4. 2 1289 1 C5AB BACUD Q61282 mus musculu<br>4. 2 1289 1 C5AB BACUD Q61282 mus musculu<br>4. 2 1289 1 C5AB BACUD Q61282 mus musculu<br>4. 2 1289 1 C5AB BACUD Q61282 mus musculu<br>4. 2 1289 1 C5AB BACUD Q61282 mus musculu<br>5. 1045 1 PRTT_SERMA P0206 Serratia ma | ALIGNMENTS | STANDARD; PRT; 2628 AA. (Rel. 39, Created) (Rel. 39, Last sequence update) (Rel. 42, Last annotation update) n A precursor. | HAGA. Prophyromonas gingivalis (Bacteroides gingivalis). Bacteria, Bacteroidetes; Bacteroides (class); Bacteroidales; Porphyromonadaceae; Porphyromonas. [1] SEOURICE FROM N.A. | PubMed=8926061; Progulske-Fox A.; gene A (tagA) of Porphyromonas gingiv. e, contiguous, direct repeats."; 4000-4007(1996). utinates erythrocytes. longs to peptidase family C25. | Tentry is copyright. It is puss Institute of Bioinformat ioinformatics Institute. The roll institutions as long his statement is not removed. Thes a license@isb.sib.ch). | AAB17128.1; T28651. 1 Virulence; Hydrolase; Thiol protease; Signal; Repeat. 25 2628                                                                   | 100.0%; Score 2443; DB 1; Length 2628;<br>larity 100.0%; Pred. No. 1.1e-163;<br>Conservative 0; Mismatches 0; Indels 0; Gaps 0 | PNPNPGTITLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSALCASSASYI 60 | NFEGPONPONYLVTPELSLENGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALL 12 |
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |            | 0 0 0 0                                                                                                                     | nonas gi<br>Bacter<br>nonadace<br>ID=837;                                                                                                                                       | 11;<br>37047672<br>Whitlock<br>Agglutir<br>four la<br>four la<br>mmun. 6                                                                                                         | SS-PROT<br>the Swi<br>bean Bic<br>non-prc<br>and thi<br>require                                                                                                           | 728651, T28<br>728651, T28<br>731utinin; V<br>2 25<br>7 25<br>7 25<br>1 2540<br>1 1452<br>1 2074                                                      | ję .                                                                                                                           | PNPNPGT<br>       <br>PNPNPGT                                   | NFEGPON<br>                                                     |
| 103.5<br>103.1<br>103.1<br>103.1<br>103.5<br>102.5<br>102.5<br>102.5<br>101.5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |            | LT 1 PORGI HGA2 PORGI CH36-5; 30-MAY-2000 (Re 10-CA7-2003 (Re Hemagglutinin A                                               | HAGA.<br>Porphyron<br>Bacteria,<br>Porphyron<br>NCBI_Tax1<br>[1]<br>SEQUENCE                                                                                                    | STRAIN=381; MEDLINE=9704762; Han N., Whitlock J. "The hemagglutinin Gentains four larg Infect. Immun. 64: -1- FUNCTION: Aggl1- SIMILARITY: Be                                    | This SWISS-PP<br>between the<br>between the<br>the European<br>use by non-<br>modified and<br>entities requ<br>or send an em                                              | EMBL, U41807; As PIR; T28651; T28 Hemagglutinin; V SIGNAL 1 1 25 DOMAIN 25 DOMAIN 540 DOMAIN 1452 DOMAIN 1452 DOMAIN 1452 DOMAIN 2074 SEQUENCE 2628 J | atch<br>cal<br>45                                                                                                              | 1500                                                            | 61                                                              |
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RESULT 3
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                                                                                                                           ANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASFS
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83."; Usacteriol. 185:581-5601(2003).
-!- FUNCTION: Agglutinates erythrocytes (By similarity).
-!- SIMILARITY: Belongs to peptidase family C25.
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PEPTIDASE C25-LIKE 1.
PEPTIDASE C25-LIKE 2.
PEPTIDASE C25-LIKE 3.
W; 6DFAB22832586C63 CRC64;
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                                                                                                                                                                                                                                                                         1072 EEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIK 1131
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BEDINE=95012612; PubMed=7927685;

Pletcher H.M., Schenkein H.A., Macrina F.L.;

"Cloning and characterization of a new protease gene (prtH) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fletcher H.M., Schenkein H.A., Macrina F.L.;
Infect. Immun. 62:5707-5707(1994).
-!- FUNCTION: CLEAVES HUMAN COMPLEMENT COMPONENT C3. MAY ENABLE
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
99.6%; Pred. No. 3.7e-163; ive 1; Mismatches 1; Indels
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protease prtH (EC 3.4.22.-).
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Infect. Immun. 62:4279-4286(1994)
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HSSP; P95493; 1CVR.
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
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01-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT--2003 (Rel. 42, Last annotation update)
Gingipain R1 precursor (EC 3.4.22.37) (Gingipain 1) (Arg-gingipain)
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales.
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Okamoto K., Misumi Y., Kadowaki T., Yoneda M., Yamamoto
                                                                                                                                                                                                                                  989 AA; 110238 MW; FA85FE8A3AC8944C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 228-290 AND 517-541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ikehara Y.;
"Structural characterization of argingipain, a novel
                                                                                                                                                                                                                                                                          59.8%; Score 1460; DB 1;
85.2%; Pred. No. 4.5e-95;
ive 11; Mismatches 29;
                                                                                                         MERCPS; C25.001; -.
InterPro; IPR002376; formyl_transf.
Pfam; PR00551; formyl_transf; 1.
Hydrclase; Thiol protease; Repeat; Virulence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         991 AA.
                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OFNPVKNLKAQPDGGDVVLKWEAPS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92406812; PubMed=1527017;
                                                           EMBL; L27483; AAA51298.1;
HSSP; P23882; 1FMT.
                                                                                                                                                                                                                                                                                              Local Similarity 85.29
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                                                                                                   MEROPS; C25.001;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                  immunoglobulins, with a preference for Arg in P1, and hydrophobic residues in P2 and P3.

RENZYME REGULATION: Requires cysteine for activation and Ca(2+) and/or Mg(2+) for stabilization. It is stimulated by glycine-containing dispeptides. It is resistant to inhibition by proteinase inhibitors in human plasma.

SIMILARITY: Belongs to peptidase family C25.
FUNCTION: Thiol protease which is believed to participate in FUNCTION: Thiol protease which is believed to participate in intracellular degradation and turnover of proteins. Its proteolytic activity is a major factor in both periodontal tissue destruction and in bacterial host defense mechanisms. Activates complement C3 and C5.

CATALYTIC ACTIVITY: Cleavage of proteins, including collagens and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 TIDADGDGNNWTTTPPPPGGTSFAGHNSAICASSASYINFEGPONPDNYLVTPELSLPNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 TLIFWYCAQDANYASEHYAVYASSTG--NDASNFANALLEEVLTAKTVVTAPEAIRGTRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----OGOKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              738 -GYQILLDADHDQYGQVIPSDTHTLWPNCSVPANLFAPFEYTVPENADPSCSPTNMIM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 PAEWTTIDADGDGGWLCLSSGQLDWLTAHGGTNVVASFSWN-----GMALNPDNYLLSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 DVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                812 ---AAPQANAKIWIAGQGPTKEDDYVFEAGKKY----HFLMKKMGSGDGTELTISEGGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS, C25.001, -...
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR005536; Peptidase_C25_C.
Pfam; PF01364; Peptidase_C25_1.
Pfam; PF03785; Peptidase_C25_C, 1.
Virulence; Hydrolase, Thiol protease; Calcium; Signal; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.9%; Score 266; DB 1; Length 991;
25.9%; Pred. No. 4.7e-11;
ive 50; Mismatches 164; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             595 SVNVSCDYNGAIATISANGKMF---GSAVVENGTATINLTG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GINGIPAIN R1.
PROTON DONOR (BY SIMILARITY
NUCLEOPHILE (BY SIMILARITY)
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281

639 432

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        -----YVPYAFKGKEMLG--YDDTISFSYKAMYVKREHFGGAMVWTLDMDDVRGTFC 367
                                                                                                                                                                                                   428 GGEAMTTEVHRRYENMITVPSDGS-----VTPGGTASPRKHAVTPENNTM 472
                                                                                                                                                                                                                                           237 AS-----FSWNGMALNPDNYLISKDVTGATKV-----KYYYAVNDGFPGDHYAVM
                                                                                                                                                                                                                                                                              473 AAEAKTMSTLDFFSKTTTGVSKTTTGVSKTTTGVSKATAGISKTIPEISKATA
                                                                                                                 368 GNGPFPLVHILNELLVQTESNSTPLPQFWFTSSVNASGPGSENTALTEVLTTDTIKILPP
                                                                                                                                                                                                                                                                                                                               282 -ISKIGINAGDFIVVFEETPNGINKGGARFGLSTEADGAKPQSVWIER-TVDLPAGTKYV
                                                                                                                                                                                                                                                                                                                                                                         533 GVSKTTTGVSKTTTGISKTITGVSK--TTTGISKTTTGISKTTTGVSKITTGVSKTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKTTTGIS------QTTTTGISKTTTDISKTT-TGISKTTPGISKTTPGMTVIVQTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----CVNVTVDPVQFNPVQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 ANEAETTATMDHQSVTPTEMDTTLFYLKTMTPSEKETSRKKTMVLEKATVSPREMSATPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-layer with tetragonal symmetry.
                                                                                                                                                         HGEAPA-----EWITIDADGDGQGWLCLSSGQLDWLTAHGGT-----
                                                                                                                                                                                                                                                                                                                                                                                                                 340 AFRHYNCSDLNYILLDDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lactobacillus brevis.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2BE2403392E65A2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-layer protein precursor (Surface layer protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 390 -FEEDGVATGNHEYCVEVK-----YTAGVSPKE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-LAYER PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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Q05044;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTGHNSPLFSLPEDSKSSAYAMNYWRKLGTPADKLIMGFPTYGRNFYLLKESKNGLQTAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and characterization of a mouse oviduct-specific
                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ICR; TISSUE=Oviduct;
MEDLINE=96115001; PubMed=7492680;
Sendai Y., Komiya H., Suzuki K., Onuma T., Kikuchi M., Hoshi H.,
                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Estrogen-dependent oviduct protein).
OVGP1 OR OGP OR CHITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 0.22;
53; Mismatches 178; Indels 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.2%; Score 126; DB 1; Length 721; 18.6%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 MGPASPGKY----TKQAGFLAYYEVCSFVQRAKKHWIDYQ-
                                                                                                                                                    721 AA
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                                                                                                                                                    PRT;
  426 QFNPVQN-LTGSAVGQKVTL 444
                            922 ADVTAQKPYTLTVVGKTITV 941
                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
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                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                      musculus (Mouse)
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es 103; Conser
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycoprotein."
Biol. Reprod.
                                                                                                                                                OGP MOUSE
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OGP MOUSE

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                                                                                                                                                                                                                                                                                                                                                                                                                                309 DATYGNTVYATVSQAATSKVALKVSGTPVTTALTTADANDKVAANDTTANGSSVAGSTVY 368
                                                                                                                                    FEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALLE 121
                                                                                                                                                                                                                                     ----KSAETITKADMPARTIGFYLTDISKNTLWTAPKYTQYKASK------ 173
                                                                                                                                                                                                                                                                                                                                                                              ---GTQVGSNTWV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----YTVY 375
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                                                                        61
                                                                                                        80
                                                                                      || ::|: | :: || :: || | 26 TTASARSYATAĞAYSTLKTDAATRNVEATGTNALYTKP--GTV---KGAKVVASKATMAK
                                                                 7 TITLSESFEN-GIPASWKTIDA----DGDGNNWTTTPPPGGTSFAGHNSAICASSASYIN
                                                                                                                                                                    81 LASSKKSADYFRAYGVKTTNRGSVYYRVVTMDGKYRGYVYG-----GKSDTAFAGGI--
                                                                                                                                                                                                                                                                                                      VSLYGVAKDTKFTVDQAATKTREGSLYYHVTATNGSGISGWIYAGKG---FSTTATGTOV
                                                                                                                                                                                                                                                                                                                                        236 VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV
                                                                                                                                                                                                                                                                     177 VEIKANGKRADFTETFESSTHGEAPABWTTIDADGDG-QGWLCLSSGQLDWLTAHGGTNV
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                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shen H., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.; "Cellublobydxolase B, a second exo-celloblobydxolase from the cellulolytic bacterium Cellulomonas fimi."; Biochem. J. 311:67-74 (1995).
                                      153;
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     DB 1; Length 465;
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01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Exoglucanase B precursor (EC 3.2.1.91) (Exocellobiohydrolase (1,4-beta-cellobiohydrolase B) (CBP120).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Cellulomonadaceae; Cellulomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---ILLDDIOFTMGGSPTPTDYT----
                                   201;
                                                                                                                                                                                                                                                                                                                                                                         231 LGGLSTDK-----SVTATNDNSVKIVYRTTD-
 5.0%; Score 121.5; DE 19.8%; Pred. No. 0.25; ive 48; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 456-461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96003898; PubMed=7575482;
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MEDLINE=94197708; PubMed=8147863;
                                   Conservative
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                 Similarity
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Query Match
Best Local
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               Best Loca
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Warren R.A.J., Miller R.C. Jr.; Kilburn D.G.,

Warren R.A.J., Miller R.C. Jr.; Kilburn D.G.,

"Esterecohemical course of hydrolysis catalysed by Cellulomonas fimi
"Esterecohemical course of hydrolysis catalysed by Cellulomonas fimi
"Esterecohemical course of hydrolysis catalysed by Cellulomonas fimi
"Esterecohemical course of hydrolyse cellohexaose to a mixture of cellotetraose,
"Cellotriose and cellohiose, with only a trace of glucose. It
hydrolyzed callopentaose to cellotriose and cellohiose, and
"Cellotetraose to cellohiose, but it did not hydrolyze cellotriose."
"Cellotetraose to cellohiose, but it did not hydrolyze cellotriose."
"Cellotetraose to cellohiose, but it did not hydrolyze glucosidic bonds with inversion of anomeric configuration.
"Cellotetraose and cellohiose, releasing cellohiose from the non-
reducing ends of the chains."
"Cellotetraose from the non-
reducing ends of the chains."
"Cellotetraose from the non-
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"Cellotetraose from the non-
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"Cellotetraose from the non-
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reducing ends of the chains."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 VIAPEAIRGIRVOG-----TWYOKIVQLPAGIKYVAFRHFGCIDFFWINLDD 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              574 TASRDKAKALLD----AIWANNQDP----LGVSAVETRGDYKRFDDTYVAN----GDG
                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO CELLULASE FAMILY L (FAMILY 48 OF GLYCOSYL HYDROLASES).
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R PIR; S59077; S59077

InterPro; IPR008965; Cellul bind.

InterPro; IPR008965; Rollil-like.

InterPro; IPR008965; Rollil-like.

InterPro; IPR003961; FN III.

R InterPro; IPR003961; FN III.

R InterPro; IPR003961; FN III.

R InterPro; IPR0041; fn3; 3.

R Pfam; PF00513; CBM 2; 1.

R Pfam; PF00513; CBM 2; 1.

R Pfam; PF0011903; Glyco-hydro-48; 1.

R PRIMES; PR00644; GlyCo-hydro-48; 1.

R PRIMES; PR00644; GlyCo-hydro-48; 1.

R PRIMES; PR00664; GlyCo-hydro-48; 1.

R PRIMES; PR00664; GlyCo-hydro-48; 1.

R SWART; SW00651; CBD II; 1.

R SWART; SW00651; CBD II; 1.

R CGlullose degradation; Hydrolage; Repeat; Signal.

R CRAILL
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FIBRONECTIN TYPE-111 1.
FIBRONECTIN TYPE-111 2.
FIBRONECTIN TYPE-111 3.
CELLULOSE-BINDING (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.0%; Score 121; DB 1; Length 1090;
22.3%; Pred. No. 0.85;
:ive 53; Mismatches 197; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114829 MW; 046BB9D956F2F399 CRC64;
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700 78
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1090 AA;
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AP002559; BAB36199.1; ALT\_FRAME

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                                                                              292
        VEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVV 236
                                        677 AQTAVAGALADYARLFDDGT-----TTPDTTAP-----TVPTG----LQAGVVTSTE 719
                                                                                                              --GTATITSFIDIGLIASTAYAY 766
                                                                                                                                           293 TVVFBETPNGINKGGARFGLSTEA---DGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDL 349
                                                                                                                                                                       767 TVRAFDAAGNVSAPSAALTVTTKATPSDTTAP-----SVPALTS-----SSSTA 810
                                                                                                                                                                                                                 401
                                                                                                                                                                                                                                                861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C157.H7 / RIMD 0509952;
MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Complete genome sequence of enterchemorrhagic scherichia coli "Complete genome sequence of enterchemorrhagic scherichia coli O157.H7 and genomic comparison with a laboratory strain K-12.";
                                                                           ASFSWNGMALNPDNYLISKDV-TGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGD---F
                                                                                                                                                                                                          350 NYILLDDIQFTWGGSPTPTDYT-----YTVYRDGTKIKEGLTETTFEEDGV-ATGNHE
                                                                                                                                                                                                                                         811 NSV-----TIGMSAS-TDNAGGSGLAGYDVYRGATRVAQ-TTALTFTDTGLTASTAYE
                                                                                                                                                                                                                                                                                   448
                                                                                                                                                                                                                                                                                                          862 YTVRARDVAGNVSAPSTAVSVTTKSDTTPDTTAPSVPAGLAAMTVTETSVALTWNA 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=0157:H7 / EDL933 / ATCC 700927;
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074335; PubMed=11205551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Apodaca J., Alattner F.R.,
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533 (2001).
                                                                                                                                                                                                                                                                           402 YCVEVKYTAG--VSPKECVNVTV-----DPVQFNPVQNLTGSAVGQ-KVTLKWDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        suctionima coli 015/18/.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 8:11-22(2001).
-!- SIMILARITY: Contains 16 Big-1 domains.
-!- SIMILARITY: Belongs to the intimin/invasin family.
-!- CAUTION: Ref. 2 sequence differs from that shown due to a
                                                                                                                                                                                                                                                                                                                                                           RESULT
YEDJECOS7
ID ZELJECOS7
AC (08X8V7; O8X2B9; O8X2C0;
DT 28-FEB-2003 (Rel. 41, Created)
PT 28-FEB-2003 (Rel. 41, Last sequence update)
PT 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                            720 ATISWT--ASTDDTRVTGYDVYRGATKV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       frameshift in position 1315.
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SEQUENCE FROM N.A.
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EMBL; AE005423; AAG57041.1; -. EMBL; AP002559; BAB36198.1; ALT\_FRAME.

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1572 -----VITATVVDNNGFPVKGVTVNFTSNAATAEMTNGGQAVTNEQGKATVTYTNTRS 1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1625 SIE---SGARPD---TVEASLENGSSTLSTSINVNADASTAHLTLLQALFDTVSAGDTTN 1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1679 LYIBVKDNYGNGVPQQEVTLSVSP----SEGVTPSNNAIY----TTNHDGNFYA---SF 1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 GPQNPDNYLVTPELSLPNGG----TLTF---WVCAQDANYASEHYAVYASSTGNDASNF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 V---VASFSWNG------MALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 IGINAGDFTVV-----FEETPNGI-NKGGARFGLSTEADGAKPQSVWIERTVDLPAG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 TKYVAFRHYNC---SDLNYILLDDIQ--FTMGGSPTPTDYTYTVYRDGTKI----KEGLTE 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATL STAAU STANDARD; PRT; 1256 AA.
PS2081;
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bifunctional autolysin precursor [Includes: N-acetylmuramoyl-L-alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 DVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGO-GWLCLSSGQLDWLTAHGGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 TTTLSESFE---NGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASYINFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1520 GEQ-----TVTASLANNGASDNKTVHFIGDTAAAKIIELTPVPDSIIAGTPQNSSGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Mismatches 198; Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | : | | : | | | | 1827 VILK--GIKAGAH--TVIASMAGGKSEQLVVNFIADILIADILIAQVNLNVI 1869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 120; DB 1; Length 2660;
Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 TIFEEDGVATGNHEYCVEVKYTAGVSPKECVNVTVDPVQFNPVQNLT 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1 16.
01EB92A08F5C09D2 CRC64;
                                                                                                                                                               Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.9%; Score 120;
InterPro; IPR00334; Big 1.
InterPro; IPR00335; Intimin.
InterPro; IPR00855; Intimin.
InterPro; IPR008064; Invasin_intimin.
InterPro; IPR000601; PKD.
Pfam; PP02369; Big 1; 16.
SMART; SM00634; BID 1; 16.
SWART; SM00634; BID 1; 16.
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                                                                                                                                                               protein;
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                                                                                                                                                                                                                                                                                                                                                                      1751
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2157
2254
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                                                                                                                                                           Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105;
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Matches
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1519

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                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ENDOHYDDLYSIS OF THE DI-ACETYLCHITOBIOSYL UNIT IN HIGH-MARNOSE GLYCOPEPTIDES AND GLYCOPROTEINS COWTAINING THE -[(MAN) 5 (GLCNAC) 2]-ASN STRUCTURE. ONE N-ACETYL-D-GLUCOSAMINE RESIDUE REMAINS ATTACHED TO THE PROTEIN; THE REST OF THE OLIGOSACCHARIDE IS RELEASED INTACT.
-!- CAPALYTIC ACTIVITY: Hydrolyzes the link between N-acetylmuramoyl residues and L-amino acid residues in certain bacterial cell-wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Endohydrolysis of the di-N-acetylchitobiosyl unit in high-mannose glycopetides and glycoproteins containing the -[Man(GloMAC)2]Asn-structure. One N-acetyl-D-glucosamine residue remains attached to the protein; the rest of the oligosaccharide is released intact.
                                                                                                                                                                                                                      "A Staphylococcus aureus autolysin that has an N-acetylmuramoyl-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETYLMURAMOYL-L-ALANINE AMIDASE FAMILY 2.
SIMILARITY: IN THE C-TERMINAL SECTION, BELONGS TO FAMILY 73 OF
                                                                                                                                                                                                                                           alanine amidase domain and an endo-beta-N-acetylglucosaminidase domain: cloning, sequence analysis, and characterization."; Proc. Natl. Acad. Sci. U.S.A. 92:285-289(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
BIFUNCTIONAL AUTOLYSIN.
N-ACETYLMURANOYL-L-ALANINE AMIDASE.
ENDO-BETA-N-ACETYLGLUCOSAMIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.8%; Score 117.5; DB 1; Length 1256; 22.1%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Secreted.
PTM: UNDERGOES PROTEOLYTIC PROCESSING TO GENERATE THE TWO
                                                                                                                                                                                   Oshida T., Sugai M., Komatsuzawa H., Hong Y.-M., Suginaka H.,
Tomasz A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multifunctional enzyme; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE N-
amidase (EC 3.5.1.28); Mannosyl-glycoprotein endo-beta-N-acetylglucosamidase (EC 3.2.1.96)].
                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 205-214 AND 776-792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137384 MW; 2BB76CAA292FDD20 CRC64;
                                                  Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                               MEDLINE=95116542; PubMed=7816834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR LYTIC ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D17366; BAA04185.1; -.
EMBL; L41499; AAA99982.1; -.
InterPro; IPR002502; Amidase_2.
InterPro; IPR002901; Amidase_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01510; Amidase 2; 1
Pfam; PF01832; Amidase 4; 1.
SMART; SM0644; Ami 2; 1.
SMART; SM00047; LYZZ; 1.
Cell wall; Hydrolase; Signal; I SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     596 75
770 93
1256 AA;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=NCTC 8325-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glycopeptides.
                                                                                           NCBI_TaxID=1280;
                                                                                                                                                STRAIN-RN450;
                                                                                                                                                                                                                                                                                                                                                          Foster S.J.:
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-----GTLIFWVCAQDANYASEHYAVYASSTGNDASNFAN-----ALLEEVLT 125
                                                                                                                                                                                                                                                                                                                                                                                        126 AKT-----VVTAPEAIR------GTRVQGTWYQKTVQLPAGTKYVAFRHFGCT-- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                     262 KVK-----YYYAVNDGFPGDHYAVMISKIGT-----NAGDFTVVFEETPNG--- 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  936 AVKPITSAAKDYNYIYVIKNG-NGYYYVIPNSDIAKYSLKAFNEQPFAVVKEQVINGQIW 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license ascement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                      714 QEAGAVSGTGNQTFKATKQQQIDKS----IYLFGTVNGKSGWVSKAYLAVPAAPKKAVAQ 769
                                                                                                       41 ---GGTSF---AGHNSA----ICASSASYINFEGPQN-PDNYLVTPE---LSLPNG--- 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             827 RAHGNETYVLINNTSHNIFLGWENVKDLNVQNLGKEVKTIQKYTVNKSNNGLSMVPWGT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----DFFWINLDDVEIKANGKRADFTE--TFESSTHGEAPAEWTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 DADGDGQGWLCLSSGQLDWLTAHGGTNVVASFSWN-----GMALNPDNYLISKDVTGAT
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-!- CATALYTIC ACTIVITY: Pectin + N H(2)O = N methanol + pectate.
-!- SIMILARITY: Belongs to the pectinesterase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspergillus aculeatus.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=KSM 510;
MEDLINE=97079238; PubMed=8920970;
Christgau S., Kofod L.V., Halkier T., Andersen L.N., Hockauf M.,
Dorreich K., Dalboege H., Kauppinen S.;
"Pectin methyl esterase from Aspergillus aculeatus: expression
cloning in yeast and characterization of the recombinant enzyme.";
Biochem. J. 319:705-712[1996].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pectinesterase precursor (BC 3.1.1.11) (Pectin methylesterase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----INKGGARFGLSTEADGAK-----PQSVWIERTVDLPAGTKY 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR000070; Pectinesterase.
Pfam; PF01095; Pectinesterase; 1.
PROSITE; PS00800; PECTINESTERASE 1; 1.
PROSITE; PS00503; PECTINESTERASE 2; 1.
Hydrolase; Aspartyl esterase; Cell wall; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U49378; AAB42153.1; -.
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Q12535;
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26; 40

Gaps

153;

Indels

47; Mismatches 163;

22.1%;

Similarity

Local

Conservative

103;

Matches

1 PNPNPGTTT----LSESFENGIPASWKTIDADGDG---NNWTTTPPP-

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                AVYASSTGNDASNFANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGT-KYVA 160
                                                                                                                                                                                                203
                                                                                                                                                                                                                       80 YGQTENTDSYADNLVTITHAISYEDAGESDDLTATFRNKAVGSQVYNLNIANTCGQACHQ 139
                                                                                                                                                                                                                                                        236
                                                                                                                                                                                                                                                                                      199
                                                                                                                                                                                                                                                                                                               -----ASFSWNGMALNPDN--YLISKDVTGA-----TKVKYYYAVNDGFPGDHYAV 280
                                                                                                                                                                                                                                                                                                                                                                            338
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2011 (Rel. 40, Last annotation update)
Pesticidial crystal protein crysAa (Insecticidal delta-endotoxin
CryvA(a)) (Crystaline entomocidal protoxin) (152 kDa crystal protein).
CRYSAA OR CRYVA(A) OR CRYVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                  : | | | | : | | | | : | | | | | : | 140 ALALSAWADQQGYYGCNFTGYQDTLLAQTGNQLYINSYIEGAVDFIFGQHARAWFQNVDI
                                                                                                                                                                                           161 FRHFGCTDFFWINL----DDVEIKANGKRADFTETFE------SSTHGEAPAE
                                                                                                                                                                                                                                                                                                                                                                         281 MISKIGINAGDFIVVFEET -- PNGINKGGARFGLSTEADGAKPOSVWIERTVDLPAGIKY
                                                                                                                                                                                                                                                                                                                                                                                                      ----WTEWSTSTP-NTEY
                                                                                                                                                                                                                                                                                                                                200 RVVEGPTSASITANGRSSETDTSYYVINKSTVAAKEGDDVAEGTYYL----GRPWSEYA-
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the spore coat. MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                  98; Indels 105;
                                                                         DB 1; Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ENRL B-18243 / PS17;
SIGA A.J., Schwab G.E., Payrne J.M.;
Sick A.J., Schwab G.E., Payrne J.M.;
Sick A.J., Schwab G.E., Payrne J.M.;
Sick A.J., Schwab G.E., Payrne J.M.;
Sick A.J., Schwab G.E., Payrne J.M.;
Sick A.J., Schwab G.E., Payrne J.M.;
Patent number US5281530, 25-7AN-1994.
-!- FUNCTION: ENDOTOXIN WITH NEMATICIDAL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                          1F1C81BF1E32174F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                     204 WTTIDADGDGGGWL-CLSSGQLDWLTAHGGTNVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus thuringiensis (subsp. darmstadiensis)
                                                                       ; Score 116.5; DE; Pred. No. 0.36; 33; Mismatches
PECTINESTERASE.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1385 AA
                                                                                                                                                                                                                                                                                                                                                                                                      ------RVVFOOTSMINVINSLG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L07025; AAA67694.1; -.
PIR; T18213; T18213.
InterPro; IPR005638; endotoxin_C.
331 PE
162 BY
183 BY
35681 MW;
                                                                      4.8%;
                                                                                    22.9%;
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
18 3
162 1
183 1
331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    339 VAFRHY 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTFGEY 290
                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=132264;
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          ACT_SITE
ACT_SITE
SEQUENCE
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SEQUENCE B
                                                                      Query Match
Best Local S
Matches 70
                                                                                                                                102
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CSAA BACUD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            743 FFATFPVPEGF----NEVRILAGLPEVSGNITVQSNNPPQPSNNGGGDGGGNGGGDGGO-- 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GVATGNHEYCV 404
                                                                                                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474 AGMGGGFADTIYSLPATHYLSYLYGTPYQTSDNYSGHVGALVGVSTPQEATLPNIIGQPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                       534 EQGNVSTMGFPFEKASYGGTVVKEWINGANAMKLSPGQSIGIPITNVTSGEYQIRCRYAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OLPAGTKYVAFRHFGCTDFFWINLDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 KY-YYAVNDGFPGDHYAVMISKTGTNAGDFTVVFBETPNGINKGGARFGLSTEADGAKPQ
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                                                                                                                                                                                                                                                                              416 DPQAGPNYVSIDSSNPIIQINMDTWKTPPQGASG--WNTNLMRGSVSGLSFLQRDGTRLS
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405 E---VKYTAGVS-PKECVNVT--VDPVQFNPVQNLTGSAVG----QKVTLKWDA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         884 KSPNVNYDRSFKLPIDLQNITTQVNALFASGTQNMLAHNVSDHDIEEVVLKVDA 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98049343; PubMed=9389475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
                                                                                                                                                                                                                                                                                                                            ----AGHNSAICASSA----SYINFEGPONPONY------LVTP-ELSLPN-
                                                                                                                                                                                                                                     2 NPNPGTTTLSESFENGI----PASWKTIDADGDGNNWTTTPPPPG---GTSF---
                                                                                                                                                                                            219;
                                                                                                                                               Length 1385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDASNF-----ANALLEEVLTAKTVVTAPEAIRGTRVQG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 GDGQGWLCLSSGQLDWLTAHGGTNVVASFSWNGMALNPDNYLISK----
                                                                                                                                                                                            Indels
                                                                                                      1385 AA; 152439 MW; E29FF11FC799DE95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 SVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSPTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                             4.8%; Score 116.5; DB 1; 20.0%; Pred. No. 2.4; ive 67; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 DYTYT-----VYRDGTKIKEGLTETTF-----EED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-701-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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IPR005639; endotoxin N. IPR008979; Gal_bind_like.
                                    Pfam; PF03944; endotoxin_C; 1.
Pfam; PF03945; endotoxin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein AF2028
                                                                                                                                                                      Best Local Similarity 20.0
Matches 119; Conservative
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                                                                           Toxin; Sporulation.
SEQUENCE 1385 AA:
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028251;
                    InterPro;
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                                                                                                                                                 Query Match
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YK28 ARCFU
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSSVTLTVNKNLNTSYDTNWKTLEFADGSSNPKQIISGTLDNNKWLTTFFKVKGNYSTDE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---SAICASSASYINFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYAS 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 AFVSRLVGFGEAYFOF-GPINGN------ISGTKIIDV-----FAIGNASIGVN 302
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Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mascon T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                             "The complete genome sequence of the hyperthermophilic, sulphate-
                                                                                                                                                                                                                                                                                                             reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: TO M.JANNASCHII MJ1393 AND MJ1394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.7%; Score 114.5; DB 1; Length 18.4%; Pred. No. 1.1; ative 67; Mismatches 187; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothelical protein; Transmembrane; Complete proteome.
TRANSMEM 16 36 POTENTIAL.
TRANSMEM 583 603 POTENTIAL.
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607 AA; 66215 MW; F46F116BF2AAFBE1 CRC64;
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PIR; C69503; C69503.
TIGR; AF2028; -.
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tes 90; Conserv
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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Button G.G., Blake J.A., Fitzderald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Trond J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 STSLNNDPNGGYKLLPKEIGRDVVISGWYRPSNWGGGPIDRIGLEDENFDGYSFEVNHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 TITLSESFENGIPASWKIIDADGDGNNWTTTPPPGG------TSFAGHNSAICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SASYINFEGPONPONYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 VASFSWNGMALNPDNYLISKDVTGATKV-----KYYYAVND-----GFPGDHYAVMISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               615 INAINWINITINWSN-----DSATLVFNVLGNYSYSERDNILAKYGFA----KILFNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 273:1058-1073(1996).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: TO M.JANNASCHII MJ1393 AND A.FULGIDUS AF2028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.6%; Score 112.5; DB 1; Length 987; Best Local Similarity 19.5%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         534 ONGSL----AATVST-----IDNT-YTKFDRVVIHGGYVYY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                              Archaea; Buryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 ----YNCSDLNYILLDDIQFTMGGSPTPTDYTYTVYRDGT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              958 978 POTENTIAL.
987 AA; 112360 MW; D1E628FFB28CA86D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69; Mismatches 143;
(Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / DSM 2661 / ATCC 43067;
                                                                                                                                 Hypothetical protein MJ1394. MJ1394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U67579; AAB99404.1; -. PIR; A64474; A64474.
                                                                                                                                                                                                                         Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                       Keeler C.L. Jr., Hnatow L.L., Whetzel P.L., Dohms J.E.;
Cloning and characterization of a putative cytadhesin gene (mgcl)
from Mycoplasma gallisepticum ";
Infect. Immun. 64:1541-1547(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93371270; PubMed-8363503;
Dohms J.E., Hnatow b.L., Whetzel P., Morgan R., Keeler C.L. Jr.,
"Identification of the putative cytadhesin gene of Mycoplasma
gallisepticum and its use as a DNA probe.";
Avian Dis. 37:380-388(1993).
                                                                                                                                                                                           Mycoplasma gallisepticum.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goh M.S., Geary S.J.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Could be involved in cytadherence.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
-!- SIMILARITY: Belongs to the adhesin Pl family.
-!- CAUTION: Ref. 4 sequence differs from that shown due to a frameshift in position 159 to 213.
                                                                                                         Q49379; Q49437; Q53351;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Adhesin Pl precursor (Cytadhesin Pl) (Attachment protein)
GAPA OR MGC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155C34DA2D6C3C65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hnatow L.L., Keeler C.L. Jr., Tessmer L., Dohms J.E.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
706 AKSYSFNLTNLNIWAVNKSAYELYWNP----FNKSIWIDGS 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y -> F (IN REF. 3).
I -> T (IN REF. 3).
R -> G (IN REF. 3).
T -> A (IN REF. 3).
DIL -> VYT (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POLY-ILE.
DM -> IW (IN REF. 4).
                                                                                               PRT; 1122 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 111.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U34842; AAB02987.1; -.
EMBL; U44804; AAC83385.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U44804; AAC83385.1; ALT_FRAME.
PIR; T18346; T18346.
CYtadherence; Signal; Transmembrane.
SYSGNAL 30 POTEWIN
                                                                                                                                                                                                                                                                                                      MEDLINE=96201559; PubMed=8613358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 159-1122 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
SEQUENCE OF 378-570 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.68;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-12 FROM N.A.
                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1122
1021
1009
314
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568
570
693
1122 AA;
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=S6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=S6;
                                                                                               MYCGA
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TRANSMEM
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CONFLICT
SEQUENCE
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                                                            DOMAIN
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                      26;
                                                                                                                         96 YASEHYA-----ALLEEVLTAKTV 129
                                                                                                                                                                                                                                                                185 RAD--FIETFESSTHGEAPAEWTTID-----ADGDGQGWLCLSSGQLDWLTAHGGTNVV 236
                                                                                                                                                                                                                                                                                                                                                                          709
                                                                                          -----NGLALAPALGODVG 479
                                                         95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDDTV-FSVSKIPFEKEITAAVNVRSLDSYYVQLNGETSVNTVARVSPDSSA-LTLNPKR
                                                     TTPPPGGTSFAGHNSAICASSASYINFEGPONPONYLVTPELSLPNGGTLTFWVCAQDAN
                                                                                                                                                          Y---HFVPRLAVGGVSSPRGANGNIFLGSAITWGTNGGNFLDTKWHSPAVIEDAPTTFIT
                                                                                                                                                                                                                                                                                                                                      237 ASFSWN------GMALNPDNYLIS------KDV-----TGATKVKYYYAV
                                                                                                                                                                                                                                                                                                                                                                         650 NNFTYNTQQQLASTAAGENANPRNILNALTTAKGFDRRDIGNVDILYSNNTNKFTYYYQV
                                                                                                                                                                                                                                                                                                                                                                                                          270 ND-----GPPGDHYAVMISKTGTNAGDFTVVFEETPNGINK-GGARFGLSTEADG
                                                                                                                                                                                                                                                                                                                                                                                                                                             710 GGAITTWPEVQVNYKTSANITYYNLTRTDFGSTTPATQDANTVSSKLNGAYLSSTGDQQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 AKPQSVWIERTVDLPAGTKYV -- AFRHYNCSDLNYILLDDIQFTMGGSPTPTDYTYTVYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGTKIKEGLTETTFEEDGVATGN----HEYCVE-----VKYTAGVSFKECVNVTVDPVQ
                                                                                                                                                                                             130 VTAPEAIRGTRVQGTWYQKTVQLP--AGTKYVAFRHFGCTDFFWINLDDVEIK----ANGK
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-galactose residues in beta-D-galactosides.
-!- SIMILARITY: Belongs to family 2 of glycosyl hydrolases.
19.0%; Pred. No. 4.1;
Live 77; Mismatches 193; Indels 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                           437 TAEAPGNTKTVGYPYGILLSA---ISFDATR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Beta-galactosidase (EC 3.2.1.23) (Lactase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1034 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; T30574; T30574.
HSSP; P00722; IBGL.
InterPro; IPR008979; Gal_bind_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ000733; CAA04267.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 F-NPVONLTGSAVGO 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||: | ::||
877 ITNPLMN-RDNVIGQ 890
                    94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus megaterium.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=DSM 319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 SAIC-----ASSASYINFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            488 FQHMYTFFKEKDSTRLVHYEGIFHHRDYDASDIES-----TMYVKPADV----ERYAL 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----YASSTGNDASNFAN--ALLEEVLTAKTVVTAPEAIRGTRVQG----TWY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 QKTVQLPA--GIKYVAF-RHFGCT----DFFWINLDDVEIKANGKRADFTETFESSTHGE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 APAEWTIIDADGDGQGWLCLSSGQLDWLTAHGGTNVVA-SFSW----NG------MA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 -YYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLSTE----ADGA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        537 MNPKKPYILCEYSHAMGNSCGNLXXXWELFDQY-------PILQGGFIWDWK 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 636 -PVKWTAVDP------AKGKFAVQNKHLFTNLNAYDFVWTVEKNGELVEKHASLLN 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                685 VAPDGTDELTLSYPLYEQENETDEFVLTLSLRLSKDTAWASAGYEVAYEQFVLPAKAAMP 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             320 KPQSVWIERTVDLPAGTKYVAFRHYNCS--------DLNYILLDDIQFTM 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 849 DNŚLASCYVTYTLYNDGEMKIEQSLAPSETMPELPEIGMLFTMNAAFDSLTWYGRCPHEN 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 GT-TILSESFENGIPAS---WK--TIDA-----DGDGNN-----WTTTPPPGGTSFAGHN 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
4.5%; Score 110.5; DB 1; Length 1034;
Best Local Similarity 19.9%; Pred. No. 4.3;
Matches 114; Conservative 70; Mismatches 169; Indels 221; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---KVKY---KDVTGAT---KVKY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTON DONOR (BY SIMILARITY).

NUCLEOPHILE (BY SIMILARITY).

118673 MW, 38644C9A649415E9 CRC64;
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InterPro; IPR006101; Glyco hydro 2.
InterPro; IPR006102; Glyco hydro 21g.
InterPro; IPR006103; Glyco hydro 21g.
InterPro; IPR006103; Glyco hydro 2TIM.
InterPro; IPR004109; Glyco hydro 42C.
InterPro; IPR004109; Glyco hydro 42C.
InterPro; IPR004109; Glyco hydro 42C.
Pfam; PF02930; Bgal small C; 1.
Pfam; PF02930; Bgal small C; 1.
Pfam; PF02930; Glyco hydro 2; 1.
Pfam; PF02836; Glyco hydro 2; 1.
Pfam; PF02836; Glyco hydro 2; 1.
PROSITE; PR00713; GLYCOFYL HYDROL F2 1; 1.
PROSITE; PR00719; GLYCOSYL HYDROL F2 2; 1.
Hydrolase; Glycosidase.
ACT SITE 481 481 PROTON DONOR (BY ACT SITE 487 547 NUCLEOPHILE (BY SEQÜENCE 1034 AA; 118673 MW; 38644C9A6494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: May 18, 2004, 11:43:32 Job time : 10.4245 sec8
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bordetella

Q7wn54

14

OM protein

Run on:

Sequence:

Searched:

Database

1111111 10084921 10111111

Result

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Quepzi mechanosarc
Quaj9 rhodopirell
Q98443 homo sapien
Q912m3 pseudomonas
Q912m3 pseudomonas
Q812m3 pseudomonas
Q858b6 enterobacte
Q8172 methanosarc
Q9mu3 paracentrot
Q7uvzg rhodopirell
Q2644 ruminococcu
Q90365 shewnella
Q8736 ralstomia s
Q8366 unidentifie
Q91369 pseudomonas
Q8151 photorhabdu
Q85151 photorhabdu
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Pavloff N., Pemberton P.A., Potempa J., Chen W.-C.A., Pike R.N.,

Prochazka V., Kiefer M.C., Travis J., Barr P.J.;

"Molecular cloning and characterization of Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1723;
                                                                                                                                                                                                                                                                                                                                                            Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Lys-gingipain...;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U54691; AAA99810.1;
R GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000524; F:ATP binding; IEA.
GO; GO:000310; F:DNA ligase (ATP) activity; IEA.
GO; GO:0006281; F:DNA repair; IEA.
GO; GO:0006281; P:DNA repair; IEA.
GO; GO:0006281; P:DNA replication; IEA.
GO; GO:0006280; P:DNA replication; IEA.
GO; GO:0006260; P:DNA replication; IEA.
GO; GO:0006508; P:Proteolysis and peptidolysis; IEA.
InterPro; IPR000977; DNA ligase.
InterPro; IPR001769; Peptidase C25.
R InterPro; IPR001769; Peptidase C25.
R InterPro; IPR001769; Peptidase C25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ptidase_C25_C; 1.
DNA_LIGASE_A1; 1.
A; 186831 MW; 4508A7E50197CEBD_CRC64;
                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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Pred. No. 3.1e-127;
                                                                                                                                                                                                                                                                                                      PRT; 1723 AA
                                                                                                                                                                                                                                                              ALIGNMENTS
                        Q7UQJ9
Q88WI9
Q9HD43
                                                                                          Q7UWZ8
Q52644
                                                          Q912M3
O858B6
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Q8Y366
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Q8PVIO
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Q8X2T1
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Pfam; PF03785; Peptidase C25 C
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                                                        1723 AA;
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Best Local Similarity
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SEQUENCE 1723 AA
NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                             Lys-gingipain.
KGP.
P72197
P72197;
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P72197
xanthomonas
                                                 May 18, 2004, 11:36:20 ; Search time 32.8982 Seconds (without alignments) 4315.838 Million cell updates/sec
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   5.1.6
Compugen Ltd.
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    GenCore version
Copyright (c) 1993 - 2004
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                                   - protein search, using sw model
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                                                                                                                             Gapop 10.0 , Gapext 0.5
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Q51816
Q51839
P72194
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Q51838
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007442
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Q9KIB3
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sp_unclassified:*
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sp_mammal:*
sp_mhc:*
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sp_bacteriap:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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Maximum DB seq length: 2000000000
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sp_plant:*
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Match
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Perfect score:
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2063
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2041
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2016
5016
5016
5016
51
561
561
561
563
152
33
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Q8pviO methanosarc Q9cfa2 lactococcus Q8eka6 shewanella Q826w1 streptomyce

Q8tq91 methanosarc Q8x2t1 escherichia Q9rzs7 deinococcus Q8thc8 methanosarc

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                                                                                                                                                                                                                                                                              120 LEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI
                                                                                                                                                                                                                                                                                                                                                                   KANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF
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                                                                    9
                            Length 1687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              051816,
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Arg-grangiant-1 proteinase.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria, Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; C25.01; -..

(GO; GO:000524; F:ATP binding; IEA.

(GO; GO:000524; F:ATP binding; IEA.

(GO; GO:000314; F:DNA ligase (ATP) activity; IEA.

(GO; GO:0005310; F:DNA recombination; IEA.

(GO; GO:0005281; P:DNA repair; IEA.

(GO; GO:0005281; P:DNA replication; IEA.

(GO; GO:0005280; P:DNA replication; IEA.

(GO; GO:0005508; P:DNA replication; IEA.

(GO; GO:0005508; P:DNA replication; IEA.

(GO; GO:0005508; P:DNA ligase.

(InterPro; IPR001710; IG-Like.

InterPro; IPR001709; Peptidase_C25.
                                                                    39; Indels
                        b; Score 2063; DB 2;
b; Pred. No. 3.5e-127;
17; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1354 VIINPTOPNPVKNLKAQPDGGDVVLKWEAPS 1384
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                          84.48;
86.38;
             Ouery Match
Best Local Similarity 86.34
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                                                                                                                          60 INFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANAL
                                       1 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASY-
                                                                                                                                                                                                              LEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI
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Han N., Dong H., Progulske-Fox A.;
"Cloning and characterization of hagE from P. gingivalis 381.";
Submitted (SPP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF026461; AAD01810.1;
HSSP; P95493; ICVR.
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
  39; Indels
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GO; GO:0008234; F:ATP binding; IEA.
GO; GO:0008234; F:Cysteine-type peptidase activity; IEA.
GO; GO:0008210; P:DNA recombination; IEA.
GO; GO:0006281; P:DNA repair; IEA.
GO; GO:0006280; P:DNA replication; IEA.
GO; GO:0006280; P:DNA replication; IEA.
INTERPRO, IPRO00977; DNA ligase.
InterPro; IPRO00977; DNA ligase.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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  17; Mismatches
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InterPro; IPR005536; Peptidase C25 C.
Pfam; PF01364; Peptidase C25, I.
Pfam; PF03785; Peptidase C25 C; 1.
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NCBI_TaxID=837;
  Conservative
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Matches 389;
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SEQUENCE
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1133 KANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVSSF 1192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 LEEVITAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI 179
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      "Characterization of a Porphyromonas gingivalis gene prtR that encodes an arginine-specific thiol proteinase and multiple adhesins."; Biochem. Biophys. Res. Commun. 224:605-610(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 INFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.0%; Score 2051; DB 2; Length 1706;
85.8%; Pred. No. 2.2e-126;
tive 18; Mismatches 40; Indels 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                    A GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005234; F:ATP binding; IEA.

GO; GO:0005314; F:Cysteine-type peptidase activity; IEA.

GO; GO:0005310; F:DNA ligase (ATP) activity; IEA.

GO; GO:0006210; P:DNA recombination; IEA.

R GO; GO:0006260; P:DNA replication; IEA.

GO; GO:0006260; P:DNA replication; IEA.

R GO; GO:0006508; P:DNA replication; IEA.

R InterPro; IPR007710; Ig-like.

R InterPro; IPR007710; Ig-like.

R InterPro; IPR007710; Peptidase.

R InterPro; IPR005536; Peptidase.

R Pfam; PF01364; Peptidase.

R Pfam; PF01364; Peptidase.

R Pfam; PF03785; Peptidase.

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                                                                                                                                                                                                                                                                                                                                 Slakeski N.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL: 1.26341; AAC18876.1; -.
HSSP; P95493; 1CVR.
                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
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Best Local Similarity 85.8
Matches 387; Conservative
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1706
                                                                                                                                                                             Reynolds E.;
Submitted (JAN-1994)
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                           SEQUENCE FROM N.A
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1013 LGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASNFTNAL 1072
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                                                                                                                                                                                                                                                                                                                                                                                                           956 PNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYSESFG 1012
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                                                                                                                                                                                                                                                                                                                                                             59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 INFEGPONPONYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 LEEVLTAKTVVTAPBAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI
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Kirszbaum L., Sotiropoulos C., Jackson C., Cleal S., Slakeski N.,
Reynolds E.C.;
"Complete nucleotide sequence of a gene prtR of Porphyromonas
specific thiol endopeptidase domain and a haemagglutinin domain.";
Blochem. Blophys. Res. Commun. 207:424-431(1995).
                                                                                                                                                                                                                                                                                                  6 ;
                        Pfam; PF01364; Peptidase C25; I. –
Pfam; PF03785; Peptidase C25 C; 1.
PROSTIE; PS00697; DML LIGASE A1; 1.
CHAIN 228 719 — MATURE 50-KDA CYSTEINE PROTEINASE
                                                                                                                                                                                                                                          Length 1704;
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                               39; Indels
                                                                                                                                              GINGIPAIN.
1704 AA; 185436 MW; 6A34B40131C2A676 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         051839; Q51840;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Arginine-specific thiol protease precursor.
                                                                                                                                                                                                                                 84.4%; Score 2063; DB 2;
86.3%; Pred. No. 3.5e-127;
ive 17; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||::||||||||||||VIINPIQENENEAPS 1401
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MEDLINE=96311339; PubMed=8713096;
Slakeski N., Cleal S.M., Reynolds E.C.;
   InterPro; IPR005536; Peptidase_C25_C.
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NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                            389; Conservative
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SEQUENCE FROM N.A.
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59

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1252

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PRT; 1723 AA

PRELIMINARY;

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420 VTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 450
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                                                                                                                     Hemagglutinin.
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                                                                                                                                                                                       Okamoto K., Kadowaki T., Nakayama K., Yamamoto K., "Cloning and sequencing of the gene encoding a novel lysine-specific cysteine proteinase (Lys-gingipain) in Porphyromonas gingivalis: structural relationship with the arginine-specific cysteine proteinase
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9
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BMENCPS, C25.002; -.

GG, GG:0005524; F:APP binding; IEA.

GG; GG:0008234; F:Cysteine-type peptidase activity; IEA.

GG; GG:00082310; F:DNA ligase (ATP) activity; IEA.

GG; GG:0006281; P:DNA recombination; IEA.

GG; GG:0006281; P:DNA replication; IEA.

GG; GG:0006281; P:DNA replication; IEA.

GG; GG:0006281; P:DNA replication; IEA.

RG; GG:0006281; P:DNA replication; IEA.

RG; GG:0006281; P:DNA replication; IEA.

RG; GG:0006281; P:DNA replication; IEA.

RG; GG:0006281; P:DNA replication; IEA.

RICEPTO; IPRO01769; Peptidase. C25.

R InterPro; IPRO05565; Peptidase. C25.

R Pfam; PRO1364; Peptidase. C25.

R Pfam; PRO1364; Peptidase. C25.

R Pfam; PRO1364; Peptidase. C25.

R Pfam; PRO3785; Peptidase. C25.

R Pfam; PRO3785; Peptidase. C25.

R Pfam; PRO3785; Peptidase. C25.

R PROSITE; PSO0697; DNA LIGASE. A1; 1.

SEQUENCE 1723 AA; IB7261 MW; 5628963D251493EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 1723;
                                                                                      Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Indels
                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.9%; Score 2049; DB 2,
85.8%; Pred. No. 3e-126;
live 17; Mismatches 41
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                                                                                                                                                               STRAIN=381;
MEDLINE=97044756; PubMed=8889827;
                                                                                                                                                                                                                                           (Arg-gingipain).";
J. Biochem. 120:398-406(1996).
                      01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity 85.8
387; Conservative
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                             NCBI_TaxID=837;
                                                              Lys-gingipain.
           P72194;
01-FEB-1997
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THATED MULLIGENE family in Porphyromonas gingivalis."

THATED MULLIGENE FAMILY STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND THE STRAINS AND
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                                                                                                                                                                                                                                                                                                       Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Indels
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1358 AA; 147102 MW; 47FCA0B25B06DEDB CRC64;
                                                                                                                            Last sequence update)
Last annotation update)
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83.5%; Score 2041; DB 2;
Best Local Similarity 85.6%; Pred. No. 7.4e-126;
Matches 386; Conservative 17; Mismatches 42;
    1358 AA
                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                    Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
                                                                              01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-OCT-2003 (TrEMBLrel. 25,
PRELIMINARY;
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1253 PNGINKGGARFGLSTBADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIOF 1312
                                                                                                                                                                                                                                                                                                                                                                                    1313 TMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSFKKCVN 1372
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                                                                                                     SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET
                                                                                                                                                            1193 SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGRPGDHYAVMISKTGTNAGDFTVVFEET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 TMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 1223;
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Bacteria, Bacteroidetes; Bacteroides (class); Bacteroidales;
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J. Biol. Chem. 274:5012-5020(1999).

BMBL; AB013363; BAA34311.1; -

GO, GO:0005224; F:AFT binding; IEA.

GO; GO:000524; F:Cysteine-type peptidase activity; IEA.

GO; GO:0005310; F:DNA ligase (ATP) activity; IEA.

GO; GO:0005310; P:DNA repair; IEA.

GO; GO:0005260; P:DNA replication; IEA.

GO; GO:0005260; P:DNA replication; IEA.

GO; GO:0005508; P:Droteolysis and peptidolysis; IEA.

InterPro; IPR001769; Peptidase_C25.

InterPro; IPR001569; Peptidase_C25.

InterPro; IPR00536; Peptidase_C25.

Pfam; PF01364; Peptidase_C25.

Pfam; PF03785; Peptidase_C25.

Pfam; PF03785; Peptidase_C25.

PFAM; PF03785; Peptidase_C25.

PFAM; PF03785; Peptidase_C25.

PFAM; PF03785; Peptidase_C25.

PFAM; PF03785; Peptidase_C25.

PFAM; PF03785; Peptidase_C25.

PFAM; PF03785; Peptidase_C25.

PFAM; PF03785; PEPTIGASE_A1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
130k-HMGD (Fragment).
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85.6%; Pred. No. 2.7e-125;
ive 15; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1373 VTVNSTQFNPVKNLKAQPDGGDVVLKWEAPS 1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 450
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MEDLINE=99143166; PubMed=9988746;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 KANGKRADFTETFESSTHGEAPAEWITIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rangarajan M., Aduse-Opoku J., Slaney J.M., Young K.A., Curtis M.A., "The prpRl and the prR2 arginine-specific protease genes of Porphyromonas gingivalis W50 produce five biochemically distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96071894; PubMed=7591131;
Aduse-Opoku J., Muir J., Slaney J.M., Rangarajan M., Curtis M.A.;
Carardererization, genetic analysis, and expression of a protease antigen (PrpRI) of PorpNromonas gingivalis W50.";
Infect. Immun. 63:4744.4754(1995).
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85.6%; Pred. No. 1.2e-125;
tive 17; Mismatches 42; Indels 6,
                                                                                                                                                                                                                                                                                                                                                                                                       Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GG; GG: 0005524; F:ATP binding; IEA.
GG; GG: 0005524; F:ATP binding; IEA.
GG; GG: 0005314; F:ATP binding; IEA.
GG; GG: 0006310; F:DMA ligase (ATP) activity; IEA.
GG; GG: 0006310; F:DMA repair; IEA.
GG; GG: 0006281; P:DMA replication; IEA.
GG; GG: 0006281; P:DMA replication; IEA.
R GG; GG: 0006280; P:DMA replication; IEA.
R GG; GG: 0006508; P:DMA replication; IEA.
R InterPro; IPR000977; DNA ligase.
R InterPro; IPR00110; IG-IAR.
R InterPro; IPR001769; Peptidase C25.
R InterPro; IPR005536; Peptidase C25.
R PR031184; Peptidase C25.
R PF0311E; PS00697; DNA_LIGASE_A1; 1.
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228 719 ALPHA-PROTEASE.
720 1262 BETA-ADHESIN.
1706 AA; 185705 MW; 0E56DCD87FDA8CDD CRC64;
                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
||::| ||||:|| vrinpt@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvknlka@fileshpvk
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NCBI_TaxID=837;
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EMBL; X82680; CAA57997.1; -.
HSSP; P95493; LCVR.
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                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel.
01-MAY-1997 (TrEMBLrel.
                                                                                                                                                                                                                                                                                  01-MAY-1997 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                   Protease precursor.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; C25.001;
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Best Local Simil
Matches 386; (
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SIGNAL
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977 PNPNPG-TILSESFENGIPASWKIIDADGDGHGWKPGNAPG---IAGYNSNGCVYSESFG 1032
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                                     LEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI 179
                                                                                                                                                                                      240 SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET 299
                                                                                                                                                                                                                                                                  PNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQF 359
                                                                                                                                                                                                                                                                                                      636 PNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQF 695
                                                                                                                                                                                                                                                                                                                                                                                 696 IMGGSPIPIDYTYTVYRDGIKIKEGLIFITFBEDGVATGNHEYCVEVKYTAGVSPKKCVN 755
398 LGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASNFTNAL 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99235907; PubWed=10219167; Slakeski N., Cleal S.M., Bhogal P.S., Reynolds E.C.; "Characterization of a Porphyromonas gingivalis gene prtK that encodes a lysine-specific cysteine proteinase and three sequence-related adhesins."
                                                                                                                                                                                                                    576 SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET
                                                                                                             180 KANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF
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                                                         1 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASY-
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Bacteria, Bacteroidetes, Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
NCBI TaxiD=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doral Microbiol. Immunol. 14:92-97(1999).

R EMBL; U75366; AAB60809.1; -.

R MGD; GO:0005524; F:ATP binding; IEA.

GO; GO:0005310; F:ATP binding; IEA.

GO; GO:0006310; F:DNA ligaee (ATP) activity; IEA.

R GO; GO:0006281; F:OFF COMBINATION; IEA.

R GO; GO:0006281; F:DNA replication; IEA.

R GO; GO:0006280; P:DNA repair; IEA.

GO; GO:0006508; P:DNA replication; IEA.

R GO; GO:0006508; P:DNA replication; IEA.

R InterPro; IPR001769; Peptidase C25.

R InterPro; IPR001769; Peptidase C25.

R InterPro; IPR00536; Peptidase C25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2016.5; DB 2 Pred. No. 4.2e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                       420 VIVDPVQFNPVQNLTGSAV--GQKVTLKWDAP 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                         756 VIVNSTOFNPVONLTAEQAPNSMDAILKWNAP 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lysine-specific cysteine proteinase.
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                                                                                                                             761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The tla gene of Porphyromonas gingivalis W50: a homologue of the arginine-specific protease precursor (PrpRI) which shares sequence similarity to TonB-linked receptors.;

J. Bacteriol. 179:4778-4788 (1997).

C. -! SUBCELLULAR LOCATION: OUTER MEMBRANE (BY SIMILARITY).

EMBL; Y07618; C. CA468897.1; -..

GO; GO:0005524; F.ATP binding; IEA.

GO; GO:0005524; F.ATP binding; IEA.

GO; GO:0005210; F.DNA ligase (ATP) activity; IEA.

RO; GO:0005211; P.DNA ligase activity; IEA.

RO; GO:0005211; P.DNA recombination; IEA.

RO; GO:0006281; P.DNA repair; IEA.

RO; GO:0006281; P.DNA replication; IEA.

RO; GO:0006281; P.DNA replication; IEA.

RO; GO:0006281; P.DNA replication; IEA.

RO; GO:0006281; P.DNA replication; IEA.

RO; GO:0006281; P.DNA replication; IEA.

RO; GO:0006281; P.DNA replication; IEA.

RICEPRO; IPRO00531; TonB_boxC.
                                                                                                                       SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFBET
                                                                                                                                                            PNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQF
             KANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF
                                                                                     SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET
                                                                                                                                                                                                PNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQF
                                               642 KANGKRADFTETFESSTHGEAPAEWITIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF
                                                                                                                                                                                                                                        TMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVN
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MEDLINE=97386416; PubMed=9244265;
Aduse-Opoku J., Slaney J.M., Young K.A., Muir J., Rangarajan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.5%; Score 2016.5; DB 2; Length 1097;
85.0%; Pred. No. 2.3e-124;
iive 18; Mismatches 41; Indels 9;
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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PROSITE; PS00697; DNA_LIGASE_A1; 1.
Membrane; Outer membrane; Receptor; Signal; TonB box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 02, Created)
(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                 420 VIVDPVQFNPVQNLTGSAV--GQKVTLKWDAP 449
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1331 TMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKKCVD 1390
                                                                        60 INFEGPONPONYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANAL 119
                                                                                                                                              LEEVLTAKTVVTAPBAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI 179
                                                                                                                                                                                                                                                                                                                                                                                                                             IMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVN 419
       PNPNPGTITLSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSALCASSASY- 59
                                                                                                                                                                                                                                                                                                                   1211 SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFBET
                                                                                                                                                                                                                 KANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF
                                                                                                                                                                                                                                                                                    SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET
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                                                                                                                                                                                                                                                                                                                                                                                        1271 PNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lewis J.P., Macrina F.L.; "18195, an insertion sequence-like element associated with protease
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01-UUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Lysine specific cysteine protease protess.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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G0; G0:000524; F:DNA ligase (ATP) activity; IEA.

G0; G0:0005281; P:DNA repair; IEA.

G0; G0:0006281; P:DNA replication; IEA.

R G0; G0:0006281; P:DNA replication; IEA.

R G0; G0:0006508; P:DNA replication; IEA.

R InterPro; IPR00177; DNA ligase.

R InterPro; IPR001769; Peptidase. C25.

InterPro; IPR001769; Peptidase. C25.

R Pfam; PF03186; Peptidase. C25. I.

R Pfam; PF03186; Peptidase. C25. I.

R Pfam; PF03186; Peptidase. C25. I.

R Pfam; PF03186; Peptidase. C25. I.

R Pfam; PF03186; Peptidase. C25. I.
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Infect. Immun. 66:3035-3042(1998).
EMBL; AF017059; AAC26523.1; -.
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PROSITE; PS00697; DNA_LIGASE_A1; 1
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MEDLINE=98298016; PubMed=9632563;
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 INFEGPONPONYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANAL 119
                                                                                       151 KANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLDWLTAHGGSNVVSSF
                                                                   LEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI
                                                                                                                                      KANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF
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82.3%; Score 2011.5; DB 2; Length 1732;
Best Local Similarity 84.7%; Pred. No. 9e-124;
Matches 383; Conservative 19; Mismatches 41; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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**REROPS; C25.002; -...

GO; GO:0008234; F:ATP binding; IEA,

GO; GO:0008234; F:Cysteine-type peptidase activity; IEA.

GO; GO:0008239; F:DNA ligase (ATP) activity; IEA.

GO; GO:0006281; P:DNA recombination; IEA.

GO; GO:0006281; P:DNA replication; IEA.

R GO; GO:0006281; P:DNA replication; IEA.

R GO; GO:0006281; P:DNA replication; IEA.

R InterPro; IPR00097; DNA ligase.

R InterPro; IPR00097; DNA ligase.

R InterPro; IPR005536; Peptidase C25.

R Pfam; PF03785; Peptidase C25.

R Pfam; PF03785; Deptidase C25.

R Pfam; PF03785; Deptidase C25.

R Pfam; PF03785; DNA LIGASE A1; I.

**R Pfam; PF03785; DNA LIGASE A1; I.

**SEQUENCE 1732 AA; I8785 MW; 654271DBEF7BCAE4 CRC64;
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Last annotation update)
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SEQUENCE FROM N.A.
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                                                                                                                 LEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYYAFRHFGCTDFFWINLDDVEI
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                               1 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAICASSASY-
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               Gaps
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Hocking D., Webb E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ross B.C., Czajkowski L., Hocking D., Margetts M., Webb E., Rothel Patterson M., Agius C., Camuglia S., Reynolds E., Barr I.G., "Identification of vaccine candidates from genomic analysis of
               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.0%; Score 683; DB 2; Length 925; 30.2%; Pred. No. 1.3e-36;
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "P. gingivalis polypeptides and nucleic acids.",
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Porphyromonas gingivalis.", Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AY007522; AGG24228.1; -InterPro; IPR003961; FN III. SWART; SM00060; FN3; 1. SEQUENCE 925 AA; 103632 MW; 5FF2198D6914DAE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative outer membrane protein PG57.
              43;
  ; Pred. No. 7.5e-123; 19; Mismatches 43;
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84.38;
Similarity 84.3
81; Conservative
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SEQUENCE FROM N.A.
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Best Local Similarity
Matches 176; Conserv
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10 LSESFENG-IPASWKTIDADGDGNNWTTTPPPGG-----TSFAGHNSAICASSASYINF

Mismatches 132; Indels 212;

62;

Conservative

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EGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALLEE 122
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421 TMTAKPT------GAWYERTINLPEGTKYIAWRHYNCTDIYFLKLDDITVFGT 467
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ANGA----WYERTITLFAGTKYIAWRHYDCTDMFFLLLDDITVYRSTETVPEPVTDFVV 745
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                                                                                                               364 IGPVTPDNYLITPKVE--GAKRVKYWVSTQDANWAAEHYAVMASTTGTAVGDFV-ILFEE
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Bacteria, Bacteroidetes, Bacteroides (class), Bacteroidales,
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32.8%; Pred. No. 3.2e-29;
Live 23; Mismatches 73
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01-OCT-2000 (TrEMBLrel. 15, Last sequence
01-OCT-2002 (TrEMBLrel. 22, Last annotati
Hypothetical outer membrane protein PG27
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Matches 136; Conservative
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Ross B., "Barr I., Patterson M., Agius C., Rothel L., Margetts M., Hocking D., Webb E.; "Polyneptides and nucleic acids."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. SEQUENCE 293 AA; 32272 MW; CC03EAC241F7F6F1 CRC64;
                            Q9XBU9;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Immunoraeactive 32 kDa antigen PG25.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                   293 AA.
                   PRT;
                                                                                                                                Porphyromonadaceae; Porphyromonas.
                PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN=W50;
                Q9XBU9
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2; Gaps Ouery Match
9.5%; Score 233; DB 2; Length 293;
Best Local Similarity 59.0%; Pred. No. 1.3e-07;
Matches 46; Conservative 7; Mismatches 23; Indels

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370 YIYTVYRDGIKIKEGLIETIFEEDGVAIGNHEYCVEVKYIAGVSPKECVNVTVDPVQFNP 429 77 YIYIVYRDGVKIASGLIEPTFLDEDVPAGEHTYCVEVQYQGGVSDKVCVDVEVK--DFKP

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430 VONLTGSAVGOKVTLKWD 447  Search completed: May 18, 2004, 11:46:36 Job time : 34.8982 secs

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Tue May 18 14:34:48 2004
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Sequence 29, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 27, Appl Sequence 11, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 14, Appl Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 
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Sequence 14, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 1, Appl
Sequence 29, Appl
Sequence 6, Appl
Sequence 6, Appl
                                                                                                                                                                   May 18, 2004, 11:38:40 ; Search time 13.9034 Seconds (without alignments) 1670.936 Million cell updates/sec
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Sequence 9, A
Sequence 4, A
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Sequence 3,
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5: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
GenCore version 5.1.6
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US-08-370-311-22
US-08-370-311-10
US-08-350-36-310-10
US-08-370-311-27
US-08-370-311-27
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Matches 450; Conservative
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Best Local Similarity
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Patent No. 5824791
GENERAL INPORMATION:
APPLICANT: Progulske-Fox, Ann
APPLICANT: Lepine, Guylaine
APPLICANT: Lepine, Guylaine
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Batti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                          100.0%; Score 2443; DB 2; Length 450; 100.0%; Pred. No. 3.1e-203; ative 0; Mismatches 0; Indels 0
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ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
FILING DATE:
CLASSIFICATION: 424
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STREET: 2421 N.W. 41st Street, Suite A-1
LENGTH: 450 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-570-311-16
                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 450; Conservative
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US-08-570-311-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 2443; DB 2; 100.0%; Pred. No. 4.5e-202;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8800
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 25.28 amino acids
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Patent No. 5824791
GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
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367 MGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVNV 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPFGGTSFAGHNSALCASSASYI
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COMPUTER: Floppy disk

COMPUTER: IBM PC Compatible

OPREATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CARRENT APPLICATION DATA:

FILLING DATE:

US/08/570,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2436; DB 2;
Pred. No. 1.3e-202;
0; Mismatches 1;
                                                                                                                                                427 TVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Ted W. Whitlock
2421 N.W. 41st Street, Suite A-1
                                                                                                                    421 TVDPVQFNPVQNLTGSAVGQKVTLKWDAPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                         Sequence 20, Application US/08570311
Patent No. 5824791
                                                                                                                                                                                                                                                                                                                                    Progulske-Fox, Ann
Tumwasorn, Somying
Lepine, Guylaine
Han, Naiming
Lantz, Marilyn
Patti, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.7%;
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 456 amino acids amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE: protein US-08-570-311-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Wh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gainesville
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Proguls
APPLICANT: Lepine,
APPLICANT: Han, Na
APPLICANT: Han, Na
APPLICANT: Hants,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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CITY: G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 BEVLTAKTVVTAPBAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVBIK 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 WNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETP 300
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TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASYI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 1.3e-202;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                             NUMBER OF SEQUENCES: 29 CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.78;
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Best Local Similarity 99.8
Matches 449; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-570-311-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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APPLICANT: Travis, James
APPLICANT: Travis, James
APPLICANT: Inamura, Takahisa
APPLICANT: Decemba, Jan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION
FILE REFERENCE: 235.00160101
CURRENT APPLICATION NUMBER: US/09/482,500A
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 60/115,869
PRIOR FILING DATE: 1999-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 BEVLTAKTVVTAPBEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVBIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                     61 NFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 EEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDEVEIK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 WNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 ANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 MGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKVCVNV
                                                                                                                                                                                                                                                                                                                                                                              7 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTFPPPGGTSFAGHNSAICVSSASYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 ANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 WNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETP
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                                                                                                                                                                                                                                                                                                                                                    1 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASYI
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                   95.0%; Score 2321; DB 2; 98.4%; Pred. No. 1.1e-192; live 3; Mismatches 4;
                         UF15.C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/09482500A
; Patent No. 6627193
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-482-500A-1
REGISTRATION NUMBER: 36,965
REFRENCE/DOCKER NUMBER: UF15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 1477
                                                                                                                                           LENGTH: 439 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 TINPTOFNPVONL 439
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Best Local Similarity 98.43
Matches 426; Conservative
                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                            US-08-570-311-22
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                                            67 NFEGPONDDNYLVTPELSLPNGGTLTF#VCAQDANYASEHYAVYASSTGNDASNFANALL 126
                                                                                                                     NGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFT 360
                                                                                                                                                                                                                                                                                                                                                                                                                           361 MGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVNV 420
                                                                                                                                                                                                             187 ANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTNVVASFS 246
                                                                                                                                                                                                                                                            WNGWALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETP 300
                                                                                                                                                                                                                                                                                                 247 WNGMALNPDNYLISKDVTGATKVKXYXAVNDGFPGDHYAVMISKTGTNAGDFTVVFEBTP 306
                                                                                                                                                                                                                                                                                                                                                                                307 NGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 MGGSPIPIDYIYIVYRDGIKIKEGLIFITFEEDGVATGNHEYCVEVKYTAGVSPKECVNV 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/08570311
Patent No. 5824791
GENERAL INFORMATION:
APPLICANT: Progulate-Fox, Ann
APPLICANT: Lepine, Guylaine
APPLICANT: Hann, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: 29
                                                                                              EEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 25-JAN-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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DB 4; Length 1477; 84.4%; Score 2063; Query Match

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1056 LEETITAKG-VRSPEAIRG-RIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVEI 1113
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Patent No. 6017532
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
TITLE OF INVENTION: Porphyromonas gingivalis
TITLE OF INVENTION: Arginine-specific Proteinase Coding Sequences
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 84.4%; Score 2063; DB 2; Best Local Similarity 86.3%; Pred. No. 1.8e-169; Matches 389; Conservative 17; Mismatches 39;
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CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
TELEFRAN: (904) 375-8100
TELEFRAN: (904) 375-8100
TELEFRAN: (904) 372-5900
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1687 amino acids
                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08-570-311-29
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Best Local Similarity
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                                                                                               60 INFEGPONPDNYLVTPELSLPNGGTLTFWYCAQDANYASEHYAVYASSTGNDASNFANAL 119
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                                                                                                                                                                                                                                                            963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Progulske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Lepine, Guylaine
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Latti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                          KANGKRADFTETFESSTHGEAPAEWTTIDADGDGGWLCLSSGQLDWLTAHGGTNVVASF
                                                                1 PNPNPGTITLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASY-
                               Gaps
                               9
                            39; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
  86.3%; Pred. No. 1.5e-169;
tive 17; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 VIVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSEE: Ted W. Whitlock
[: 2421 N.W. 41st Street, Suite A-1
Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JMBER: US 07/647,119
25-JAN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                      Matches 389; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 25-JAN-10
Best Local Similarity
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TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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TELEFAX: (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 IMGGSPIPIDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVN 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 KANGKRADFIETFESSTHGEAPAEWITIDADGDGQGWLCLSSGQLDWLTAHGGINVVASF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.4%; Score 2063; DB 3; Length 1704; 86.3%; Pred. No. 1.9e-169; Live 17; Mismatches 39; Indels 6.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
RILING DATE: 08-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1371 VTINPTOFNPVKNLKAQPDGGDVVLKWEAPS 1401
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                                                                                                                                          PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/119,361
FILING DATE: 10-55E-1993
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/265,441
FILING DATE: 24-070-1994
ATTORNEY AGENT INFORMATION:
NAME: Ferber, Donna M.
                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 31,878
REFERENCE/DOCKET NUMBER: 21-97
TELECHOMINICATION INFORMATION:
TELEPHONE: (303) 499-8080
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 86.3%
Matches 389; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 1704 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-336-308A-10
                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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RESULT 9 US-08-822-324-6 'Sequence 6, Application US/08822324 'Partent No. 6129917

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GENERAL INFORMATION:

APPLICANT: Potempa, Jan S.

APPLICANT: Travis, James

APPLICANT: Travis, James

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS COMPRISING

TITLE OF INVENTION: METHODS

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

STREET: S370 Manhattan Circle, Suite 201

CITY: Boulder

COMPANIENCE ADDRESS:

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86.3%; Pred. No. 1.9e-169;
iive 17; Mismatches 39;
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REGISTRATION NUMBER: 33,878
REGISTRATION NUMBER: 103-95 WO
TELECOMMUNICATION:
TELEPHONE: (303) 488-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,945
FILING DATE: 22-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/822,324 FILING DATE: 21-MAR-1997 CLASSIFICATION: 536
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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1311 TMGGSPTPTDYTYTVYRDGTKIKBGLTETTFEBDGVATGNHEYCVEVKYTAGVSPKECVN 1370
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APPLICANT: Bapgal, Peter S.
APPLICANT: Slakeski, Nada
IITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
FILE REPERBNES: Reynolds
CURRENT APPLICATION UNMBER: US/09/066,330A
CURRENT FILING DATE: 1998-09-15
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85.8%; Pred. No. 2e-168;
ive 18; Mismatches 40; Indels 6
                                                                                                                                                                                                                                                                                                                                                           1371 VTINPTÕFNPVKALKAQPDGGDVVLKWEAPS 1401
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EARLIER FILING DATE: 1995-10-30
EARLIER FILING DATE: 1996-10-30
EARLIER FILING DATE: 1996-10-30
SUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/09066330A Patent No. 6511666 GENERAL INFORMATION:
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US-09-066-330-10
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                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
TITLE OF INVENTION: Porphyromonas gingivalis
TITLE OF INVENTION: Arginine-specific Proteinase Coding Sequences
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 2063; DB 3;
; Pred. No. 1.9e-169;
17; Mismatches 39;
                                               ||::|||||:||
1371 VTINPTQFNPVKNLKAQPDGGDVVLKWEAPS 1401
                420 VTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 450
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/265,441
FILING DATE: 24-UN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,931
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REGISTRATION NUMBER: 33,878
REFERENCE DOCKET NUMBER: 21-93C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/336,308
                                                                                                                                                                       ; Sequence 10, Application US/09490931; Patent No. 6274718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPRONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
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86.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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Best Local Similarity 86.3%
Matches 389; Conservative
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LENGTH: 1704 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                             RESULT 10
US-09-490-931-10
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574 SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET 633
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                                                                                                                                                                                                                                                                                                                                        634 PNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLDYILLDDIQF 693
                                                                                                                                                                                                                                                                                                                                                                                        360 TMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVN 419
                                                                                                                                                                                                                                                                                                                                                                                                                 LEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
396 LGGIGVLTPDNYLITPALDLANGGKLTFWVCAQDANYASEHYAVYASSTGNDASNFTNAL 455
                                                                                                                                                           LEETITAKG-VRSPEAIRG-RIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLDEVET
                                                                                                                             180 KANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF
                                                                                                                                                                                                                 SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
BLING DATE: 09-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   754 VTINPTOFNPVKNLKAQPDGGDVVLKWEAPS 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420 VIVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 418t Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-7AN-1991
CLASSIFICATION: 424
PRIOR APPLICATION ATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-353-485-8; Sequence 8, Application US/08353485; Patent No. 5830710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumwasorn, Somying
Lepine, Guylaine
Han, Naiming
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TELEPAX: (904) 372-8800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Whitlock, Ted W. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Progul
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ZIP: 32606
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1313 TMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKKCVN 1372
                                                                                                                                                                                                                                                                                      APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 2e-167;
18; Mismatches 4.
                                                                                           1373 VIVNSTÓFNPVKNLKAQPDGGDVVLKWEAPS 1403
                                                  VIVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 450
                                                                                                                                                                                                                                                                                                                                                                                                                                               AUDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 09-DEC-1994
CLASSIPICATION: 424
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-DAN-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA.
APPLICATION UNMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DALE.
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
APPLICATION NUMBER: 09-DEC-1994
                                                                                                                                                                                                 Sequence 8, Application US/08570311
Patent No. 5824791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                      Progulske-Fox, Ann
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 85.4%
Matches 385; Conservative
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MOLECULE TYPE: protein
US-08-570-311-8
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APPLICANT: Progul
APPLICANT: Tumwas
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1025 VIINPIQENPVKNLKAQPDGGDVVLKWEAPS 1055
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                            PRIOR AFFLICATION DATA:

PRELING DATE: 09-DEC-1994
CLASSIFRCATION: 144
PRIOR APPLICATION: 02-DEC-1994
PRIOR APPLICATION: 02-DA-1991
CLIASSIFRCATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLIASSIFRCATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
FREISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UP15.C3
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION IN
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APPLICANT: Progulake-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Lantz, Marilyn
APPLICANT: Datz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
                                                                                                                                                                                                                                                                                                60 INFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANAL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                      455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 LEEVLTAKTVVTAPBAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQF 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               574 SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEBT 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TWGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVN 419
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                                                                                                                                                                                                                                                                    1 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPFGGTSFAGHNSAICASSASY-
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                       . 9
                                                                                                                                                               Length 1087;
                                                                                                                                                                                                                       42; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                          83.3%; Score 2036; DB 2;
85.4%; Pred. No. 2e-167;
Live 18; Mismatches 42;
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APPLICATION NUMBER: US/08/570,311
FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-570-311-27
; Sequence 27, Application US/08570311
Patent No. 5824791
; GENERAL INFORMATION:
1087 amino acids
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                                                                                                                                                                             Best Local Similarity 85.4%
Matches 385; Conservative
                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                         amino acid
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                                            ; TOPOLOGY:
; MOLECULE TYI
US-08-353-485-8
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965 TMGGSPTPTDYTYTVXRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSFKVCVN 1024
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                                                                                                                                                                                                                                                             LEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI 179
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                                                                                                                1 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAICASSASY-
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Patent No. 6511666
GENERAL INFORMATION:
APPLICANT: Brogal, Peter S.
APPLICANT: Brogal, Peter S.
TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
FILE REFERENCE: Reynolds
                                                                9
        Length 1358;
                                                                42; Indels
83.3%; Score 2036; DB 2;
85.4%; Pred. No. 2.9e-167;
ive 18; Mismatches 42;
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1331 TMGGSPTPIDYTYTVYRDGTKIKEGLIBTITFEEDGVATGNHEYCVEVKYTAGVSPKKCVN 1390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360 TMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVN 419
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82.5%; Score 2016.5; DB 4; Length 1732;
Best Local Similarity 85.0%; Pred. No. 2e-165;
Matches 384; Conservative 18; Mismatches 41; Indels 9;
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|391 VTVNSTQFNPVQNLTAEQAPNSMDAILKWNAP 1422
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CURRENT APPLICATION NUMBER: US/09/066,330A;
CURRENT FILING DATE: 1998-09-15
EARLIER APPLICATION NUMBER: PN 6275
FARLIER FILING DATE: 1995-10-30
FARLIER APPLICATION NUMBER: PCT/AU96/00673
FARLIER FILING DATE: 1996-10-30
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 11
                                                                                                                                                                              TYPE: PRT;
CRGANISM: Porphyromonas gingivalis
US-09-066-330-11
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Search completed: May 18, 2004, 11:49:13 Job time : 14.9034 secs

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May 18, 2004, 11:42:50 ; Search time 34.8564 Seconds (without alignments) 3592.387 Million cell updates/sec
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2443
1. PNPNPGTTTLSESFENGIPA......QNLTGSAVGQKVTLKWDAPN 450
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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13 - 6/ptcodata/1/pubpaa/USO9E_PUBCOMB.pep:*
14 - 6/ptcodata/1/pubpaa/USO9E_PUBCOMB.pep:*
15 - 6/ptcodata/1/pubpaa/USO9E_PUBCOMB.pep:*
15 - 6/ptcodata/1/pubpaa/USO9E_PUBCOMB.pep:*
16 - 6/ptcodata/1/pubpaa/USO9E_PUBCOMB.pep:*
17 - 6/ptcodata/1/pubpaa/USO9E_PUBCOMB.pep:*
18 - 6/ptcodata/1/pubpaa/USO9E_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|                               |                  |                 |                |                |                |                |                 |                 |                  |                 |                 | _                   |                 |                  | _                 |  |
|-------------------------------|------------------|-----------------|----------------|----------------|----------------|----------------|-----------------|-----------------|------------------|-----------------|-----------------|---------------------|-----------------|------------------|-------------------|--|
| !<br>!<br>!                   | App]             | Appl            | \ppli          | Appli          | appli          | Appli          | Appl            | Appl            | Appl             | 24, Appl        | Appl            | 57, A               | Appl            | Appl             | , App             |  |
| i                             | 10,              | 11,             | 3, 4           | 5,             | 6,7            | 4,             | 18,             | 21,             | 23,              | 24,             | 26,             | 554                 | 17,             | 25,              | 101               |  |
| Description                   | Sequence         | Sequence        | Sequence       | Sequence       | Sequence       | Sequence       | Sequence        | Sequence        | Sequence         | Sequence        | Sequence        | Sequence            | Sequence        | Sequence         | Seguence          |  |
|                               | US-10-229-066-10 | 1-10-229-066-11 | 1-10-174-695-3 | 3-10-174-695-5 | 3-10-174-695-6 | 3-10-174-695-4 | 3-10-387-977-18 | 3-10-387-977-21 | US-10-387-977-23 | 3-10-387-977-24 | 3-10-387-977-26 | 3-10-282-122A-55467 | 3-10-387-977-17 | JS-10-387-977-25 | JS-10-387-977-101 |  |
| QI .                          | SD               | US              | SD             | S              | ä              | S              | ä               | US              | ä                | ä               | B               | ğ                   | ğ               | ğ                | ğ                 |  |
| DB                            | 14               | 14              | 15             | 15             | 15             | 15             | 15              | 15              | 15               | 7.5             | 15              | 12                  | 15              | 15               | 15                |  |
| %<br>Query<br>Match Length DB | 1706             | 1732            | 419            | 419            | 231            | 196            | 29              | 29              | 29               | 29              | 29              | 872                 | 29              | 29               | 509               |  |
| %<br>Query<br>Match           | 84.0             | 82.5            | 28.7           | 27.9           | 15.8           | 8.5            | 6.3             | 6.3             | 6.3              | 6.3             | 6.3             | 6.1                 | 0.9             | 5.9              | 5.9               |  |
| Score                         | 2051             | 2016.5          | 700            | 680.5          | 385            | 206.5          | 153             | 153             | 153              | 153             | 153             | 148                 | 147             | 145              | 144               |  |
| Result<br>No.                 | 1                | 7               | æ              | 4              | S              | 9              | 7               | 80              | σ                | 10              | 11              | 12                  | 13              | 14               | 15                |  |

| Sequence 20, Appli<br>Sequence 4, Appli<br>Sequence 3, Appli<br>Sequence 3, Appli<br>Sequence 10, Appli<br>Sequence 11, Appli<br>Sequence 11, Appli<br>Sequence 12, Appli<br>Sequence 13, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 6, Appli<br>Sequence 14, Appl<br>Sequence 82, Appl<br>Sequence 84, Appl<br>Sequence 14592, A<br>Sequence 14592, A<br>Sequence 14592, A<br>Sequence 14592, A<br>Sequence 14592, A<br>Sequence 34, Appl<br>Sequence 34, Appl<br>Sequence 14592, A<br>Sequence 34, Appl<br>Sequence 34, Appl<br>Sequence 34, Appl<br>Sequence 34, Appl<br>Sequence 34, Appl<br>Sequence 34, Appl |                                        |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------|
| US-10-387-977-20<br>US-10-175-282-4<br>US-10-175-282-4<br>US-10-175-282-3<br>US-10-1387-977-77<br>US-10-387-977-11<br>US-10-387-977-11<br>US-10-387-977-11<br>US-10-387-977-13<br>US-10-387-977-13<br>US-10-282-122A-6335<br>US-10-282-122A-6335<br>US-10-282-122A-6335<br>US-10-282-122A-6335<br>US-10-387-977-81<br>US-10-387-977-81<br>US-10-387-977-81<br>US-10-387-977-82<br>US-10-387-977-84<br>US-10-387-977-84<br>US-10-387-977-84<br>US-10-387-977-84<br>US-10-387-977-84<br>US-10-387-977-84<br>US-10-387-977-84<br>US-10-387-977-84<br>US-10-387-977-84<br>US-10-387-977-84<br>US-10-387-977-84<br>US-10-387-977-84<br>US-10-387-977-84<br>US-10-387-977-84<br>US-10-387-977-84                                                                        | .0-387-977<br>.0-387-977<br>.0-206-576 |
| 2 4 4 4 4 5 5 5 5 5 6 6 6 7 4 4 4 5 5 5 5 6 6 7 4 7 5 5 6 7 6 7 6 7 7 7 7 7 7 7 7 7 7 7 7                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 1221                                   |
| 29<br>19933<br>19933<br>1992<br>25<br>27<br>2122<br>2468<br>2434<br>2434<br>25<br>25<br>26<br>26<br>1095<br>1095<br>1095<br>1095<br>1095                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 491<br>1638<br>1638                    |
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| RESULT 1  US-10-229-066-10  IS equence 10. Application US/10229066  Publication No. US20030157637A1  GENERAL INFORMATION: APPLICANT: Reynolds, Eric C. APPLICANT: Blogal, Peter S. APPLICANT: Blogal, Peter S. APPLICANT: Blogal, Poter S. APPLICANT: Blogal, Poter S. APPLICANT: Blogal, Poter S. APPLICANT: Blogal, Poter S. APPLICANTON UNBER: US/10/229,066 CURRENT FILING DATE: 2002-08-28 FILE REFERENCE: REPLICATION NUBER: US/09/066,330 PRIOR FILING DATE: 1998-09-15 PRIOR FILING DATE: 1998-09-15 PRIOR FILING DATE: 1996-10-30 PRIOR FILING DATE: 1996-10-30 PRIOR PELICATION NUMBER: POT/AU96/00673 PRIOR APPLICATION NUMBER: POT/AU96/00673 PRIOR PELING DATE: 1996-10-30 NUMBER OF SEQ ID NOS: 15 SOFTWARE: PATENTIN Ver. 2.0 SEQ ID NO 10 LENGTH: 1706 TYPE: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: PRI VER: P | Query Match  84.0%; Score 2051; DB 14; Length 1706; Best Local Similarity 85.8%; Pred. No. 9.8e-176; Matches 387; Conservative 18; Mismatches 40; Indels 6; Gaps | 1 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASY | 60 INFEGPONFDNYIVTPELSLPNGGTLTFWVCAQDAYASEHAVYASSTGNUASNFANAL<br> |
| US. US. US. US. US. US. US. US. US. US.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                                                                                  | S A                                                           | A 48                                                              |

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1211 SWNGWAINPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET 1270
                                                              120 LEBVITAKTVVTAPBAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVBI
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                                                                                                                 TWGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVN
                                         PNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDINYILLDDIQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 28.7%; Score 700; DB 15; Length 419; Best Local Similarity 74.7%; Pred. No. 1.8e-54; Matches 139; Conservative 11; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Slakeski, Nada

APPLICANT: Chen, Chao Guang

APPLICANT: Chen, Chao Guang

TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION

FILE REFERENCE: 529282000700

CURRENT APPLICATION NUMBER: US/10/174,695

CURRENT FILING DATE: 2002-06-18

PRIOR APPLICATION NUMBER: PCT/AU00/01588

PRIOR APPLICATION NUMBER: AU PQ 4859

PRIOR FILING DATE: 1999-12-24

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PASELSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/10174695;
Publication No. US20030232022A1
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric Charles
APPLICANT: Chen, Chao Guang
APPLICANT: Barr, Ian George
TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REFERENCE: 5.29282000700
CURRENT APPLICATION NUMBER: US/10/174,695
                                                                                                                                                                                                                                 1391 VTVNSTOFNPVONLTAEQAPNSMDAILKWNAP 1422
                                                                                                                                                                                            VIVDPVOFNPVQNLTGSAV--GOKVTLKWDAP 449
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                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/10174695 Publication No. US20030232022A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                         LEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI 179
                                                                                                                                                                                        60 INFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANAL 119
                                                1132
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           LEBVLTAKTVVTAPBAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVBI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/10229066

Sequence 11, Application US/10229066

Publication No. US20030157637A1

GENERAL INFORMATION:

APPLICANT: Reynolds, Eric C.

APPLICANT: Blogal. Peter S.

APPLICANT: Blogal. Peter S.

TITLE OF INVENITON: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE

TITLE OF INVENITON: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE

CURRENT APPLICATION NUMBER: US/10/229,066

CURRENT FILING DATE: 1990-18

PRIOR FILING DATE: 1990-15

PRIOR FILING DATE: 1995-10-30

PRIOR PELING DATE: 1995-10-30

PRIOR PELING DATE: 1995-10-30

PRIOR PELING DATE: 1996-10-30

PRIOR PELING DATE: 1996-10-30

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PATENTIN UNIVER: PATENTING DATE: 1996-10-30

NUMBER OF SEQ ID NOS: 15
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                                                                                                             KANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASF
                                                                                                                                                                SWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEET
                                                                                                                                                                                                                                       PNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQF
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85.0%; Pred. No. 1.3e-172;
iive 18; Mismatches 41; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                             |||: ||||||||| VIVISTQFNDVKNLKAQPDGGDVVLKWEAPS 1403
                                                                                                                                                                                                                                                                                                                                                                                          VTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 450
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Best Local Similarity
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WESULO. 187-977-18
; Sequence 18, Application US/10387977
; Sequence 18, Application US/10387977
; Publication No. US2004000527641
; Publication No. US2004000527641
; Publication No. US2004000527641
; APPLICANT: Reymolds, Eric Charles
; APPLICANT: O'Brien-Simpsen, Neil Martin
; APPLICANT: Slakeski, Nada
; TITLE OF INVENTION: DYAGNOSIS AND TREATMENT OF PERIODONITITS ASSOCIATED WITH
; TITLE OF INVENTION: DYAGNOSIS AND TREATMENT OF PERIODONITITS ASSOCIATED WITH
; TITLE OF INVENTION: DYAGNOSIS AND TREATMENT OF PERIODONITITS ASSOCIATED WITH
; TITLE OF INVENTION: SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SOURCES SO
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                                                                                                                                                              142 EGLTATTFEEDGVAAGNHEXCVEVKYTAGVSFKVCKDVTVEGSNEFAPVQNLTGSSVGQK 201
                                        ----DSPASYTYTVYRDGTKIK 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Revolutions, Eric Charles
APPLICANT: Slakeski, Nada
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REPERENCE: 529282000700
CURRENT APPLICATION NUMBER: US/10/174,695
CURRENT FILING DATE: 2002-06-18
PRIOR PLILING DATE: 2000-12-21
PRIOR FILING DATE: 1999-12-24
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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8.5%; Score 206.5; DB 11
Best Local Similarity 37.5%; Pred. No. 2.4e-10;
Matches 57; Conservative 13; Mismatches 63
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                                        92 RYDDFTFE--AGKKYTFTMRRAGMGDGTDMEVED--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-174-695-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10174695 Publication No. US20030232022A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        202 VTLKWDAPN 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 IGGIĞVLTPDNYLITPALDIPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASNFINAL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 LEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 PNPNPG-TILSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYSESFG 295
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27.9%; Score 680.5; DB 15; Length 419;
Best Local Similarity 73.7%; Pred. No. 1e-52;
Matches 137; Conservative 12; Mismatches 30; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 231;
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Publication No. US2003023202A1
GENERAL INFORMATION:
APPLICANT: Reprodus, Eric Charles
APPLICANT: Chen, Cheo Guang
APPLICANT: Chen, Cheo Guang
APPLICANT: Chen, Cheo Guang
APPLICANT: Barr, Ind George
TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
CURRENT APPLICATION NUMBER: US/10/174,695
CURRENT FILING DATE: 2002-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 15.8%; Score 385; DB 15; Best Local Similarity 41.4%; Pred. No. 2.2e-26; Matches 103; Conservative 31; Mismatches 69;
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: PCT/AU00/01589
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: AU PQ 4859
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 419
TYPE: PRI
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PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: AU PQ 4859
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 231
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US-10-174-695-5
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PRIOR FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 29
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                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                     TYPE: PRT
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| Publication No. US20040005276A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Reynolds, Eric Charles
| APPLICANT: Slakeski, Nada
| APPLICANT: Slakeski, Nada
| TITLE OF INVENTION: DIAGNOSIS AND TREATHENT OF PERIODONTITIS ASSOCIATED WITH
| TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
| TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
| TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
| TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
| TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
| FILE REFERENCE: 52922000301
| CURRENT APPLICATION NUMBER: US/10/387,977
| CURRENT PILING DATE: 2000-03-22
| PRIOR FILING DATE: 2000-03-22
| PRIOR FILING DATE: 1998-04-30
| PRIOR APPLICATION NUMBER: AU PO 6528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Eric Charles
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
FILE REPRENCE: 5.29282000301
CURRENT APPLICATION NUMBER: US /10/387,977
CURRENT FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: BCT/AU98/00311
PRIOR APPLICATION NUMBER: AU PO 6528
PRIOR FILING DATE: 1994-04-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE FEALSEQ FOF Windows Version 4.0
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100.0%; Pred. No. 1e-06;
cive 0; Mismatches 0; Indels
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        NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
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                                                                                                                  TYPE: PRT
ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 21, Application US/10387977; Publication No. US20040005276A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 29; Conservative
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JAPELICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Neil Martin
APPLICANT: Slakeski, Nada
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: POREPHYROMONAS GINGIVALIS
TITLE OF INVENTION: POREPHYROMONAS GINGIVALIS
TITLE OF INVENTION: POREPHYROMONAS GINGIVALIS
TITLE OF INVENTION NUMBER: US 09/423,056
PRIOR APPLICATION NUMBER: US 09/423,056
PRIOR PELING DATE: 1098-0311
PRIOR PILING DATE: 1998-04-30
PRIOR PILING DATE: 1997-04-30
PRIOR FILING DATE: 1997-04-30
PRIOR FILING DATE: 1997-04-30
PRIOR FILING DATE: 1997-04-30
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APPLICANT: Reyrolds, Eric Charles
APPLICANT: Reyrolds, Eric Charles
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: PORPHYROWONAS GINGIVALIS
FILE REFERENCE: 529220000301
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CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 09/423,056
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: PCT/AU98/00311
PRIOR FILING DATE: 1998-04-30
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; ORGANISM: Porphyromonas gingivalis US-10-387-977-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-387-977-24
; Sequence 24, Application US/10387977
; Publication No. US20040005276A1
; GENERAL INFORMATION:
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Sequence 17, Application US/10387977
; Sequence 17, Application US/10387977
; Publication No. US20040005276A1
; Publication No. US20040005276A1
; Publication No. US20040005276A1
; Publication No. US20040005276A1
; APPLICANT: Slakeski Nada
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONITIIS ASSOCIATED WITH
; TITLE OF INVENTION: DORPHYROWONAS GINGIVALIS
; FILE REFERENCE: 529282000301
; CURRENT PILING DATE: 2003-07-18
; PRIOR PELLICATION NUMBER: US 09/423.056
; PRIOR PELLICATION NUMBER: PCT/AU98/00311
; PRIOR PELLING DATE: 1999-04-30
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
                                          293 NTGTGTHNVTVDTGLPS--VAFNAISDDNVLNAVEKGODLSVSGTSANLAEGTVVTVTLN 350
                                                                                                                                                                 351 G----KNYAATTAAD----GTWSLTVPAADLAGLGDHYTLSATATNGVGNSVSNTANLLV 402
                                                                                                                                                                                                                                                      121 EEVLTAKT------VVTAPEAIRGTRVQGTWYQKTVQLPAG---TKYVAFRHFGCT-- 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 ----YTYTVYRDG----TKIKEG----LIETTFEEDGVATGNHEYCVEVKYT 409
                                                                                                                                                                                                                                                                                                              403 DTALPTVTINTVAGDNVINAAEVAAGQTISG----KVANAEAGNTVTVTIGGNSYTATVQ 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 AVMISKTGT------NAGDFTVVFEETPNGINKGGARFGLSTEADGAKPOSVW 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           554 AASVLADGTWSAAIPAADVGALAAGTVTV----TAAGQSAAG-------NPVTIS 597
4 NPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASYINFE 63
                                                                                                                                                                                                                                                                                                                                                                                                                           598 HDVTVDLSA----VAI----SIDAIATDDVINAAEKGADLVLSGSTSNVEENQTVTIT
                                                                                                                             64 GPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASST---GNDASNFANALL
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US-10-387-977-17
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US-10-387-977-17
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                 Query Match 6.3%; Score 153; DB 15; Length 29; Best Local Similarity 100.0%; Pred. No. 1e-06; Matches 29; Conservative 0; Mismatches 0; Indels
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US-10-282-122A-55467
Sequence 55467, Application US/10282122A
PUBLICATION NO. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Allone, Carlos
APPLICANT: Allone, Carlos
APPLICANT: Allone, Carlos
APPLICANT: Allone, Carlos
APPLICANT: Allone, Carlos
APPLICANT: Allone, Vari
APPLICANT: Offlsen, Kari
APPLICANT: Offlsen, Kari
APPLICANT: Trawick, John
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: AU PO 6528
PRIOR FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 1.05
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-06
PRIOR PAPLICATION NUMBER: 60/230,335
PRIOR PELING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                    TYPE: PRT; ORGANISM: Porphyromonas gingivalis
US-10-387-977-26
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Search completed: May 18, 2004, 11:52:20 Job time : 35.8564 secs
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APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DORPHYROMONAS GINGIVALIS
FILE REFERENCE: 529282000301
CURRENT APPLICATION NUMBER: US/10/387,977
CURRENT PELLING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US/9/423,056
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1997-04-30
PRIOR FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 105
                                                                          APPLICANT: Reynolds, Exic Charles
APPLICANT: Reynolds, Exic Charles
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREAPMENT OF PERIODONITIS ASSOCIATED WITH
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
FILE REFERENCE: 5.29282000301
CURRENT FILING DATE: 2003-07-18
PRIOR PLING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: US 09/423,056
PRIOR PLING DATE: 1998-04-30
PRIOR PLING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 105
SEQ ID NOS: 105
SEQ ID NOS: 105
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96.6%; Pred. No. 5.4e-06;
tive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 101, Application US/10387977; Publication No. US20040005276A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ), ORGANISM: Porphyromonas gingivalis US-10-387-977-25
            Sequence 25, Application US/10387977
Publication No. US20040005276A1
GENERAL INFORMATION:
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Matches 28; Conserv
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US-10-387-977-101
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48 HNSAICASSAS-YINFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAV-YA 105 

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380 PASIPQNQASYSIQASAGSYVAISKDGVLYGTGVANAS----GVATVSMTKQITENGNYD 435
106 SSTGNDASNFANALL---EEVLTAKTVVTAPEAIRGTRVQGTWYOKTVQ--LPAGTKXVA 160
                                                                                                                         161 FRHFGCTDFFWINLDDVEIKANGKRADFTETFESSTHGEAPABWTTIDADGDGOGWL--C 218
                                                                                                                                                                                               181 NQEHGYTDVY-----NYLKAPYTGCYSHLNTGVSFANYT---AHGSETAWADPL 226
                                                                                                                                                                                                                                                                                                        272 GFPGDH--------YAVMISKTGTNAGDFTVVF-EETPNGINKGGARFGLSTEA 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------GNHE 401
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                  Copyright
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- protein search, using sw model OM protein May 18, 2004, 11:33:39 ; Search time 47.0287 Seconds (without alignments) 2739.638 Million cell updates/sec Run on:

US-08-570-311-18

2480 1 GTENPNPNPNPNPGTTTLSESF......QNLTGSAVGQKVTLKMDAPN 456 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

1586107

Minimum DB Maximum DB

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:\* 1: geneseqp1980s:\* Database

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp1980s:\* geneseqp1990s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

## SUMMARIES

|                     | Aar96023 P. qinqiv | <u>.</u> | Hae      | _        |          | 8 Hae    | Aar96021 P. gingiv | Aaw69489 Haemaqqlu | Aar96024 P. gingiv |          | Aar96033 P. gingiv | Aaw69495 Haemagglu | Aar70188 Arg-gingi | Aaw34843 Arg-qingi | Aay67396 Arg-gingi | <u>а</u> | Aaw24786 PrtR anti | Aar96028 P. gingiv | Aaw69486 Haemagglu | Aar96032 P. gingiv | Aaw69494 Haemagglu | Aar96029 P. gingiv | Aaw24787 PrtK anti | Aaw69487 Haemagglu | Aau03572 P. gingiv |
|---------------------|--------------------|----------|----------|----------|----------|----------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| QI .                | R96                | AAR96022 | AAW69491 | AAW69490 | AAR96030 | AAW69488 | AAR96021           | AAW69489           | AAR96024           | AAW69492 | AAR96033           | AAW69495           | AAR70188           | AAW34843           | AAY67396           | AAU08938 | AAW24786           | AAR96028           | AAW69486           | AAR96032           | AAW69494           | AAR96029           | AAW24787           | AAW69487           | AAU03572           |
| n DB                |                    |          |          | 2        |          |          |                    |                    |                    |          | 7                  |                    |                    |                    |                    |          | 7                  |                    |                    |                    |                    |                    | 2                  |                    | 4                  |
| Length              | 45(                | 45       | 456      | 456      | 2628     | 2628     | S                  | 45                 | 3                  | 43       | 1687               | 1687               | 1704               | 170                | 1704               | 170      | 1706               | 1087               | 1087               | 35                 | 35                 | 73                 | 1733               | 73                 |                    |
| %<br>Query<br>Match | 100.0              | 100.0    | 8        | 100.0    | $\circ$  | 0        |                    | 98.2               |                    | •        | 84.0               |                    |                    | 84.0               | 84.0               |          | 83.5               | ω.                 | Э.                 |                    | <u>ب</u>           | ς.                 | ς.                 | ć,                 | 29.3               |
| Score               | 2480               | 2480     | 48       | æ        | 2480     | 2480     | 2436               | 2436               | 2351               | 2351     | 2082               | 2082               | 2082               | 2082               | 2082               | 2082     | 2070               | 2066               | 2066               | 2066               | 0                  | 034                | 034                | 2034.5             | 726                |
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| Abp55081 Porphyrom   |          | Aay34522 Porphorym | Aay34521 Porphorym | Aay34520 Porphorym |          | Aay34359 Porphorym | Aay34484 Porphorym |          | Aaw69483 Haemagglu | Aar72458 Porphyrom | Aau03575 P. gingiv | Aar77313 Porphyrom | Aaw34805 Arg-speci | Aay34483 Porphorym | Aay34358 Porphorym | Aau03573 P. gingiv | Aaw34798 Arg-speci | Aaw83085 Peptide f |
|----------------------|----------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| ABP55081<br>AAU03574 | AAB49217 | AAY34522           | AAY34521           | AAY34520           | AAY34392 | AAY34359           | AAY34484           | AAR96025 | AAW69483           | AAR72458           | AAU03575           | AAR77313           | AAW34805           | AAY34483           | AAY34358           | AAU03573           | AAW34798           | AAW83085           |
| 135 6                | 134 4    | 921 2              | 922 2              | 925 2              | 938 2    | •                  | 312 2              | 497 2    | 497 2              | 970 2              | 231 4              | 991 2              | 49 2               | 293 2              | 299 2              | 196 4              |                    | 29 2               |
| 720 29.0             | 28.4     | 27.5               | 27.5               |                    | 27.5     | 22.8               | 22.6               | 22.0     |                    | 16.7               |                    | 10.8               | 9.5                | 4.6                | 233 9.4            | 9.4                | 189 7.6            | 153 6.2            |
| 26 27 71             | 28       | 53                 | 30                 | 31                 | 32       | 33 56              | 34 56              | 35 54    | 36 54              | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43 23              | 44                 | 45                 |

## ALIGNMENTS

```
Haemagglutinin; hagA; periodontal disease; vaccine; antibody; HArep3

    P. gingivalis haemagglutinin hagA HArep3 product.

       AAR96023 standard, protein; 456 AA
                         (revised)
(first entry)
                        16-OCT-2003
04-SEP-1996
                AAR96023;
RESULT 1
    AAR96023
```

Porphyromonas gingivalis; strain 381.

WO9617936-A2.

95WO-US016108. 11-DEC-1995;

13-JUN-1996.

94US-00353485. 09-DEC-1994;

(UYFL ) UNIV FLORIDA. (UABR-) UAB RES FOUND.

Patti JM; Lantz M, Han N, Lepine G, Tumwasorn S, WPI; 1996-287181/29. Progulske-Fox A, N-PSDB; AAT30647. Porphyromonas gingivalis genes and proteins - used in the detection and vaccination against periodontal disease.

Claim 4; Page 110-112; 153pp; English.

HArep3 (AAR96023) is the product of the HArep3 repeat unit (AAT30647) of the hagA gene (AAT30654) of P. gingivalis 318. It forms part of haemagglutinin hagA (see also AAR96030). HArep3 and other hagA repeat unit products (see also AAR96021-22 and AAR96024) can be obtd. from transformed host cells and used as vaccines to protect humans or animals against periodontal disease. Expression in Salmonella cells allows product of live vaccine. HArep1-4 can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)

Sequence 456 AA;

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entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gingivalie
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                                                                                        Sequence 456 AA;
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09-DEC-1994;
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                                                                              61 SSASYINFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASBHYAVYASSTGNDASN 120
                                                                                                         180
                                                                                                                    121 FANALLEEVLTAKTVVTAPBAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINL 180
                                                                                                                                          240
                                                                    SSASYINFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASN 120
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                                                                                                                                                                         VVASFSWNGMALNPDNYLISKDVTGATKVKYYXAVNDGFPGDHYAVMISKTGTNAGDFTV 300
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                                                                                                                                                 DDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTN
                                                 1 GTPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICA
                                  GIPNPPNPNPGTITLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICA
                                                                                                      FANALLEBULTAKTVVTAPBAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINL
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                    Gaps
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  Length 456;
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                  Indels
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100.0%; Score 2480; DB 2;
llarity 100.0%; Pred. No. 7.5e-191;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                           KECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
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                                                                                                                                                                                                                                                                                                                                                                                                        P. gingivalis haemagglutinin hagA HArep2 product
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-00353485
                                                                                                                                                                                                                                                                                                                                             AAR96022 standard; protein;
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         Similarity
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HArep2 (AAR86022) is the product of the HArep2 repeat unit (AAT30646) of the hag4 gene (AAT30654) of P. gingivalis 318. It forms part of haemagglutinin hag4 (see also AAR96030). HArep2 and other hag4 repeat unit products (see also AAR96021 and AAR96023-24) can be obtd. from transformed host cells and used as vaccines to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of live vaccine. HArep1-4 can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)
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Best Local Similarity 100.0%; Pred. No. 7.5e-191;
Matches 456; Conservative 0; Mismatches 0;
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94US-00353485.
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                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagA haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as
                                                                                                                                                                                                                                                                                                                                        encoding haemagglutinin and/or
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100.0%; Pred. No. 7.5e-191;
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vaccines against periodontal
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                                                       Tumwasorn S,
                                                                                                                                               Porphyromonas gingivalis genes
                                                                                                                                                                                                   Claim 1; Col 133-138; 101pp; English.
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                                                                                                                                                                   protease poly:peptide(s))
                                                       Han N, Lantz
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                   UAB RES FOUND
(UXFL ) UNIV FLORIDA (UABR-) UAB RES FOUN)
                                                                                        WPI; 1998-582627/49.
N-PSDB; AAV58878.
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                                                     Patti JM,
                                                                                                                                               Isolated
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AAW69490 RESULT 4

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                                                                                       1310 DDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSP 1369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated Porphyromonas gingivalis genes - encoding haemagglutinin and/or protease poly:peptide(8)).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagA haemagglutinin protein. T polypeptides are used to produce antibodies to organisms associated wi periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
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91US-00647119.
94US-00353485.
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09-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P. gingivalis 381 haemagglutinin hagA (AAR96030) was identified as the product of the hagA gene (AAT30654) isolated as an BCORV fragment of genomic DNA. The haemagglutinin, or portions of it (see also AAR96021-24), can be obtd. from transformed host cells and used as a vaccine to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of a live vaccine. The haemagglutinin can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise os field)
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                                                                                                                                                          Porphyromonas gingivalis; strain 381
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/label= Sig_peptide
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                                                                                     P. gingivalis haemagglutinin hagA
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                 DDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLGWLTAHGGTN
                                                                 1190 VVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTV
                                                                                             VFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILL
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DDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTN
                                             VVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTV
                                                                                                                                            DDIQFIMGGSPTPIDYTYTVRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Han N,
                                                                                                                                                                                                                                                                                                                                                                    P. gingivalis haemagglutínin hagA HArepl product
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 103-104; 153pp; English.
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N-PSDB; AAT30645.
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98.2%; Score 2436; DB 2; Length 450; ilarity 99.8%; Pred. No. 2.6e-187; Conservative 0; Mismatches 1; Indels

Query Match Best Local Similarity Matches 449; Conserv

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306
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                                                                              EEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIK 186
                                                                                                                                             BEVITAKTVVTAPBAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIK 180
                                                                                                                                                                                                               ANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLDWLTAHGGTNVVASFS 240
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             PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASYI
                                                         67 NFEGPONPONYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 450
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protease poly:peptide(s)).
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91US-00647119.
94US-00353485.
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(UABR-) UAB RES FOUND.
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N-PSDB; AAV58876.
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09-DEC-1994;
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N-PSDB; AAT30648.

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                                                                                                                                                                                                                                                                                                                                                            polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
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                                                                                          Gape
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                                                                    Length 450;
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                                                                                        Indels
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                                                                  98.2%; Score 2436; DB 2;
99.8%; Pred. No. 2.6e-187;
iive 0; Mismatches 1;
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(UABR-) UAB RES FOUND.
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Best Local Simi
Matches 449;
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                                                                                               HAREP4 (AAR96024) is the product of the HAREP4 repeat unit (AAJ30648) of the hagA gene (AAT30654) of P. gingivalis 318. It forms part of haemagglutinin hagA (see also AAR96030). HAREP4 and other hagA repeat unit products (see also AAR96011-23) can be obtd. from transformed host cells and used as vaccines to protect humans or animals against cells and used as vaccines to protect humans or animals against beriodontal disease. Expression in Salmonella cells allows prodn. of live vaccine. HAREP1-4 can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)
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      nseq
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Pred. No. 1.7e-180;
3; Mismatches 5;
Porphyromonas gingivalis genes and proteins vaccination against periodontal disease.
                                                              English
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                                                        Claim 4; Page 114-115; 153pp;
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Best Local Similarity 98.2%;
Matches 431; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSP
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                            Lepine
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                                                                                                                          Progulske-Fox A,
                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                     Score 2351; DB 2;
Pred. No. 1.7e-180;
                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                          Tumwasorn S,
                                                                                                                                                                               Isolated Porphyromonas gingivalis genes
protease poly:peptide(s)).
                                                                                                                                                                                                                      English
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                                   88US-00241640.
91US-00647119.
94US-00353485.
             95US-00570311
                                                                                                                                                                                                                   Col 139-144; 101pp;
                                                                                                                                                                                                                                                                                                                                                     94.8%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lantz M,
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                   UNIV FLORIDA.
UAB RES FOUND
                                                                                                                                             WPI; 1998-582627/49.
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 431; Conserv
                                                                                                                       Han N,
                                                                                                                                                        N-PSDB; AAV58879
                                                                                                                                                                                                                                                                                                                             Sequence 439 AA;
                                                                                  (UYFL ) UNIV
                                             25-JAN-1991;
09-DEC-1994;
            11-DEC-1995;
                                   08-SEP-1988;
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                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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                                                                                              (UABR-)
                                                                                                                       Patti
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1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             991
                                                                                                                                                                                                                                                                                                                                                                                                            P. gingivalis 381 haemagglutinin hagE (AAR96033) was identified as the product of a gene (AAT30656) identified in P. gingivalis 318 genomic DNA The haemagglutinin can be obtd. from transformed host cells and used as vaccine to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of a live vaccine. The haemagglutinin can also be used to detect the presence of anti-P. appln. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                               used in the detection and
                                                                                                                                                                                                                                                                           Patti JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  935 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PNPNPPNPNPRTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAICASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VASFSWNGMALNPDNYL I SKDVTGATKVKYYYA VNDGFPGDHYA VMI SKTGTNAGDFTVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1687;
                                                     Haemagglutinin; hagE; periodontal disease; vaccine; antibody
                                                                                                                                                                                                                                                                           Lantz M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40; Indels
                                                                                                                                                                                                                                                                          Han N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.0%; Score 2082; DB 2;
86.2%; Pred. No. 5.2e-158;
ive 17; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                               genes and proteins -
                                                                                                                                                                                                                                                                          Lepine G,
                                                                                    Porphyromonas gingivalis; strain FDC381
                                                                                                                                                                                                                                                                                                                                                           vaccination against periodontal disease.
                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 138-143; 153pp; English.
                            P. gingivalis haemagglutinin hagE
                                                                                                                                                                                                                                                                        Tumwasorn S,
                                                                                                                                                                                                 94US-00353485.
                                                                                                                                                                        95WO-US016108
 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 86.2³
Matches 392; Conservative
                                                                                                                                                                                                                                                                                                                                           Porphyromonas gingivalis
                                                                                                                                                                                                                          (UYFL ) UNIV FLORIDA.
(UABR-) UAB RES FOUND
                                                                                                                                                                                                                                                                                                WPI; 1996-287181/29.
N-PSDB; AAT30656.
                                                                                                                                                                                                                                                                       Progulske-Fox A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1687 AA;
                                                                                                                                                                                                09-DEC-1994;
                                                                                                              WO9617936-A2
                                                                                                                                                                       11-DEC-1995;
  04-SEP-1996
                                                                                                                                          13-JUN-1996
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ECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456

standard; protein; 1687 AA.

AAR96033

AAR96033

HXXXH

(revised)

16-OCT-2003

421

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1290 DIQFIMGGSPIPIDYIYIVYRDGTKIKEGLIETIFEEDGVAIGNHEYCVEVKYTAGVSPK 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A low mol.wt. arginine-specific gingipain (AG-1) and high mol.wt. AG (AG-2) were isolated from P. gingivalis strains H66 (ATCC 33277) and W50 (ATCC 53973). The sequences of the proteins were used to design PCR primers and probes to isolate AG DNA. Lambda DASH and lambda ZAP libraries were screened with a probe based on amino acids 11-22 of the AG protein to obtain DNA encoding AG-1 (AAQB3484) and AG-2 (AAQB3489). AG-2 correct PN field.)
               302 FEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding Arg-gingipain proteins - used to develop prods. for detection, treatment and prevention of periodontal disease.
                                                                                                                                                                                                                                                                                                              Arg-gingipain-2; gingivalis; periodontal disease; vaccine; arginine-specific protease.
                                                                                                                                                                                                                                                                                                                                                                                      228. .719
/label= Protease
/note= "corresponds to Arg-gingipain-1"
                                                                                                                            422 ECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1092. .1429
/label= Hemagglutinin
1430. .1704
/label= Hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                        720. .1091
/label= Hemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 70-77; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                  AAR70188 standard; protein; 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barr PJ,
                                                                                                                                                                                                                                                                                        Arg-gingipain-2 prepolyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93US-00119361.
93US-00141324.
94US-00265441.
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                                                                                                                                                                                                                                                    (revised)
(first entry)
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                                                                DIQFTMGGSPTPTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-123373/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ83489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9507286-A1
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21-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Travis J,
                                                                362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagE haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding haemagglutinin and/or
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                                                                                                                                                                                                                                                                                                                                                                                  Tumwasorn S, Progulske-Fox A,
                                                                                                                                                                      Haemagglutinin protein; periodontal disease; vaccine; hagE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
ECVNVTINPTQFNPVKNLKAQPDGGDVVLKWEAPS 1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2082; DB 2;
Pred. No. 5.2e-158;
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86.2%; Pred. No. 5.1.
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                                                                     AAW69495 standard; protein; 1687
                                                                                                                                                                                                                                                                      95US-00570311
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94US-00353485.
                                                                                                                                                                                                                                                                                                                                                                                Patti JM, Han N, Lantz M,
                                                                                                                                             Haemagglutinin protein hagE
                                                                                                                       (first entry)
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nes 392; Conservative
                                                                                                                                                                                             Porphyromonas gingivalis
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UAB RES FOUND.
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                                                                                                                       22-DEC-1998
                                                                                                                                                                                                                                                                     11-DEC-1995;
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09-DEC-1994;
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                                                                                                                                                                          DVEIKANGKRADFTETFESSTHGEAPAEWTIDADGDGQGWLCLSSGQLGWLTAHGGTNV
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               Length 1704;
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ECUNVIINPIQENPVKNLKAQPDGGDVVLKWBAPS 1401
         84.0%; Score 2082; DB 2;
86.2%; Pred. No. 5.2e-158;
iive 17; Mismatches 40;
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                                           Matches 392; Conservative
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N-PSDB; AAT93872.
   Query Match
Best Local Similarity
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EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLDWLTAHGGTNV 1186
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Porphyromonas gingivalis Arg-specific gingipain protease peptide(s) -
useful for protecting animals and humans from gingivalis and periodontal
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; Pred. No. 5.2e-158;
17; Mismatches 40;
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                                                                                                                                                                                                                                       Disclosure; Page 68-73; 95pp; English
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Best Local Similarity 86.23
Matches 392; Conservative
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New Porphyromonas gingivalis arginine-specific protease preparation useful for preparing vaccines against periodontal disease and for screening for Arg-gingipain inhibitors.
                                                                                               (UYGE-) UNIV GEORGIA·RES FOUND INC.
                                                                                                           Potempa JS, Travis J;
                                                                                                                       2000-136659/12.
                                                                                                                              N-PSDB; AAZ60181.
                                                                 08-NOV-1994;
                                                                             10-SEP-1993;
24-JUN-1994;
                                          US6017532-A
                                                     25-JAN-2000
      Key
Region
                        Region
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PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS 1008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
                                             This sequence represents a Porphyromonas gingivalis arginine-specific proteinase known as Arg-gingipain/gingipain-2 amino acid sequence. Gingipain-2 consists or a 50kD protease component non-covalently associated with a 44kD haemagglutinin component. The proteinase is stimulated by glycine containing peptides and glycine analogues. It is trimibited by cysteine protease group specific inhibitors. The protease preparation can be used in immunogenic compositions and vaccines against inflammatory response and tissue damage caused by P. gingivalis in periodontal disease. It can also be used to screen for agents that modulate Arg-gingipain proteinase activity inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1009 ESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEETPNGINKGGARFGLSTEADGAKPOSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 ASY-INFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                               Length 1704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   40; Indels
                                                                                                                                                                                                                                                                                                                                                                                          84.0%; Score 2082; DB 3;
86.2%; Pred. No. 5.2e-158;
iive 17; Mismatches 40;
Claim 1; Col 29-42; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 86.2
Matches 392; Conservative
                                                                                                                                                                                                                                                                                                                                    Sequence 1704 AA;
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1307 DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 1366

DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 421

362

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422 ECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456 à g

229. .719"
/note= "Amino acids 229-719 are specifically claimed" 720. .1185
/note= "Amino acids 720-1185 are specifically claimed"

94US-00336308 93US-00119361 94US-00265441

Location/Qualifiers

Search completed: May 18, 2004, 11:42:42 Job time : 49.0287 secs

|           | Ltd.      |
|-----------|-----------|
| 5.1.6     | Compugen  |
| version   | - 2004    |
| GenCore v | (c) 1993  |
|           | Copyright |

OM protein - protein search, using sw model

Run on:

May 18, 2004, 11:37:00 ; Search time 11.906 Seconds (without alignments) 3684.135 Million cell updates/sec

US-08-570-311-18 Title: Perfect score:

2480 1 GTPNPNPNPNPNPGTTTLSESF.....QNLTGSAVGQKVTLKWDAPN 456 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|        | Description | agglutini | ~   | . ^   | 71.610 | Joneph     | onserved | (a)   | 'n |       | ₽     |       | _     | ŭ   |       | ical  | tail-host specific | •     | probable RTX famil | transferrin-like p | S-layer protein - | large repetitive p | tt<br>tt | al  | hypothetical prote | alkaline serine pr |        |     | rvata | rized |
|--------|-------------|-----------|-----|-------|--------|------------|----------|-------|----|-------|-------|-------|-------|-----|-------|-------|--------------------|-------|--------------------|--------------------|-------------------|--------------------|----------|-----|--------------------|--------------------|--------|-----|-------|-------|
|        | dr<br>      | T286      | Æ   | 54976 | T3     | 14022      | AF295    | H9832 |    | A8341 | C8987 | AH251 | S1078 |     | A8668 | C8682 | T1325              | F9069 | B8554              |                    | A4702             |                    | S59077   |     | T34416             | JC4908             | T30944 |     | T1821 | B970  |
|        | Length DB   | 628       | 704 | 526   | 732    | 16         | 52       | m     | 91 | 468   | 248   | 936   | ₹*    | 13  | 441   | 649   | 904                | 16    | 188                | 274                | 465               | 24                 | 060      | 806 | 83                 | 15                 |        | 26  |       | 817   |
|        | Match       | 0         |     | ω.    | 2      | •          | •        | 5.6   | •  |       |       | •     |       |     |       |       |                    |       |                    | •                  | ٠                 | •                  | •        | •   | •                  | 4.8                | 4.8    | 4.8 | 4.8   | 4.8   |
|        | Score       | 2480      | 0   | 0     | 2034.5 | $^{\circ}$ | 39       | 139.5 | 32 | 31    | 28    | -     | 127.5 | 127 | 126   | Н     | 24                 | 24    | 23                 | 55                 | 121.5             | 7                  | 121      | 120 | 120                | 119                | ~      | 138 | 118.5 | 18    |
| Result | NO.         | 1         | 0   | m     | 4      | S          | 9        | 7     | σο | ø,    | 10    | 11    | 12    | 13  | 14    | 15    | 16                 | 17    | 18                 | 19                 | 20                | 77                 | 22       | 23  | 24                 | 25                 | 56     | 27  | 28    | 29    |

1250 VFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILL 1309

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à 원 장

301 VFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILL 360

1310 DDIQFTWGGSPTPTDYTYTVXRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSP 1369

421 KECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456

361 DDIQPTMGGSPTPTDYTYTVXRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSP 420

| hypothetical prote | hypothetical prote | hypothetical profe | beta-dalactosidase | hemolvsin limporte | major surface prot | probable outer mem | protein-tyrosine-p | microbial colladen | probable S-laver n | probable secreted | outer membrane pro | hypothetical prote | cellulase - Cellul | hypothetical prote | internalin-like pr |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| S76412             | E90696             | A85547             | T30551             | AI0452             | S48753             | AF0472             | A49724             | JC4393             | D97316             | AD1507            | JC1340             | 876109             | S49541             | H90975             | AF1772             |
| N                  | (1)                | N                  | (7                 | N                  | 7                  | 7                  | Н                  | α                  | ~                  | 7                 | ~1                 | N                  | 2                  | ~                  | 0                  |
| 4199               | 1461               | 1461               | 1034               | 1635               | 702                | 875                | 1118               | 1282               | 1939               | 821               | 1651               | 3029               | 872                | 1345               | 938                |
| 4.8                | 4.8                | 4.8                | 4.7                | 4.7                | 4.7                | 4.7                | 4.7                | 4.7                | 4.7                | 4.6               | 4.6                | 4.6                | 4.6                | 4.6                | 4.5                |
|                    |                    | æ                  | .5                 | 'n                 | 5.5                | 5.5                | 115.5              | 5.5                | 5.5                | 115               | 115                | 115                | 114                | 113                | 112.5              |
| 118.5              | 118                | 딤                  | 117                | 116                | 17                 | H                  | 7                  | 11                 | H                  |                   |                    |                    |                    | •                  | 11                 |

## ALIGNMENTS

| RESULT 1 T28651 Chemagglutinin A - Porphyromonas gingivalis CSPGC468: Porphyromonas gingivalis CSPGC468: Porphyromonas gingivalis CSPGC468: Porphyromonas gingivalis CSPGC468: Porphyromonas gingivalis CSPGC68: T28651 FFHan, N; Whildock, J; Progulske-Fox, A. FFHan, N; Whildock, J; Progulske-Fox, A. FFHan, N; Whildock, J996 A;Title: The hemagglutinin gene A (hagA) of Porphyromonas gingivalis 381 contains A;Reference number: Z20494; MUID: 97047672; PMID: 8926061 A;Reference number: Z20494; MUID: 97047672; PMID: 8926061 A;Reference number: Z20494; MUID: 97047672; PMID: 8926061 A;Residues: 1-2628 cHAN. A;Residues: 1-2628 cHAN. A;Residues: 1-2628 cHAN. A;Residues: 1-2628 cHAN. A;Coss-references: EMBL: U41807; NID: 91552410; PID: 91469916; PIDN: AAB17128.1 A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;G |  |
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Gaps

9

1010

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1070

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Dp

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lysine-specific cysteine proteinase porphypain (EC 3.4.22.-) - Porphyromonas gingivalis lysine-specific cysteine proteinase 1, 60K

Nylternate names: lysine-specific cysteine proteinase 1, 60K
C;Species: Porphyromonas gingivalis
C;Species: Porphyromonas gingivalis
C;Date: 22-Oct-1999 #sequence revision 22-Oct-1999 #text_change 17-Nov-2000
C;Accession: 170836; T30837; T30826; A53113
R;Barkcoy-Gallagher, G.A.2741, 1996
A;Ritle: Analysis of the prtP gene encoding porphypain, a cysteine proteinase of Porphy.
A;Reference number: 220895; MUID:96213011; PMID:8631659
A;Reference number: 220895; MUID:96213011; PMID:8631659
A;Reference number: T30886
A;Reference si ENBL:U42210; NID:g1314325; PID:g1314326; PIDN:AAB06565.1
A;Residues: 1-1732 <BBR.
A;Cross-references: ENBL:U42210; NID:g1314325; PID:g1314326; PIDN:AAB06565.1
R;Slakeski, N; Cleal, S.M.; Reynolds, E.C.
Submitted to the EMBL Data Library, October 1996
A;Reference number: 220896
A;Reference number: 220896
A;Reference number: 220896
A;Reference number: 220896
A;Reference number: 220896
A;Reference number: 220896
A;Reference number: Data Library, translated from GB/EMBL/DDBJ
A;Status: preliminary;
C;Accession: 849763
R;Aduse-Opoku, J.; Muir, J.; Slaney, J.M.; Rangarajam, M.; Curtis, M.A.
submitted to the EMBL Data Library, November 1994
A; Description: Cloning, sequence analysis and expression in Escherichia coli of prpRl
A;Reference number: 849763
A;Reference number: 849763
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A;Resarreferences: EMBL;R82680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 ASY-INFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1526;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 2059; DB 2;
; Pred. No. 7.4e-134;
17; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.5%;
Matches 389; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182
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ANAlternate names: 50K high molecular mass arginine-specific cysteine proteinase; HGP; R

C.Species: Porphyromonas gingivalis

C.Species: Porphyromonas gingivalis

C.Species: Porphyromonas gingivalis

C.Species: Porphyromonas gingivalis

C.Species: Porphyromonas gingivalis

C.Species: Porphyromonas gingivalis

C.Species: Porphyromonas gingivalis

C.Species: Porphyromonas gingivalis

C.Species: Porphyromonas gingivalis

R.Pavloff, N.; Potempa, J.; Pike, R.N.; Prochazka, V.; Kiefer, M.C.; Travis, J.; D.S. J. Barr, F. J. Bol. Chem. 270, 1007-1010, 1995

A.Title: Molecular cloning and structural characterization of the Arg-gingipain proteina

A.Reference number: ASS426, MUID:95138080; PMID:7836351

A.Scatus: preliminary

A.Molecule type: DNA

A.Reference number: ASS113; MUID:951300; PIDN:AAA69539.1; PID:GS57068

R.Pike, R.; McGraw, W.; Potempa, J.; Travis, J.

J. Balol. Chem. 269, 466-411, 1994

A.Title: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolat

A.Reference number: ASS113; MUID:94103245; PMID:8276827

A.Molecule type: protein

A.Residues: 228-249 - FIKA

A.Residues: 228-249 - FIKA

A.Residues: 228-249 - FIKA

A.Residues: 228-249 - FIKA

A.Residues: 228-249 - FIKA

A.Residues: 228-249 - FIKA

A.Residues: Sale-249 - FIKA

A.Residues: Sale-249 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

A.Residues: C.Sale-240 - FIKA

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A.Residues: C.Sale-240 - FIKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNV 1186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        952 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 PNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSALCASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTNV
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1370 KECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 1405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.0%; Score 2082; DB 2;
86.2%; Pred. No. 2.2e-135;
iive 17; Mismatches 40;
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Matches 392; Conservative
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à qq ò DP  $\delta$ gg à Db  $\stackrel{>}{\circ}$ g ð a à g  $\stackrel{>}{\circ}$ a m

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Cisperies: Agrobacterium tumefaciens (imported) - Agrobacterium tumefaciens (strain C5 C; Species: Agrobacterium tumefaciens (c) Species: Agrobacterium tumefaciens (c) Species: Agrobacterium tumefaciens (c) Species: Agrobacterium tumefaciens (c) Species: Agrobacterium tumefaciens (c) Species: Ascassion: AF2959 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I seage, G.; Gilelt, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-2323, 2001 Science 294, 2317-
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A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            680 ILKWDAPSTKTNATIN-TARSVDGIRELVLLSVSDAPELLRSGQAEIVLEAHDVWNDGS- 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----QGQKV 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 QGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDV-EIKANGKRADFTETFESSTHGEA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLIFWVCAQDANYASEHYAVYASSTG--NDASNFANALLEEVLTAKTVVTAPEAIRGTRV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 PAEWITIDADGDGQGWLCLSSGQLGWLTAHGGINVVASFSWN-----GMALNPDNYLISK 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GYQILLDADHDQYGQVIPSDTHTLWPNCSVPANLFAPFEYTVPENADPSCSPTNMIM-- 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 ADGAKPQS---VWI-----ERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSP 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --SDYTYTVYRDGTKIKEGLTETTYRDAGMSAQSHEYCVEVKYAAGVSPKVCVDYIPDGV 921
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A;Cross_references: GB:AE008689; PIDN:AAL44092.1; PID:g17741659; GSPDB:GN00187
                                                                                                                                                                                                                                                                                                                                                30 TIDADGDGNNWTTTPPPPGGTSFAGHNSAICASSASYINFEGPQNPDNYLVTPELSLPNGG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVNVTVDPV
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                                                A;Molecule type: DNA
A;Residues: 1-991 <RES>
A;Cross-references: GB:D26470; NID:g927644; PIDN:BAA05484.1; PID:g927645
                                                                                                                                                                                              5.6%; Score 139.5; DB 2; Length 1052;
20.9%; Pred. No. 0.12;
Live 67; Mismatches 159; Indels 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             538 TLTLTV----VGYNKETVIKTINTNGEPNPYQPVSN----LTATT-
                                                                                                                                                                                                                                                                                                                                                                                                               595 SVNVSCDYNGALATISANGKMF---GSAVVENGTATINLTG-
                  preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 25.9%
Matches 114; Conservative
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Matches 123; Conservative
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A; Title: The Genome of
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A, Status: preliminary
A, Molecule type: DNA
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross.1-1350,'N', 1352-1363,'Y', 1365-1447,'H',1449-1732 <LEW>
A;Cross-references: EMBL:AF017059; NID:g2738802; PID:g2738803; PIDN:AAC26523.1
B;Pike, R.; McGraw, W.; Potempa, J.; Travis, J.
J. Biol. Chem. 269, 406-411, 1994
A;Title: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolat
A;Reference number: A53113; MUID:94103245; PMID:8276827
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R;Okamoto, K.; Misumi, Y.; Kadowaki, T.; Yoneda, M.; Yamamoto, K.; Ikehara, Y.
Arch. Biochem. Biophys. 316, 917-925, 1995
A;Title: Structural characterization of argingipain, a novel arginine-specific cysteine A;Accession: 140229; MUID:95168884; PMID:7864651
                                                                                                    Infect. Immun. 66, 3035-3042, 1998
A;Title: IS185, an insertion sequence-like element associated with protease genes in A;Reference number: Z20844; MUID:98298016; PMID:9632563
A;Recession: T30526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
A,Residues: 1-795,'I',797-1389,'N',1391-1478,'Y',1480-1732 <SLA>
A,Cross-references: EMBL.U75366; NID:g2182811; PID:g2182812; PIDN:AAB60809.1
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C, Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1204 SNVVSSFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.0%; Score 2034.5; DB 284.3%; Pred. No. 4.3e-132; iive 19; Mismatches 44;
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Matches 387; Conservative
                                                                          R; Lewis, J.P.; Macrina, F.L.
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A;Residues: 229-249 <PIK>
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| Db 452YSGGTTISAGMIKGTAKEGGGGINNAELVVDGGGTLSNAISGTGSFEKTGDGNLLL 509  Qy 403 TGNHEYCVEVKYTAGVSPKECVNVTVDEVQFNPVQNLTGSAVGKYTL 450  Db 510 TGNSTYSGATAVSAGKLSVNGSLASAVSVGSGATVGGTGI 550  RESULT 7  H93323  Hypothetical protein AGR L 3085 [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens  C; Species: Agrobacterium tumefaciens  C; Species: Agrobacterium tumefaciens  C; Species: Agrobacterium tumefaciens  C; Species: Agrobacterium tumefaciens  C; Species: Agrobacterium tumefaciens  C; Species: Agrobacterium tumefaciens  C; Species: Agrobacterium tumefaciens  C; Species: Agrobacterium tumefaciens  C; Species: Agrobacterium tumefaciens  C; Species: Agrobacterium tumefaciens  C; Species: Agrobacterium tumefaciens  C; Accession: H99323  R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;  A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194  A; Molecule type: DNA  A; Molecule type: DNA  A; Residues: -1344 . AKUR>  A; Cross-references: GB:Ab007870; PIDN:AAK90114 1; PID:G156160.06. Gebra. Groba.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | RESULT 8 By5622 hypothetical protein - Deinococcus radiodurans (strain R1) C;Species: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000 C;Accession: B75622 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; S, Smith, M.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Recession: B75622 A;Residues: 1-691 <whi> A;Residues: 1-691 <whi> A;Residues: 1-691 <whi> A;Residues: strain R1 C;Genetics: A;Gene: DR80037 A;Map position: megaplasmid A;Gene: plasmid MP1 A;Gene: plasmid MP1</whi></whi></whi> |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Query Match 5.3%; Score 132.5; DB 2; Length 691;<br>Best Local Similarity 21.9%; Pred. No. 0.21;<br>Matches 111; Conservative 46; Mismatches 178; Indels 171; Gaps 23;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| Query Match         5.6%; Score 139.5; DB 2; Length 1341;           Best Local Similarity         20.9%; Pred. No. 0.16;           Matches 123; Conservative 67; Mismatches 159; Indels 239; Gaps 33;           QY         13 TTLISESFENGIPASWITIDADGDGNWTTTPPPGGTSFAGHNSAICASSAS 64           Db         341 TVTSGRAIIGRHSASEATV-TGDGSKWTTGDLQVGGDTSDFGG-LAGNGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ASWKTIDADGDGNNWTTTP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |

| Db 1044 TPSTPLADGTVVNATATDPAG-N'  Qy 348 RHYNCSDLNYILLDDIQI  Db 1095TAEFGSTVILTDGNGNPIAB'  QY 402 ATGNHEYCVEVKYTAGVSPKECYI  Db 1144 ASGNSSPPATVTVDSSAPPAPVII  RESULT 10  C8987 10  C8987 2010 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 100  C8987 | autolytain limported; Staphylococcus aureus (strain N315)  G;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: C89874 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001 A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Recession: C89874 A;Accession: C89874 A;Status: preliminary A;Moclecule type: DA A;Residues: 1-1248 «KUR» A;Residues: 1-1248 «KUR» A;Cross-references: GB:BA000018; PID:g13700854; PIDN:BAB42150.1; GSPDB:GN00149 A;R. Lim, C;Generics: strain N315 | tic pathc                                                                      | QY         128 EVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAPRHFG 171           Db         758 AVAQPKTAVKXTVTKPQTTQTVSKIAQVKENNTGIRASVYEKTAKNGAKY-ADRTFY 814           QY         172 CT |
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| QY         196                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | osa PA01, an opportur<br>6; PIDN:AAG05263.1;<br>mgth 2468;<br>dels 189; Gaps 2 | 0 4 6 2 4 8 4 8 8 9 9 4                                                                                                                                                            |

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A; Cross-references: EMBL: X53373; NID: 948305; PIDN: CAA37453.1; PID: 948306
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Best Local Simi
Matches 129;
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                                       Query Match
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C;Species: alkaliphilic eubacterium 163-26
C;Species: alkaliphilic eubacterium 163-26
C;Species: alkaliphilic eubacterium 163-26
C;Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 15-Oct-1999
C;Acadession: S10789
Bur. J. Blochem: 191, 177-185, 1990
A;Title: Blochemical and genetic analysis of a maltopentaose-producing amylase from A;Reference number: S10789; MUID:90336627; PMID:1696201
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                          3161 GLSNPN---TPGTYQLQVDATTVQDNAGN------SGDAARTTFFIAAPPTPGV 3206
                                                                                                                                                                                                                                                                                                                                                                                                                 T-----ITQSGGSTAVIEG-GNTDSYTLVLRTQPTADVTVTLNTGSQITTDKTTLTF 3257
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A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr7304
A;Genome: plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VASFSWNGMALN--PDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKT 291
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C;Species: alkaliphilic eubacterium 163-26
C;Date: 21-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                                                                                                                     ----TILSESFENGIPASWKTIDADGDGNNWTT-----TPPPGG
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                                                                                                                                                                                                                                                                           5.2%; Score 12%; DB 2; Length 4936;
20.4%; Pred. No. 5.5;
.ive 60; Mismatches 171; Indels 190;
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                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 20.4¹
Matches 108; Conservative
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A Molecule type: DNA
A Residues: 1-1684 < CAN>
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T.; Zalewski,
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                                                                                                                                                                                               ELSLPNGGTLTFWVCAQD-ANYASEHYAVYASSTGNDASNFANALLEEVLTAKTV-VTAP 139
                                                                                                                                                                                                                                                                                            EAIRGT-RVQGTWYQKTVQLPAGTKYVAFRHFGCTDFF--WINLDDVEIKANGKRADFTE 196
                                                                                                                                                                                                                                                                                                                                       281 PILRNKWNDQASGYEDWF-VPAAEPYRQDLNIAPKDYLIKWITSWVEEFGIDGFRVDTAK 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281 GDHYAVMISKTGTN----AGDFTVVF-EETPNGINKGGARFGLSTEADGAKPQSVW--IE 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cispecies: Deinococcus radiodurans
Cibate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
Cibacession: B/5489
R;White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale S.; Smith, H.O.; Venter, J.C.; Frager, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----NGMALNPDNYLISKDVTGATKVKYYYAVNDGFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395 FGFDSVINFEFQNANFNNLEGLFSRYANSINTDPDFNMLSYVSSHDTKL---YSRDD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 DYTYTVYRDGTKIKEGLT--ETTFEEDGVATGNHBYCVEVKYTAGVSPKECVNVTVDPVQ
                                                                                                                                                                                                                                            ------WIRADETAGY-----DNCGGSEQTMCIGFLPDIKTEVTTGVDLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 GIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICA-SSASYINFEGPQNPDNYLVTP
                                                                                                                                            204 GLPRDWTPNQA--QGQNWHT-----HNDIMNKDNBAAWANWWGSD-----
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                                                       149;
       Length 1684;
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                                                                                                                                                                                                                                                                                                                                                                                      197 TFESSTHGEAPAE-----WTTIDADGDGQGWLCLSSGQLGWLTA----HG-
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                                                       IndelB
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5.1%; Score 127.5; DB 2;
20.9%; Pred. No. 1.5;
tive 53; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein - Deinococcus
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                                                    Conservative
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NCBI_TaxID=837;
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Infect. Immun. 62:4279-4286(1994).
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Dewhirst F.E., Fraser C.M.;
"Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivalis strain W83.";
"Jacteriol. 185:5591-5601 (2003).
"Bacteriol. 185:5591-5601 (2003).
"Bacteriol. 185:5591-5601 (2003).
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Hemagglutinin; Virulence; Hydrolase; Thiol protease; Signal; Repeat;
Complete proteome.
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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PEPTIDASE C25-LIKE 3.
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Infect. Immun. 62:5707-5707(1994).
-!- FUNCTION: CLEAVES HUMAN COMPLEMENT COMPONENT C3. MAY ENABLE
P.GINCIVALIS TO EVADE COMPLEMENT—MEDIATED KILLING DURING THE
IMMUNE RESPONSE. PLAYS AN IMPORTANT ROLE IN SOFT TISSUE INFECTIONS
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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16-OCT-2001 (Rel. 40, Last annotation update)
Protease prtH (EC 3.4.22.-).
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01-DEC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence indate)
Gingipain R1 precursor (EC 3.4.22.37) (Gingipain 1) (Arg-gingipain)
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                                                                                                                                                                                                                                                                   Length 989;
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Bacteria, Bacteroidetes; Bacteroides (class); Bacteroidales
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MEDLINE=95168884; PubMed=7864651;
Okamoto K., Misumi Y., Kadowaki T., Yoneda M., Yamamoto K.,
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InterPro; IPR002376; formyl transf.
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J. Biol. Chem. 267:18896-18901(1992).

-I. FUNCTION: Thiol protease which is believed to participate in intracellular degradation and turnover of proteins. Its proteolytic activity is a major factor in both periodontal tissue destruction and in bacterial host defense mechanisms. Activates complement C3 and C5.

-I. CATALYTIC ACTIVITY: Cleavage of proteins, including collagens and immunoglobulins, with a preference for Arg in P1, and hydrophobic residues in P2 and P3.

-I. ENZYME REGULATION: Requires cysteine for activation and Ca(2+) and/or Mg(2+) for stabilization. It is stimulated by glycine-containing dipeptides. It is resistant to inhibition by proteinase inhibitors in human plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
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HSSP; P40229; 140229.
HSSP; P5433; ICVR.
HSRP; D5433; ICVR.
MEROPS; CZS.001; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR007536; Peptidase CZS.
InterPro; IPR00536; Peptidase CZS.
InterPro; IPR00536; Peptidase CZS.
InterPro; IPR03785; Peptidase CZS.
InterPro; IPR03785; Peptidase CZS.
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InterPro; IPR03785; Peptidase CZS.
InterPro; IPR037
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25.9%; Pred. No. 8.6e-11;
Live 50; Mismatches 164; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GINGIPAIN R1.
PROTON DONOR (BY SIMILARITY)
NUCLBOPHILE (BY SIMILARITY).
RT -> TK (IN REF. 2).
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264
991 AA;
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N-ACETYLMURAMOYL-L-ALANINE AMIDASE. ENDO-BETA-N-ACETYLGLUCOSAMIDASE.

BIFUNCTIONAL AUTOLYSIN

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DOMAIN
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- FUNCTION: ENDOHYDROLYSIS OF THE D.N-ACETYLCHITOBLOSYL UNIT IN HIGH-MANNOSE GLYCOPEPTIDES AND GLYCOPROTEINS CONTAINING THE HIGH-MANNOSE GLYCOPEPTIDES AND GLYCOPROTEINS CONTAINING THE HIGH-MANNOSE GLYCOPEPTIDES AND GLYCOPROTEINS CONTAINING THE RESIDUE REMAINS ATTACHED TO THE PROTEIN; THE REST OF THE CUIGOSACCHARIDE IS RELEASED INTACT.
-!- CATALYTIC ACTIVITY: Hydrolyzes the link between N-acetylmuramoyl residues and L-amino acid residues in certain bacterial cell-wall glycopeptides.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the di-N-acetylchitobiosyl unit in high-mannose glycopeptides and glycoproteins containing the -[Man (GloNac) 2] Asn-structure. One N-acetyl-D-glucosamine residue remains attached to the protein; the rest of the oligosaccharide is released intact.
-!- TYM: NUDERGOSE PROTEOLYTIC PROCESSING TO GENERATE THE TWO EVENTALED IN AUGUST AND ENGEDATICE.
                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bifunctional autolysin precursor [Includes: N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28); Mannosyl-glycoprotein endo-beta-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR LYTTC ENZYMES.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE N-ACETYLMURAMOYL-L-ALANINE AMIDASE FAMILY 2.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A Staphylococcus aureus autolysin that has an N-acetylmuramoyl-L-alanine antidase domain and an endo-beta.N-acetylglucosaminidase domain: cloning, sequence analysis, and characterization."; Proc. Natl. Acad. Sci. U.S.A. 92:285-289 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oshida T., Sugai M., Komatsuzawa H., Hong Y.-M., Suginaka H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 205-214 AND 776-792.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Foster S.J.;
Submitted (APR-1995) to the EMBL/GenBark/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                        PRT; 1256 AA
                                 | | : ||: ||:
922 ADVIAQKPYTLTVVGKTITV 941
432 QFNPVQN-LTGSAVGQKVTL 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95116542; PubMed=7816834;
                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=NCTC 8325-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=RN450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tomasz A.;
                                                                                                                                                                                                     ATL STAAU P52081;
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                                                                                                                                                                                                                                                                                                                                                                                            ------GILTFWVCAQDANYASEHYAVYASSTGNDASNFAN-----ALLE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                 710 GTYKQEAGAVSGTGNQTFKATKQQQIDKS----IYLFGTVNGKSGWVSKAYLAVPAAPKK 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 EVLTAKT-----VVTAPEAIR------GTRVQGTWYQKTVQLPAGTKYVAFRHFG 171
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                                                                                                                                                                                                                                                                                                            47 -----GGTSF---AGHNSA----ICASSASYINFEGPON-PDNYLVTPE---LSLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            823 VIKERAHGNETYVLLNNTSHNIFLGWFNVKDLNVQNLGKEVKTTQKYTVNKSNNGLSMVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 CT-----TFESSTHGEAPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 WITIDADGDGQWLCLSSGQLGWLTAHGGTNVVASFSWN-----GMALNPDNYLISKDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            883 WGT------KNQVILTGNNI----AQGTFNATKQVSVGKDVYLYGTINNRTGWVNAKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 TGATKVK------YYYAVNDGFPGDHYAVMISKTGT-----NAGDFTVVFEETPN
                                                                                                                                                                                                     Gaps
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Biol. Reprod. 53:285-294(1995).

-!- FUNCTION: Binds to oocyte zona pellucida in vivo. May play a rol in the fertilization process and/or early embryonic development.
-!- SUBCELLUIAR LOCATION: Secretory granules.
-!- TISSUE SPECIFICITY: Epithelial cells of the oviduct.
-!- SIMILARITY: Belongs to family 18 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning and characterization of a mouse oviduct-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Oviductal glycoprotein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ICR; TISSUE=Oviduct;
MEDLINE=96115001; PubMed=7492680;
Sendai Y., Komiya H., Suzuki K., Onuma T., Kikuchi M., Hoshi H.,
                                                                                                                                                                                               Indels 153;
                                                                                                                                                          Length 1256;
                                                                                                                                                                                                                                  PNPNPNPNPGTTT----LSESFENGIPASWKTIDADGDG----NNWTTTPPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        308 G-----INKGGARFGLSTEADGAK-----PQSVWIERTVDLPAGTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             991 GOTWYYGKLSNGKLAWIKST--DLAKELIKYNOTGMTLNOVAQIQAGLQY
                                                                                                                   2BB76CAA292FDD20 CRC64;
                                                                                                                                                        5.3%; Score 131.5; DB 1;
22.3%; Pred. No. 0.24;
live 47; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oviduct-specific glycoprotein precursor (Oviduct (Oviductin) (Estrogen-dependent oviduct protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                   425 589 1.
596 758 2.
770 932 3.
1256 AA; 137384 MW;
                                                                                                                                                                        al Similarity 22.3
105; Conservative
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1256
775
1256
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932
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                                                                                                                                                      Query Match
Best Local
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Q62010;
                                                                                                                                                                                          Matches
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OGP_MOUSE
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SWART, SM00644, Ami 2; 1. SWART; SM00047, LYZ2, 1. Cell wall; Hydrolase; Signal; Multifunctional enzyme; Repeat.

InterPro, IPR002502; Amidase 2.
InterPro, IPR002901; Amidase 4.
Pfam; PF01510; Amidase 2; 1.
Pfam; PF01832; Amidase 4; 1.

EMBL; D17366; BAA04185.1; -.

POTENTIAL

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SLAP
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           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                         FIGHNSPLFSLPEDSKSSAYAMNYWRKLGTPADKLIMGFPTYGRNFYLLKESKNGLQTAS 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----YVPYAFKGKEMLG--YDDTISFSYKAMYVKREHFGGAMVWTLDMDDVRGTFC 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                 EGPONPONYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---FSWNGMALNPDNYLISKDVTGATKV-----KYYYAVNDGFPGDHYAVM-ISKTGTNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 GNGPFPLVHILNELLVQTESNSTPLPQFWFTSSVNASGPGSENTALTEVLTTDTIKILPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       428 GGEAMTTEVHRRYENMTTVPSDGS-----VTPGGTASPRKHAVTPENNTMAAEAKTMST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   482 LDFFSKTTTGVSKTTTGVSKTTTGVSKATAGISKTIPEISKATAGVSKTTTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 VLTAKTVVTAPBAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 HGEAPA-----EWITIDADGDGQGWLCLSSGQLGWLTAHGGT---NVVAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 GDFTVVFBETPNGINKGGARFGLSTEADGAKPQSVWIER-TVDLPAGTKYVAFRHYNCSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542 SKTTIGISKTITGVSK--TITGISKTITGISKTITGVSKITIGVSKTITGISKTITGISK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                649 MDHQSVTPTEMDTTLFYLKTMTDSEKETSRKKTMVLEKATVSPREMSATPN-----GQS
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                      POTENTIAL.

OVIDUCT-SPECIFIC GLYCOPROTEIN.

21 X 7 AA TANDEM REPEATS OF S-K-T-T-
[TAP] -G-[IV].

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---EIKANGKRAD---FTETFESST---
                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 0.28; 55; Mismatches 185; Indels 202;
                                                                                                                                                                                                                                                                                                                                     5.1%; Score 126; DB 1; Length 721; 18.9%; Pred. No. 0.28;
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                                                                                                                                                                                                                                                                                                              37246C8F01665652 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 MGPASPGKY----TKQAGFLAYYEVCSFVQRAKKHWIDYO
                                                                                                                      MGD; MGI:106661; Ovgpl.
InterPro; IPR001223; Glyco_hydro_18.
InterPro; IPR001223; Glyco_hydro_18.
Fean: PF00704; Glyco_hydro_18; 1.
ProDom; P0000471; Glyco_hydro_18; 1.
SWART; SW00636; Glyco_18; 1.
PROSITE; PS01095; CHITINASE_18; FALSE_NEG.
Glycoprotein; Fertilization; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                             Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                   FAGHNSAICA----SSASYINF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 404 GNHEYCVEVK-----YTAGVSPKE-
                                                                                                                                                                                                                                                                                                            78807 MW;
                                                                                                          EMBL; D32137; BAA06863.1; -.
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                          721 AA;
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103; Conserv
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Best Local
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RESULT 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 LASSKKSADYFRAYGVKTTNRGSVYYRVVTMDGKYRGYVYG-----GKSDTAFAGGI-- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---TSTDGTKAGSKVSDKAADQTALEAYINANKPSGYTVTNPNAA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --YTVY 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382 RDGTKIKEGLTETTFE------EDGVATGNHEYCVEV-----KYTAGVSPK 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTLSESFEN-GIPASWKTIDA----DGDGNNWTTTPPPPGGTSFAGHNSALCASSASYIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 EVLTAKTVVTAPEAIRGTRVQGTWYQKTVQ----LPAGTKYVAFRHFGCTDFFWINLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 VSLYGVAKDTKFTVDQAATKTREGSLYYHVTATNGSGISGWIYAGK---GFSTTATGTQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTASAKSYATAGAYSTLKTDAATRNVEATGTNALYTKP--GTV---KGAKVVASKATMAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 FEGPONPONYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALLE
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=33054358; PubMed=1429463; Vidgren G., Palva A.; Vidgren G., Palva I., Pakkanen R., Lounatmaa K., Palva A.; Vidgren G., Palva I., Pakkanen R., Lounatmaa K., Palva A.; "S-layer protein gene of Lactobacillus brevis: cloning by polymerase chain reaction and determination of the nucleotide sequence."; J. Bacteriol. 174:7419-7427(1992)
-!- FUNCTION: The S-layer is a paracrystalline mono-layered assembly of proteins which coat the surface of bacteria.
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 VEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDG-QGWLCLSSGQLGWLTAHGGTNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GTQVGSNTWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201; Indels 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-layer with tetragonal symmetry.
-!- SIMILARITY: SOME, TO THE S-LAYER PROTEIN OF L.ACIDOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 465;
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                                                                                                                                                                                                                Bacteria, Firmicutes, Lactobacillales, Lactobacillaceae,
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 FEETPNGINKGGARFGLSTEADGAKPOSVWIERTVDLPAGTKYV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48159 MW; 2BE2403392E65A2C CRC64;
                                                                                                                                            S-layer protein precursor (Surface layer protein).
                                                    (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 LGGLSTDK-----SVTATNDNSVKIVYRTTD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 121.5; Di
Pred. No. 0.32;
         Z
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                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-ATCC 8287 / DSM 20556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal; Glycoprotein; Cell wall; S-layer.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z14250; CAA78618.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99; Conservative
   STANDARD;
                                                                                                                                                                                      Lactobacillus brevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A47023; A47023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                  NCBI_TaxID=1580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 ----
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01-JUN-1994 (
01-OCT-1994 (
LACBR
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PROSITE; PS00561; CED BACTERIAL; 1.
Cellulose degradation; Hydrolase; Glycosidase; Repeat; Signal.
SIGNAL 33

SIGNAL PROPEP CHAIN DOMAIN DOMAIN

InterPro; IPR003961; FN III.
InterPro; IPR000356; Glyco\_hydro\_48.
InterPro; IPR000556; Glyco\_hydro\_48.
InterPro; IPR000528; CBM\_2; 1.
Pfam; PF00553; CBM\_2; 1.
Pfam; PF002011; Glyco\_hydro\_48; 1.
PRINTS; PR00841; GLHFDRLASE48.
ProDom; PD011903; Glyco\_hydro\_48; 1.
SMART; SM00637; CBD\_II; 1.

FN III-like.

EXOGLUCANASE B.

```
MEDLINE=94197708; PubMed=8147863;

RA Shen H., Tomme P., Weinke A., Gilkes N.R., Kilburn D.G.,

RA Shen H., Tomme P., Meinke A., Gilkes N.R., Kilburn D.G.,

RA Warren R.A.J., Miller R.C. Jr.;

R. Cerecochemical course of hydrolysis catalysed by Cellulomonas fimi

R. Cens, a member of a new family of beta-1,4-glucanases.";

R. Sichen. Biochbys. Res. Commun. 199:1223-1228(1994).

C. -! FUNCTION: Hydrolyze cellohexaose to amixture of cellotetraose, and

cellotriose and cellobiose, with only a trace of glucose. It

hydrolyzed cellopiose, with only a trace of glucose. It

cellotetraose to cellobiose, unit id did not hydrolyze cellotriose.

CC cellotetraose to cellobiose, but it did not hydrolyze cellotriose.

CC Has also weak endoglucanase activity. Hydrolyzes glucosidic bonds

CC with inversion of anomeric configuration.

CC -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages

in cellulose and cellotetraose, releasing cellobiose from the non-

CC -!- SIMILARITY: Contains 3 fibronectin type III domains.

CC -!- SIMILARITY: Contains 1 bacterial-type cellulose-binding (CBD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
| | | : : | : | | | | | | | | | | 369 AAGTKIAQLTTDLGERGQVVTLTAIDTDLEDATFTGTTTYYSDLGKAYHYTYTYNKDSA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 54-75.

MEDLINE=93209933; PubMed=8458833;

Meinke A., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;

"Cellulose-binding polypeptides from Cellulomonas fimi: endoglucanase D (CenD), a family A beta-1,4-glucanase.";

J. Bacteriol. 175:1910-1918(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO CELLULASE FAMILY L (FAMILY 48 OF GLYCOSYL HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Warren R.A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-AICC 484, MEDLINE-96003898; PubMed=7575482; Shen H. Gikkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R. "Cellobiohydrolase B, a second exo-cellobiohydrolase from the cellulolytic bacterium Cellulomonas fimi."; Biochem. J. 311:67-74(1995).
                                                                                                                                                                                                                                        -0CT-1996 (Rel. 34, Created)
-0CT-2096 (Rel. 34, Last sequence update)
-0CT-2003 (Rel. 42, Last annotation update)
coglucamase B precursor (EC 3.2.1.91) (Exocellobiohydrolase)
                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Cellulomonadaceae; Cellulomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 456-461.
                                                                                                                                                                                                            PRT; 1090 AA.
                                                             422 ECVNVTVDPVQFNPVQNLTGS 442
                                                                                                   ASSNAS---TOFG--SNVTGT 444
                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  Cellulomonas fimi
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1708;
                                                                                                                                                                                                                                                                                                       Exoglucanase B
                                                                                                                                                                                                                                          01-0CT-1996 (
01-0CT-1996 (
10-0CT-2003 (
                                                                                                                                                                                                                                                                                                                                             CENE
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SEQUENCE OF
                                                                                                                                                                                                      GUXB CELFI
                                                                                                   429
                                                                                                                                                                                                                                                                                                                                             CBHB OR
                                                                                                                                                                                 GUXB_CELFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 VTAPBAIRGTRVQG-----TWYQKTVQLPAGTKXVAFRHFGCTDFFWINLDD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              620 IYIPSGWIGIWPNGDVIKPGVSFLDIRSFYKKD---PNWSKVQIFLDGGAEPQFRYHRFW 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 TVVFEETPNGINKGGARFGLSTEA---DGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDL 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               767 İVRAFDAAGNVSAPSAALIVITKAIPSDITIAP-----SVPALIS-----SSTA 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 NYILLDDIQFTMGGSPTPTDYT-----YTVYRDGTKIKEGLTETTFEEDGV-ATGNHE 407
                                                                                                                                                                                                                                                                                                                                                                                                                        26 ASWKT---IDADGDGNNWTTTPPPGG-----TSFAGHNSAICASSASYINFEGPQNPD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                             574 TASRDKAKALLD----ALWANNQDP-----LGVSAVETRGDYKRFDDTYVAN----GDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 VEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGWLCLSSGQLGWLTAHGGINVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        677 AQTAVAGALADYARLFDDGT-----TTPDTTAP----TVPTG----LQAGVVTSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 ASFSWNGMALNPDNYLISKDV-TGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGD---F
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        911 NSV-----TIGWSAS-TDNAGGSGLAGYDVYRGATRVAQ-TTALTFTDTGLTASTAYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry5Aa (Insecticidal delta-endotoxin
CryVA(a)) (Crystaline entomocidal protoxin) (152 kDa crystal protein).
CRYSAA OR CRYVA(A) OR CRYVA.
Bacillus thuringiensis (subsp. darmstadiensis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 YCVEVKYTAG--VSPKECVNVTV-----DPVQFNPVQNLTGSAVGQ-KVTLKWDA 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                862 YTVRARDVÅGNVSAPSTAVSVTTKSDTTPDTTAPSVPAGLAAMTVTETSVALTWNA 917
                                                                                                                                                                                                                                CATALYTIC (BY SIMILARITY).
FIBRONBCTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
CELLUCOSE-BINDING (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                  120;
                                                                                                                                                                                                                                                                                                                                                               4.9%; Score 121; DB 1; Length 1090; 22.3%; Pred. No. 1.1; tive 53; Mismatches 197; Indels 12:
                                                                                                                                                                                                                                                                                                                                       046BB9D956F2F399 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1385 AA
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989 1090 CELLU
513 NUCLE
990 1089 BY SI
1090 AA; 114629 MW; C
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106; Conservative
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1090
699
785
884
978
1090
513
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Best Local S:
Matches 106
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DISULFID
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HSSP, P07986, IEXG. InterPro, IPR001919, Bac\_celose-bind. InterPro, IPR008965, Cellul\_bind.

EMBL; L38827; AAB00822.1; -.

S59077; S59077.

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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001919;
InterPro; IPR008965;
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                          Cellulomonas fimi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1EXG
                                                                                                                                                                                                                                             NCBI_TaxID=1708;
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                                                                                                                                     01-OCT-1996
01-OCT-1996
                                                                                                                GUXA CELFI
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                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAVDÉQAGPNYVSIDSSNPIIQINMDTWKTPPQGASG--WNTNLMRGSVSGLSFLQRDGT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471 RLSAGMGGGFADTIXSLPATHYLSYLYGTPYQTSDNYSGHVGALVGVSTPQEATLPNIG 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GGTLT-FWVCAQDA------NYASEHYAVYAS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     531 QPDEQGNVSTWGFPFEKASYGGTVVKEWLNGANAMKLSPGQSIGIPITNVTSGEYQIRCR 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STGNDASNF-----ANALLEEVLTAKTVVTAPEAIRGTRVQG-----TWYQ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             645 SFTEIPAKTINVHLTNQGSSDVF---LDRIEFIPFSLPLIYHGSYNTSS-GADDVLW--- 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 DADGDGQGWLCLSSGQLGWLTAHGGTNVVASFSWNGMALNPDNYLLSK-----DVTGA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 TKVKY-YYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLSTEADGA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
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                                                                                                                DEVELOPMENTAL STACE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 PNPNPNPGTITLSESFENGI----PASWKIIDADGDGNNWTITPPPG---GISF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TALB-ETSLPN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 KTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIKANGKRADFTETFESSTHGEAPPAEWTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 KPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSPTPT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------FSLSGSDHTTIYHGKLETGIH
                                                                                                                                                  MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Length 1385;
                               SEQUENCE FROM N.A.
STRAIN-NRRL B-18243 / PS17;
Sick A.J., Schwab G.E., Payne J.M.;
"Genes encoding nematode-active toxins cloned from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
  Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                     1385 AA; 152439 MW; E29FF11FC799DE95 CRC64;
                                                                                                                                                                        SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                     FUNCTION: ENDOTOXIN WITH NEMATICIDAL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EED-
                                                                                                                                                                                                                                                                                                                                                                                                         4.8%; Score 118.5; DB 1; 20.1%; Pred. No. 2.2; ative 66; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----AGHNSAICASSA----SYINFEGPONPDNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---DYTYT-----VYRDGTKIKEGLTETTF-
                                                                              thuringlensis isolate PS17.",
Patent number US5281530, 25-JAN-1994.
                                                                                                                                                                                                                                                                                                                             InterPro; IPR005639; endotoxin_N.
InterPro; IPR008979; Gal bind like.
Pfam; PF03944; endotoxin_C; 1.
Pfam; PF03945; endotoxin_N; 1.
                                                                                                                                                                                                                                                                                                                InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _
<u>:</u>
                                                                                                                                                                                                                                                                                         EMBL; L07025; AAA67694.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                    PIR, T18213, T18213
                                                                                                                                         the spore coat
                                                                                                                                                                                                                                                                                                                                                                        Toxin; Sporulation
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                     -----SFSVRAKDVAGNTSAASAVSATTQTGTVVDTTAPSVPTGLTAGTTTTSSV 691
                                                                                                                                                                                                                                                                                                                                                                                                         PAEWITIDADGDGQGWLCLSSGQLGWLTAHGGTNV--VASFSWNGMALNPDN----YLIS 260
                                                                                                                                                                                                                                                                                                                                                                                                                                              KDVTG-----ATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINK-G 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDVAGNVSAASAAVSARIQAAISGG-----CTVKYSASSWNIG-FIGIVEVKNNGIAALN 799
                                                                                                                                                                                                                                                        77
                                                                                                                                                                                                                                                  12 GTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSALCASSASYINFEGP
                                                                                                                                                                                                                                                                                                                                ---EAIRGTRVQGTW----YQKTVQLPAGTKYV
                                                                                                                                                                                                                                                                                                                                                                                                                        PLTWT---ASTDNAG----GSGVAGYEVFNGTTRVATVTSTSYTVTGLAADTAYSFTVKA
                                                                                                                                                                                                                                                                                                                                                                         ---SSTHGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                    PROSITE; PS00561; CBD BACTERIAL; 1.
PROSITE; PS00655; GLYČOSYL_HYDROL_F6_1; 1.
PROSITE; PS00656; GLYCOSYL_HYDROL_F6_2; 1.
Cellulose degradation; Hydrolase; Glycosidase; Repeat; Signal.
SIGNAL
                                                                                                                                    CELLULOSE-BINDING (BY SIMILARITY)
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                  29; Mismatches 146; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
                                                                                                                                                                                                                                                                      GTTTAT----SVPLSW---TASTDNVAVTGYDVYRGTTLVGTTAA----
                                                                                                                                                                                                                 DB 1; Length 872;
                                                                                                                                                                                             7883B407F995533B CRC64;
                                                                                               CATALYTIC.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
                                                                                                                                                                                                                                                                                                                                                                    AFRHFGCTDFFWINLDDVEIKANGKRADFTETFE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TECC. STANDARD; PRT; 2660 AA. 08X807; Q8X2B9; Q8X2C0; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last sequence update) Hypothetical protein yeeJ. 28-FEB-2003 (Rel. 41, Last annotation update) 23-135 OR ECS2775/ECS2776.
                                                                                     EXOGLUCANASE A.
                                                                                                                                                                                                                Score 114; DB
Pred. No. 2.4;
                                                                                                                                                                SIMILARITY.
SIMILARITY.
SIMILARITY.
            'n
        Prodom; PD003733; Glyco hydro 6;
SMART; SM00637; CBD II; 1.
SMART; SM00060; FN3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 GARFGLSTEADGAKPOSVW 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      799 GWTLGFSF-ADGQKVSQGW 816
                                                                                                                                                                                            89300 MW;
 PRINTS; PR00733; GLHYDRLASE6
                                                                                                                                                                                                              4.6%;
                                                                                                                                                                                                                                92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli 0157:H7.
                                                                                     872
477
563
664
768
872
188
                                                                                                                                                                                                                                                                                                                               LTAKTVVTAP--
                                                                                                                                                                                            872 AA;
                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                            529
                                                                                                                                           ACT SITE
                                                                                                                                                                                                                                                                                         72
                                                                                                                                                                                                                                                                                                                              130
                                                                                                                                                                                                                                                                                                                                                                                       641
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                                                                                                                                                                       DISULFID
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                                                                                                                                                                                   DISULFID
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                                                                                                                                                                                                               Query Match
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                                                                                                                          DOMAIN
                                                                                             DOMAIN
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                                                                                    CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPQNPDNYLVTPELSLPNGG----TLTF---WVCAQDANYASEHYAVYASSTGNDASNF 121
                                                                                                                                                                                                                                                                       Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T.-T. Tanaka M., Tobe T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Gasawara N., Yasunaga T., "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTLSESFE---NGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASYINFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."; "Mature 409:529-533 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58; Mismatches 199; Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 16 Big-1 domains.
-!- SIMILARITY: Belongs to the intimin/invasin family.
-!- CAUTION: Ref.2 sequence differs from that shown due to a frameshift in position 1315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280062 MW; 01EB92A08F5C09D2 CRC64;
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Pred. No. 1
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InterPro; IPR00355; Intimin.
InterPro; IPR008964; Invasin_intimin.
InterPro; IPR008061; PKD.
Pfam; PR02369; Big.1; 16.
SMART; SM00634; BID 1; 16.
SMART; SM00634; BID 1; 16.
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EMBL; AP002559; BAB36199.1; ALT_FRAME.
                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed=11258796;
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Matches 114; Conservative
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                                                                                                                         TATKAGVYQVTATLENGDSMQQTVTYVPNVANAEISLAASKDPV-----IANNNDLTTL 1780
ANALLBEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYYVAFRHFGCTDFFWINLD 181
                                                                                                                                                                                           241 V---VASFSWNG-----MALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISK 290
                                                                                                                                                                                                                                                                                        TGTNAGDFTVV-----FEETPNGI-NKGGARFGLSTEADGAKPQSVWIERTVDLPAG 341
                                                                                                                                                                                                                                                                                                                                                                                      342 TKYVAFRHYNC---SDLNYILLDDIQ--FTMGGSPTPTDYTYTVYRDGTKI---KEGLTE 393
                                           -----VITATVVDNNGFPVKGVTVNFTSNAATAEMTNGGQAVTNEQGKATVTYTNTRS
                                                                                           182 DVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQ-GWLCLSSGQLGWLTAHGGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-galactose residues in beta-D-galactosides.
-!- SIMILARITY: Belongs to family 2 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1827 VTLK--GTKAGAH--TVTASMAGGKSEQLVVNFIADTLTAQVNLNVT 1869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 TIFEEDGVATGNHEYCVEVKYTAGVSPKECVNVTVDPVQFNPVQNLF 440
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15-DEC-1998 (Rel. 37, Last annotation update)
Beta-galactosidase (EC 3.2.1.23) (Lactase).
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InterPro; IPRO06101; Glyco hydro 2.
InterPro; IPRO06102; Glyco hydro 219.
InterPro; IPRO06104; Glyco hydro 219.
InterPro; IPRO04200; Glyco hydro 27IM.
InterPro; IPRO04109; Glyco hydro 42C.
InterPro; IPRO04199; Glyco hydro 42C.
InterPro; IPRO04199; Glyco hydro 42N.
Pfam; PF0230; Bgal small 7; 1.
Pfam; PF0230; Bgal small 7; 1.
Pfam; PF0230; Glyco hydro 2; 1.
Pfam; PF0230; Glyco hydro 2. C; 1.
Pfam; PF02307; Glyco hydro 2. N; 1.
PRINTS; PR00132; GLHYDELASE2.
PROSITE; PS00719; GLYCOSYL HYDROL F2 1; 1.
PROSITE; PS00719; GLYCOSYL HYDROL F2 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        send an email to license@isb-sib.ch).
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HSSP; P00722; 1BGL.
InterPro; IPR008979; Gal_bind_like.
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15-DEC-1998 (Rel. 37, Last seq
15-DEC-1998 (Rel. 37, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---YASSIGNDASNFAN--ALLEEVLTAKTVVTAPEAIRGTRVQG----TWY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          796 RP-NFW-RAVTDNDLGNKL----HERCQTWRQASLEQHVKKVTVQPQVDFVII-SVELAL 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PILOGGFIWDWK 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKTVQLPA--GTKYVAF-RHFGCT----DFFWINLDDVEIKANGKRADFTETFESSTHGE 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636 -PVKWTAVDP-----AKGKFAVQNKHLFTNLNAYDFVWTVEKNGELVEKHASILN 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 -YYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLSTE----ADGA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       745 SVKAAHPALTVDQNEQTLTVTGTN---FTAIFDK-----RKKGOFISYNYERTELLASGF 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- DLNYILLDDIQFTM 367
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                                                                                                                                                                                                                                                                                                                                                   432 GTWIYLQEGEQKAVPGSKPEWKENVLDRCRSMYERDKNHPSIIIWSL----GNESFGGEN
                                                                                                                                                                                                                                                                                12 GT-TTLSESFENGIPAS---WK--TIDA----DGDGNN-----WTTTPPPGGTSFAGHN
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MEDLINE=95272392; PubMed=7752895;

Heyer L.L., Scherer S., Shatzman A.R., Livi G.P.;

"Candida albicans ALSI: domains related to a Saccharomyces cerevisiae sexual agglutinin separated by a repeating motif.";

Mol. Microbiol. 15:39-54 (1995).

-! FUNCTION: MAY PLAY A ROLE IN ADHESION AND PATHOGENESIS.
-!- PTW: N-91ycosylated and O-glycosylated (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    582 DQALQATAEDGISYLAYGGDFGDTPNDGNFCGNGLIFADGTASPKIAEVKKCYQ-
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                  221;
                                                                                                                                            Length 1034;
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                                                                                                                                 1 4.5%; Score 112.5; DB 1; Length 1 Similarity 19.9%; Pred. No. 3.9; L4; Conservative 70; Mismatches 169; Indels
481 481 PROTON DONOR (BY SIMILARITY).
547 547 NUCLEOPHILE (BY SIMILARITY).
1034 AA; 118673 MW; 38644C9A649415E9 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
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EMBL; U34842; AAB02987.1; -.
EMBL; U44804; AAC83385.1; ALT_FRAME.
PIR; T18346; T18346.
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                                                                                                                                                                                                                                                                                                                        MEDLINE=93371270; PubMed=8363503;
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                                                                                                                                                                  Mycoplasma gallisepticum
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                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
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         ----SQSYA 593
                                                                                                                            ---GGTDTV-----IIREPPNHTV 618
                                                         200 SSTHGEAPAEWTIDADGDGQGWLCLSSGQLGWLTAHGGTNVVASFSWNGMALNPDNYLI
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Q49379; Q49437; Q53351;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last aquence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Adhesin Pl precursor (Cytadhesin Pl) (Attachment protein)
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Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
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Y -> F (IN REF. 3).
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Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
                                                                                                                                                                         Indels 131;
                                                                                                                                Length 1122;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Pectinesterase precursor (EC 3.1.1.11) (Pectin methylesterase)
  I -> T (IN REF. 3).
R -> G (IN REF. 3).
T -> A (IN REF. 3).
DIL -> VYT (IN REF. 4).
WW; 155C34DA2D6C3C65 CRC64;
                                                                                                                                             19.0%; Pred. No. 5.., tive 77; Mismatches 193;
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VTFGEY 290

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entry is copyright. It is produced through a collaboration
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                                                                                                       or send an ema...

R EMBL; U49378; AAB42153.1; -.

R EMBL; U49378; AAB42153.1; -.

R INGENTE; PRO00070; Pectinesterase.

DR PROSITE; PS00800; PECTINESTERASE 1; 1.

DR PROSITE; PS00503; PECTINESTERASE 2; 1.

R Hydrolase; Aspartyl esterase; Cell wall; Signal.

FT SIGNAL 1 17 BY SIMILARITY.

FT CHAIN 18 331 PECTINESTERASE.

"" SITE 162 BY SIMILARITY.

"" SITE 162 BY SIMILARITY.

"" 1: Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              4.4%; Score 109.5; 22.5%; Pred. No. 1.4
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May 18, 2004, 11:36:20 ; Search time 33.3368 Seconds (without alignments) 4315.838 Million cell updates/sec
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1 GTRNPNPNPNPGTTTLSESF.....QNLTGSAVGQKVTLKWDAPN 456
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                             of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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sp_mammal:*
sp_mhc:*
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sp_bacteria:*
sp_fungi:*
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_unclassified:\*

sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\*

sp\_virus:\*
sp\_vertebrate:\*

sp\_rodent: \*

sp\_organelle:\*
sp\_phage:\*
sp\_plant:\*

|           |        | Description     | comonydanor 791279 |        |        |        |        |        |        | nomorphise porprovenou | Q9znb5 porphyromon | P72196 northuron |        |        | Coron porpulation | OS2050 porphyromon |        | Colline of the Colline | Cavity porphyromon | Caxona borbhyromon | Q8p377 xanthomonas |
|-----------|--------|-----------------|--------------------|--------|--------|--------|--------|--------|--------|------------------------|--------------------|------------------|--------|--------|-------------------|--------------------|--------|------------------------|--------------------|--------------------|--------------------|
| SUMMARIES |        | ΙD              | P72197             | O9R9B7 | 051816 | P72194 | P96967 | 051839 | 051838 |                        | CANAGO             | P72196           | 007442 | 051817 | 21000             | 026020             | Q9F4J0 | O9KTB3                 | 0110700            | KOPKO X            | Q8P377             |
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|           | ,      | Match Length DB | 1723               | 1687   | 1704   | 1723   | 1358   | 1706   | 1706   | 1723                   | 1225               | 1097             | 1732   | 1732   | 1733              | 4014               | 925    | 312                    | 203                | 1                  | 1742               |
| dł        | Query  | Match           | 84.4               | 84.0   | 84.0   | 83.8   | 83.5   | 83.5   | 83.0   | 0 0                    | 700                | 8.7.Z            | 82.2   | 82.0   | д<br>п            | 1 1                | 51.5   | 22.6                   | 4                  |                    | 7.0                |
|           | ,      | Score           | 2094               | 2082   | 2082   | 2079   | 2071   | 2070   | 2059   | 2054 E                 |                    | 2039.5           | 2039.5 | 2034.5 | 2020.5            |                    | 789    | 561.5                  | 233                |                    | 152.5              |
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| 3346 1            | 1341 1   | -                | 1   | ι <del>-</del> | -          | 1800 2              | Н                         | ~                | 2                 | Н        | 1 1                 | 1115 4 | Н             | 1357 1             | 2468 16 | 2219 16             |        | -                 | -                  | 0                      |       | 7716 16             |       |        | 2656 5             |        | 4936 16 | 1684 2             |  |
| 5.8               | 5.6      | 5.6              | 5.4 | 5.4            | 5.4        | 5.4                 | 5.4                       | 5.4              | 5.4               | 5.3      | 5.3                 | 5.3    |               | ۳.                 | ۳.      |                     |        | 5.3               | 5.2                |                        |       |                     |       |        | 5.2                |        | 5.2     | 5.1                |  |
| 144               | 139.5    | 139              | 135 | 134.5          | 134        | 134                 | 134                       | 133.5            | 133               | 132.5    | 132.5               | 132.5  | 131.5         | 131.5              | 131.5   | 131                 | 130.5  | 130.5             | 130                | 129.5                  | 129.5 | 129                 | 128.5 | 128.5  | 128.5              | 128    | 128     | 127.5              |  |
| 17                | 18       | 19               | 50  | 21             | 22         | 23                  | 24                        | 25               | 26                | 27       | 28                  | 29     | 30            | 31                 | 32      | 33                  | 34     | 35                | 36                 | 37                     | 38    | ďς<br>Θ             | 40    | 41     | 42                 | 43     | 44      | 45                 |  |
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## ALIGNMENTS

84.4%; Score 2094; DB 2; Length 1723; 86.2%; Pred. No. 6.8e-128;

Query Match Best Local Similarity us-08-570-311-18.rspt

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(TrEMBLrel. 01, Created)
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                                                                             Conservative
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                                                                      1204 NVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFT 1263
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                                                                                                                               SSASY-INFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDAS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDDIQFTWGGSPTPTDYTYTVYRDGTKIKEGLTETTFBEDGVATGNHBYCVEVKYTAGVS 419
                                                 9
                                        GTPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICA
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      Gaps
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"Cloning and characterization of hagE from P. gingivalis 381.";

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

R HSP; P95493; ICVR.

RRACDS 946; AADD1810.1; -.

RRACDS; C25.001; -.

RGO; GO:000524; F:ATF binding; IEA.

GO; GO:000524; F:ATF binding; IEA.

GO; GO:0005210; P:DNA recombination; IEA.

GO; GO:00062810; P:DNA repair; IEA.

GO; GO:00062810; P:DNA repair; IEA.

GO; GO:00062810; P:DNA repair; IEA.

GO; GO:00062810; P:DNA repair; IEA.

GO; GO:0006281; P:DNA repair; IEA.

RO; GO:0006281; P:DNA repair; IEA.

RO; GO:0006281; P:DNA repair; IEA.

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RO; GO:0006281; P:DNA repair; IEA.

RO; GO:0006281; P:DNA repair; IEA.

RO; GO:0006281; P:DNA repair; IEA.

RITHERPO; IPRO0110; GJ:Ike.

RITHERPO; IPRO0110; GJ:Ike.

RITHERPO; IPRO01769; Peptidase_C25.

RR Pfam; PF01785; Peptidase_C25.

RR Pfam; PF01785; Peptidase_C25.

RR Pfam; PF01785; Peptidase_C25.

RR Pfam; PF01785; DNA_LIGASE_A1; 1.

PROSITE; PS00697; DNA_LIGASE_A1; 1.
      . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||:|||||::| |||||:
1384 PKKCVNVTINPTQFNPVKNLKAQPDGGDVVLKWEAPS 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420 PKECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
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Last annotation update)
    40;
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17; Mismatches
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Matches 394; Conservative
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                                                                                                                                                                          991
                                                                                                                                             3 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASS
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                                                                  Gaps
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J. Biol. Chem. 2701007-1010(1995).
BIOL. Chem. 2701007-1010(1995).
PIR; A55426; A55426.
HSSP; P95429; ICVR.
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MEDLINE-95113080; Pubmed=7836351;
MEDLINE-95138080; Pubmed=7836351;
Pavloff N., Potempa J., Pike R.N., Prochazka V., Kiefer M.C.,
Travis J., Barr P.J.;
"Molecular cloning and structural characterization of the Arg-
84.0%; Score 2082; DB 2; Length 1687; 86.2%; Pred. No. 4e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arg-gingipain-1 proteinase.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria, Bacteroidetes; Bacteroides (class); Bacteroidales;
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MEROPS; C25.001;

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005324; F:ATP binding; IEA.

GO; GO:000310; F:DNA ligase (ATP) activity; IEA.

GO; GO:0006310; F:DNA repair; IEA.

GO; GO:0006501; P:DNA repair; IEA.

GO; GO:0006508; P:DNA replication; IEA.

R GO; GO:0006508; P:DNA replication; IEA.

R GO; GO:0006508; P:DNA replication; IEA.

R GO; GO:0006508; P:DNA rigase.

R InterPro; IPR00077; DNA ligase.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR007109; R-IIR.
                                                            Indels
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                                                   17; Mismatches
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9
                                                                                                                                                                                                                                    Length 1723;
       GO; GO:0006310; P:DNA repair; IEA.

GO; GO:0006281; P:DNA repair; IEA.

GO; GO:0006260; P:DNA replication; IEA.

R GO; GO:0006508; P:Proteolysis and peptidolysis; IEA.

R InterPro; IPR001769; Peptidase.

R InterPro; IPR001769; Peptidase.

R InterPro; IPR00184; Peptidase.

R Pfam; PF01364; Peptidase.

R Pfam; PF03185; Peptidase.

R Pfam; PR03185; Peptidase.

R PROSITE; PS00699; DNA 187261 MW; 5628963D251493EB CRC64;
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                      Indels
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1384 PKVCVNVIINPIQENPVKNIKAQPDGGDVVLKWEAPS 1420
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Last annotation update)
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                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                83.8%; Score 2079; DB 2;
85.8%; Pred. No. 6.4e-127;
ive 17; Mismatches 42;
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Matches 392; Conservative
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01-MAY-1997 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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"Cloning and Sequencing of the gene encoding a novel lysine-specific cysteine proteinase (Lys-gingipain) in Porphyromonas gingivalis: structural relationship with the arginine-specific cysteine proteinase (Arg-gingipain).",
J. Biochem. 120:398-406 (1996).

EMBL; D83258; BAA11870.1;
                                                                                                                                                                                                                                           63 ASY-INFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF
                                                                                                                                                                                                                       PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASS
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InterPro, IPR005536; Peptidase C25_C. Pfam; PF01364; Peptidase C25_C; 1. Pfam; PF037085; Peptidase C25_C; 1. PR081TB; PS00697; DMA LIGASE A1; 1. CHAIN 728
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                                                                                                                                                     DB 2; Length 1704;
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
                                                                                                                                                84.0%; Score 2082; DB 2; Length 1
86.2%; Pred. No. 4e-127;
ive 17; Mismatches 40; Indels
                                                                                             GINGIPAIN.
1704 AA; 185436 MW; 6A34B40131C2A676 CRC64;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008234; F:Cysteine-type peptidase activity; IEA.
GO; GO:0003910; F:DNA ligase (ATP) activity; IEA.
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                                                                                                                                                                                   392; Conservative
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                                                                                                              SEQUENCE
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Best Local &
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P72194

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Biophys. Res. Commun. 207:424-431(1995)
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Best Local Similarity 85.7°
Matches 390; Conservative
                                                              FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYIL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    898
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                                                                                                                                                                                                                                                                                                                                                                                         GTPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSASY-INFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGDWLCLSSGGLDWLTAHGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 LDDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVS
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95160709; PubMed=7857299; Rirszbum L., Sotiropoulos C., Jackson C., Cleal S., Slakeski N., Rirszbum L., Sotiropoulos C., Jackson C., Cleal S., Slakeski N., Reynolds E.C.; "Complete nucleotide sequence of a gene prtR of Porphyromonas gingivalis W50 encoding a 132 kba protein that contains an argininespecific thiol endopeptidase domain and a haemagglutinin domain.";
                                                                                                                                                                                                                                                                                                                                                            ;
9
                                                                                                                                                                                                                                                                                                                  Length 1358;
GO; GO:0006310; P:DNA recombination; IEA.

GO; GO:0006281; P:DNA repair; IEA.

GO; GO:0006280; P:DNA replication; IEA.

GO; GO:0006508; P:Proteolysis and peptidolysis; IEA.

InterPro; IPR000977; DNA ligase.

R InterPro; IPR001536; Peptidase.

R InterPro; IPR001536; Peptidase.

R InterPro; IPR001536; Peptidase.

R InterPro; IPR001536; Peptidase.

R Pfam; PF01364; Peptidase.

R Pfam; PF01364; Peptidase.

R SMART; SM00060; PN3; 1.

R SMART; PS00697; DNA LIGASE A1; 1.

R SEQUENCE 1358 AA; 147102 MW; 47FCA0B25B06DED8 CRC64;
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                          43; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Arginine-specific thiol protease precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PKECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
                                                                                                                                                                                                                                                                                                         83.5%; Score 2071; DB 2;
85.6%; Pred. No. 1.6e-126;
iive 17; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1706 AA
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                                                                                                                                                                                                                                                                                                                             Best Local Similarity 85.6
Matches 391; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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MEDILINE=96311339; PubMed=8713096; Slakeski N., Cleal S.M., Reynolds B.C.; Characterization of a Porphyromonas gingivalis gene prtR that an arginine-specific thiol proteinase and multiple adhesins."; Biochem. Biophys. Res. Commun. 224:605-610(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.5%; Score 2070; DB 2; Length 1706;
85.7%; Pred. No. 2.5e-126;
Live 18; Mismatches 41; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=WSO;
Slakeski N.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; L26341; AAC18876.1; -.
HSSP; P95493; 1CVR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
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GG: GG:0008234; F:Cysteine-type peptidase activity; IEA.
GG: GG:0008234; F:Cysteine-type peptidase activity; IEA.
GG: GG:0006281; P:DNA ligase (ATP) activity; IEA.
GG: GG:0006281; P:DNA repair; IEA.
GG: GG:0006281; P:DNA replication; IEA.
GG: GG:0006280; P:DNA replication; IEA.
GG: GG:0006280; P:Porteclysis and peptidolysis; IEA.
InterPro; IPRO007710; IG-like.
InterPro; IPRO01769; Peptidase.
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VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV 301
                                                                                                                                                                                                            FEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYIILD
                                                                                                                                                                                                                                                                                                               DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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U. Biol. Chem. 274:5012-5020(1999).

EMBL; ABOID3963; BAA3441.1;
EMBL; ABOID3963; BAA3441.1;
EMBL; ABOID3963; BAA3441.1;
EMBL; ABOID3963; BAA3441.1;
EMBL; ABOID3963; BAA3441.1;
EMBC; GO:0006234; F:ATP biding; IEA.

GO; GO:00062310; F:DNA ligase (ATP) activity; IEA.

GO; GO:0006281; P:DNA repair; IEA.

GO; GO:0006280; P:DNA replication; IEA.

EMBC; GO:0006260; P:DNA replication; IEA.

InterPro; IPR000977; DNA ligase.

InterPro; IPR001769; Peptidase C25.

InterPro; IPR00556; Peptidase C25.

Fram; PF01364; Peptidase C25.

R PFam; PF01364; Peptidase C25.

R PROSITE; PS00697; DNA_LIGASE_A1: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
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Pred. No. 1.6e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1223 AA
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85.28; Pred. No. 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rangarajan M., Aduse-Opoku J., Slaney J.M., Young K.A., Curtis M.A., "The prpRl and the prR2 arginine-specific protease genes of Porphyromonas gingivalis W50 produce five biochemically distinct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=W50,
MEDLINE=96071894; PubMed=7591131;
Aduse-Opoku J., Muir J., Slaney J.M., Rangarajan M., Curtis M.A.;
"Characterization, genetic analysis, and expression of a protease antigen (PrpRI) of Porphyromonas gingivalis W50.";
Infect. Immun. 63:4744-4754 [1995).
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Bacteria, Bacteroidetes, Bacteroides (class); Bacteroidales;
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720 1262 BETA-ADHESIN.
1706 AA; 185705 MW; 0E56DCD87FDA8CDD CRC64;
                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
1369 KCVNVIVNSTQENPVROLKAQPDGGDVVLKWEAFS 1403
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1.3e-125;
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85.5%; Pred. No. 1.3e
:ive 17; Mismatches
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                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Microbiol. 23:0-0(1997).
EMBL; X82680; CAA57997.1; -.
HSSP; P95493; 1CVR.
                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, 01-MAX-1997 (TrEMBLrel. 03, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                              PRELIMINARY;
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                                        SNFANALLEEVLTAKTVVTAPBAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWI
                                                            NLDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGG
                                                                                                                                                                                            TNVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDF
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Bacteria, Bacteroidetes; Bacteroides (class); Bacteroidales;
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R GO; GO:000524; F:ATP binding; IEA.

GO; GO:0005219; F:Cysteine-type peptidase activity; IEA.

R GO; GO:0005310; F:DNA ligase (ATP) activity; IEA.

GO; GO:0006281; P:DNA recombination; IEA.

GO; GO:0006281; P:DNA replication; IEA.

GO; GO:0006280; P:DNA replication; IEA.

GO; GO:0006508; P:DNA replication; IEA.

R GO; GO:0006508; P:DNA replication; IEA.

R InterPro; IPR001769; Peptidase C25.

InterPro; IPR001769; Peptidase C25.

R Pfam; PF01364; Peptidase C25.

R Pfam; PF01364; Peptidase C25.

R Pfam; PF03785; Peptidase C25.

R Pfam; PF03785; Deptidase C25.

R Pfam; PF03785; Deptidase C25.

R PROSITE; PS00697; DNA LIGASE A1; 1.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Lysine-specific cysteine proteinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    749 SPKKCVNVTVNSTQFNPVQNLTAEQAPNSMDAILKWNAP
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82.2%; Score 2039.5; DB 2;
Best Local Similarity 84.5%; Pred. No. 2.4e-124;
Matches 388; Conservative 18; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oral Microbiol. Immunol. 14:92-97(1999).
EMBL; U75366; AAB60809.1; -.
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NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                         LLDDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGV 418
                                                                                                                                                                                                                                                                 NLDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGG 238
                                TNVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDF 298
                                                                                                                  60 ASSASY-INFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDA 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEDLINE=97386416; PubMed=9244265;
Aduse-Opoku J., Slaney J.M., Young K.A., Muir J., Rangarajan M., Aduse-Opoku J., Slaney J.M., Young K.A., Muir J., Rangarajan M., Curtis M.A.;

"The tla gene of Porphyromonas gingivalis W50: a homologue of the raginine-specific protease precursor (PrpRI) which shares sequence in arginine-specific protease precursor (PrpRI) which shares sequence in Engliarity to Tonb-linked receptors.";

"The tla gene of Porphyromonas gingivalis W50: a homologue of the raginiarity to Tonb-linked receptors.";

"The tla gene of Porphyromonas gingivalis W50: a homologue of the similarity to Tonb-linked receptors.";

"The tla gene of Porphyromonas gingivalis W50: a homologue of the similarity to Tonb-linked receptors.";

"The tla gene of Porphyromonas gingivalis W50: Go. 00019867; Couter membrane; IEA.

"The tla gene of Porphyromonas Acceptors.";

"The tla gene of Porphyromonas gingivalis W60: Go. 00019867; Couter membrane; IEA.

"The tla gene of Porphyromonas gingivalis R60: Go. 0006281; PinA repair; IEA.

"The tla gene of Porphyromonas activity; IEA.

"The tla gene of Porphyromonas gingivalis R60: Go. 0006281; PinA repair; IEA.

"The tla gene of Porphyromonas Activity; IEA.

"The Go. 00006281; PinA repair; IEA.

"The tla gene of Porphyromonas gingivalis R60: Go. 0006281; PinA repair; IEA.

"The tla gene of Porphyromonas gingivalis R60: Go. 0006281; PinA repair; IEA.

"The tla gene of Porphyromonas gingivalis R60: Go. 0006281; PinA repair; IEA.

"The tla gene of Porphyromonas gingivalis R60: Go. 0006281; PinA repair; IEA.

"The tla gene of Porphyromonas gingivalis R60: Go. 0006281; PinA repair; IEA.

"The tla gene of Porphyromonas gingivalis R60: Go. 0006281; PinA repair; IEA.

"The tla gene of Porphyromonas gingivalis R60: Go. 0006281; PinA repair; IEA.

"The tla gene of Porphyromonas gingivalis R60: Go. 0006281; PinA repair; IEA.

"The tla gene of Porphyromonas gingivalis R60: Go. 0006281; PinA repair; IEA.
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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PROSITE; PRO0593; TonB dep Rec; 1.
PROSITE; PS00697; DNA_LTGASE Al; 1.
Membrane; Outer membrane; Receptor; Signal; TonB box.
POTENTIAL.
53
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Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Lat
TonB-linked adhesin precursor.
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01-OCT-2003
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MEDLINE=99235907; PubMed=10219167;
Slakeski N., Cleal S.M., Bhogal P.S., Reynolds E.C.;
"Characterization of a Porphyromonas gingivalis gene prtK that encodes
a lysine-specific cysteine proteinase and three sequence-related
adhesins.";
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SEQUENCE FROM N.A.
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       179 NLDDVEIKANGKRADFTETFESSTHGEAPAEWTŢIDADGDGQGWLCLSSGQLGWLTAHGG 238
60 ASSASY-INFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDA 118
                                                                          TNVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDF 298
                        SNFANALLEEVLTAKTVVTAPBAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWI
                                                                                                  TVVFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYI
                                                                                                                            LLDDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGV
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
                                                                                                                                                            SPKECVNVTVDPVQFNPVQNLTGSAV--GQKVTLKWDAP 455
                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 2034.5; DB 2; Pred. No. 5.2e-124; 19; Mismatches 44;
                                                                                                                                                                                                  PRT; 1732 AA.
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Best Local Similarity 84.31
Matches 387; Conservative
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SEQUENCE FROM N.A.
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01-NOV-1996
01-OCT-2003
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                                                GTPNPNPNPNPNPNPGTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGC
                                                                                                                                     60 ASSASY-INFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDA
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11-Sine specific cysteine protease protease
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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G0; G0:0005524; F:ATP binding; IEA.
G0; G0:0008224; F:Gyteline-type peptidase activity; IEA.
G0; G0:000310; F:DNA ligase (ATP) activity; IEA.
G0; G0:000510; P:DNA recombination; IEA.
G0; G0:0005281; P:DNA repair; IEA.
G0; G0:0005281; P:DNA replication; IEA.
G0; G0:000508; P:Proteolysis and peptidolysis; IEA.
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DR GO; GC.

DR GO; GO:0006310;

DR GO; GO:0006281;

DR GO; GO:0006281;

DR GO; GO:0006280;

DR GO; GO:0006280;

DR InterPro; IPR000176;

DR InterPro; IPR00176;

DR PFI PP03186;

PPpidase C25.

DR PP03186;

PPpidase C25.

DR PP03186;

PPpidase C25.

TR PP03186;

PPpidase C25.

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PPpidase C25.

TR PP03186;

PPPIGASE C25.

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PPPIGASE C25.

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PPPIGASE AI; I.
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Infect. Immun. 66:3035-3042(1998).
EMBL; AF017059; AAC26523.1; -.
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                                                                                                                 969 GTPNPNPNPNPNPGTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGC 1025
                                                                                                                                                                                                          1026 VYSESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWYCAQDANYASEHYAVYASSTGNDA 1085
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                                                                                                                                                                                                                                                          SNFANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWI 178
                                                                                                                                                                    60 ASSASY-INFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ross B.C., Czajkowski L., Hocking D., Margetts M., Webb E., Rothel L., Patterson M., Agius C., Camuglia S., Reynolds E., Barr I.G.; "Identification of vaccine candidates from genomic analysis of Porphyromonas gingivalis."; Bubmitted (ARR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AY007522; AAG24228.1; "InterPro; IRRO, 111.
                                                                              1 GIPNPNPNPNPGT-TILSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAIC
                                                                                                                                                                                                                                                                                  NLDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLDDIQFIMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGV
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=W50; Barr I., Patterson M., Agius C., Rothel L., Margetts M. Hocking D., Webb E.; Patterson M., Agius C., Rothel L., Margetts M. Hocking D., Webb E.; Proprides and nucleic acids."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.5%; Score 682; DB 2; Length 925;
30.2%; Pred. No. 4e-36;
tive 62; Mismatches 132; Indels 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative outer membrane protein PG57.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                       46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        925 AA; 103632 MW; SFF2198D6914DAE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPKECVNVTVDPVQFNPVQNLTGSAV--GQKVTLKWDAP 455
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01-MAR-2001 (TYEMBLrel. 16, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
                  Pred. No. 4.2e-123; ); Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        925 AA
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385; Conservative
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SEQUENCE 925 AA: 10
             Similarity
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             Best Local
Matches 38
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                                                                                              206 APAEWTIIDADGDGQGWLCLSSGQLGW-LTAHGGTNVVASFSWNGM--ALNPDNYLISKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            588 IPEGWILIDADGDNVNW-----DYYPWIMYGHDSEKCIASPSYLPMIGVLTPDNYLVTPR
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                                                                                                                                                           VLTAKTVVTAPBAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDV----
                                                                                                                                                                                                                                                                                             468 PASEPEPVTDFVVSLIENNKGRLKWNYPNGYEPDKTDDKDPLQLAGYNIYANGSLLVHIQ
                                                                                                                                                                                                                                                                                                                                                                                     528 DPTVLEYIDETYSSRDDQVEVEYCVTAVYNDNIESQSVCDKLIYDSQSDIILYEGFEAGS
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EMBL; AF237555; AAF81413.1; -. SEQUENCE 312 AA; 34592 MW; 0D5792C9643A25F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 ADGAKPQSVWIBRTVDLFAGTKYVAFRHYNCSDLNYILLDDI-------
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                                                                                                                                                                                                                                                          -----EIKANG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical outer membrane protein PG27.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.6%; Score 561.5; DB 2; Length 312; 32.8%; Pred. No. 7e-29; Live 23; Mismatches 73; Indels 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 EEDGVATGNHEYCVEVKYTAGV-SPKEC--VNVTV---DPVQ
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Ross B.C.;
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LSESFENG-1PASWKTIDADGDGNNWTTTPPPGG-----TSFAGHNSAICASSASYINF

176; Conservative

Matches

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NYLVTPELSLPNGG--TLTFWVCAQDANYASEHYAVYASSTGNDASNFANALLEEVLTAK 133
                                                          134 TVVTAPBAIRGTRVQGTWYQKTVQLPAGTKYYAFRHFGCTDPFWINLDDVBIKANGKRAD 193
                                                                                                                                                   194 FTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTNVVASFSWNGMALN 253
                                                                                                                                                                                                        254 PDNYLISKDVIGATKVKYYYAVNDGFPGDHYAVMISKIGINAGDFTVVFEETPNGINKGG 313
                                                                                                                                                                                                                                          ----- 172
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STRAIN-W50;
STRAIN-W50;
Hocking D., Webb E.;
W. Gingivalis polypeptides and nucleic acids.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFIS5351; AAD3410.1;
SEQUENCE 293 AA; 32272 NW; CC03EAC241F7FFFI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            OSKBUG;

01-NOV-1999 (TrEMBLrel. 12, Created)

01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

Immunoreactive 32 kDa antigen PG25.

Porphyromonas gingivalis (Bacteroides gingivalis).

Bacteria: Bacteroidetes; Bacteroides (class); Bacteroidales;

Porphyromonadaceae; Porphyromonas.

NCBI_TAXID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.4%; Score 233; DB 2; Length 293
59.0%; Pred. No. 1.7e-07;
tive 7; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                           -----RRAPC----
                                                                                                                                                                                                                                                                                                                                                                                                                  293 AA
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Job time : 35.3368 secs
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Matches 46; Conservative
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May 18, 2004, 11:38:40 ; Search time 14.0888 Seconds (without alignments) 1670.936 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-570-311-18 2480 1 GTPNPNPNPPGTTTLSESF.....QNLTGSAVGQKVTLKWDAPN BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Scoring table: Sequence: Run on:

Total number of hits satisfying chosen parameters: 389414 seqs, 51625971 residues Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued Patents AA:\*
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 14, Appl Sequence 16, Appl Sequence 2, Appl Sequence 29, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 27, Appl Sequence 27, Appl Appl Appli Appli Appli Appl Appl Sequence 20, Sequence 14, Sequence 16, Sequence 18, Sequence 10 Sequence 2, Sequence 2, Sequence 14 Sequence 14 Sequence 18 Sequence 9, Sequence 4, Sequence 4, Description Sequence 27 Sequence 11 Sequence 10 US-08-570-311-18 US-08-570-311-14 US-08-570-311-12 US-08-570-311-22 US-09-482-500A-1 US-08-570-311-22 US-09-490-931-10 US-08-82-324-6 US-09-66-330-10 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-27 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-37 US-08-570-311-3 -08-570-311-29 .08-822-324-18 .08-822-324-9 -08-621-944A-4 US-08-621-944A-3 US-08-945-567D-3 SUMMARIES Query Match Length DB 2222210984321009876 2222221098432210 Result No.

Sequence

| Sequence 30227, A    | Seguence 5434. An   |                  | , IC            | 4                | Sequence 4. Appli | 4               | -                 | 25.8              |                   |                   |                     |                 | , ,-             | Sequence 36. April | Semience 264 Ann  |                  |                 |
|----------------------|---------------------|------------------|-----------------|------------------|-------------------|-----------------|-------------------|-------------------|-------------------|-------------------|---------------------|-----------------|------------------|--------------------|-------------------|------------------|-----------------|
| US-09-252-991A-30227 | US-09-543-681A-5434 | US-09-482-500A-2 | US-08-119-361-5 | US-08-336-308A-4 | US-08-822-324-4   | US-09-490-931-4 | US-08-968-685A-10 | US-09-071-035-258 | US-09-071-035-262 | US-09-071-035-266 | US-09-134-000C-5999 | US-09-066-330-6 | US-08-822-324-19 | US-09-268-347-36   | US-09-071-035-264 | US-09-268-347-48 | US-08-822-324-8 |
| 4                    | 4                   | 4                | Н               | m                | m                 | m               | ო                 | 4                 | 4                 | 4                 | 4                   | 4               | ٣                | 4                  | 4                 | 4                | М               |
| 2736                 | 2315                | 492              | 737             | 737              | 737               | 737             | 2123              | 1638              | 1638              | 1638              | 1747                | 24              | 25               | 2411               | 699               | 2048             | 509             |
| 5.4                  | ы<br>Э.             | ы<br>Б.          | 5.3             | 5.3              | 5.3               | 5.3             | 5.3               | 5.2               | 5.2               | 5.2               | 5.2                 | 5.2             | 5.2              | 5.1                | 5.0               | 5.0              | 4.9             |
| 134.5                | 132.5               | 131.5            | 131.5           | 131.5            | 131.5             | 131.5           | 131.5             | 129.5             | 129.5             | 129.5             | 129.5               | 129             | 128              | 126                | 123.5             | 123.5            | 121             |
| 28                   | 29                  | 30               | 31              | 32               | 33                | 34              | 35                | 36                | 37                | 38                | 39                  | 40              | 41               | 42                 | 43                | 44               | 45              |

## ALIGNMENTS

```
APPLICANT: Progulske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepline, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Han, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
CORRESPONDENCE: 29
ADDRESSE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPRIATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILLING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILLING DATE: 09-DEC-1994
CLASSIFICATION A124

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILLING DATE: 25-JAN-1991
CLASSIFICATION NUMBER: US 07/241,640
FILLING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: WILLICAK, 104
RESTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
NAME: MATCH NUMBER: 16,965
REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
US-08-570-311-18
; Sequence 18, Application US/08570311
Patent No. 5824791
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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61 SSASYINFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 SSASYINFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 DDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 DDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTN
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100.0%; Pred. No. 2.8e-204;
ive 0; Mismatches 0;
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                            PRICE ATTENDANT OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF
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Patent No. 5824791
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 456 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 456; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-570-311-20
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US-08-570-311-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SSASYINFEGPQNPONYLVTPELSLFNGGTLFFWVCAQDANYASEHYAVYASSTGNDASN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 FANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 DDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLIFTTFEEDGVATGNHEYCVEVKYTAGVSP 420
                                                                                                                                                                                                                                                                                                                                                                                                                              SSASYINFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDIQFIMGGSPTPIDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSP 420
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APPLICANT: Prognalske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Tumwasorn, Somying
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Batti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
CORRESPONDENCE. ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         1 GTPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTN
                                                                                                                                                                                                                                                                                                      GTPNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICA
                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                              100.0%; Score 2480; DB 2; Length 456; 100.0%; Pred. No. 2.8e-204; ive 0; Mismatches 0; Indels 0
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 KECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-08-570-311-20
; Sequence 20, Application US/08570311
; Patent No. 5824791
: 456 amino acids
amino acid
                                                                                                                                                                                                                                          Conservative
                                                                               MOLECULE TYPE: protein US-08-570-311-18
                                                               linear
                                                                                                                                                                          Query Match
Best Local Similarity
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                                                        TOPOLOGY:
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APPLICANT: Progulske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Lepine, Guylaine
APPLICANT: Lepine, Guylaine
APPLICANT: Lepine, Marilyn
APPLICANT: Patti, Joseph
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
STREET: 2421 NW. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASYI
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                                                                                                                                                                                                      1370 KECVIVTVDPVQFNPVQNLTGSAVGQKVTLKMDAPN 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                      KECVNVTVDPVOFNPVQNLTGSAVGQKVTLKWDAPN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2436; DB 2;
Pred. No. 1.6e-200;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/353,485

FILING DATE: 09-DEC-1994

CLASSIFICATION ATA:

APPLICATION NUMBER: US 07/647,119

FILING DATE: 25-JAN-1991

CLASSIFICATION NUMBER: US 07/241,640

FILING DATE: 08-SEP-198

APPLICATION NUMBER: US 77/241,640

FILING DATE: 08-SEP-198

ATTORNEY/AGENT INFORMATION:

NAME: Whitlock, Ted W.

REGISTRATION NUMBER: 36,965

REFERENCE/DOCKET NUMBER: 36,965

REFERENCE/DOCKET NUMBER: 36,965

TELECHOME: (904) 375-8100

TELECHOME: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 16, Application US/08570311; Patent No. 5824791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (904) 372-5800 INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 98.2%;
Best Local Similarity 99.8%;
Matches 449; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 2421 N.W. CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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USA
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APPLICANT: Patti, Joseph
TITE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
SIREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GTPNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICA
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                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
FILING DATE: 09-DEC-1994
CLASSIFICATION OPTA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION ATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 09-DEC-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: WhitloCK, Ted W.
REFERENCE/DOCKET NUMBER: 36,965
REFERENCE/DOCKET NUMBER: 36,965
REFERENCE/DOCKET NUMBER: 36,965
REFERENCE/DOCKET NUMBER: 36,965
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REFERENCE/DOCKET NUMBER: 36,965
REFERENCE/DOCKET NUMBER: 36,965
REFERENCE/D
                                                                                                                                               SSEE: Ted W. Whitlock
F: 2421 N.W. 41st Street, Suite A-1
Gainesville
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Best Local Similarity 100.
Matches 456; Conservative
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ZIP: 32606
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                                                                                                                                                                                                                       CITY: (STATE:
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Gaps

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84.0%; Score 2082;
REFERENCE DOCKET NUMBER: 36,965
REFERENCE DOCKET NUMBER: UF15.C3
TELECOMUNICATION INFORMATION:
TELEFRONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 439 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECHE FOR THE FOR THE SECOND TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Porphyromonas gingivalis
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                                                                                                                                                                                                                                  94.8%;
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-570-311-22
                                                                                                                                                                                                                                                   Similarity
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Best Local S
Matches 431
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                                                                                                                           121 BEVLTAKTVVTAPBAIRGIRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIK 180
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APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naining
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
                                                     BEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIK 186
                                                                                                                                                                                                                                                            241 WNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETP
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                                                                                                                                                                                      367 MGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVNV
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                                 67 NFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALL
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 450
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APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-0AN-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 22, Application US/08570311
patent No. 5824791
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| Sequence 1, Application US/09482500A |
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| Sequence 1, Application US/09482500A |
| Sequence 1, Application US/09482500A |
| Patent No. 6627193 |
| GENERAL INFORMATION: Takehisa |
| APPLICANT: Travis, James |
| APPLICANT: Toempa, Jan |
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION |
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION |
| CURRENT FILING DATE: 235.0016.12.17 |
| PRIOR FILING DATE: 1999-01-13 |
| NUMBER OF SEQ ID NOS: 4 |
| SEQ ID NO 1 |
| LEMENTH: PatentIn version 3.0 |
| SEQ ID NO 1 |
| LEMENTH: 1477 |
| LEMENTH: 1477 |
| COARDINATE: 1477 |
| COARDINATE: PATENTH: 1477 |
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Score 2351; DB 2; Length 4 Pred. No. 3e-193; 3; Mismatches 5; Indels
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.230 FEETPNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD 1289
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APPLICANT: Barr, Philip J.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Madine
TITLE OF INVENTION: Porphyromonas gingivalis
TITLE OF SEQUENCES: 16
CORRESPONDENCE 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

84.0%; Score 2082; DB 2;
Best Local Similarity 86.2%; Pred. No. 2.5e-169;
Matches 392; Conservative 17; Mismatches 40;
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CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8400
TELEPKX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08336308A; Patent No. 6017532; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          1687 amino acids
                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                  amino acid
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STATE: Colora
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Refert No. 5824791
GENERAL INFORMATION:

APPLICANT: Progulake-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Han', Naiming
APPLICANT: Han', Naiming
APPLICANT: Han', Marilyn
APPLICANT: Patti, Joseph
ITILE OF INVENTION: Cloned Porphyromonas gingivalis Genes
ITILE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    960 VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV 1019
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                                                                                                         63 ASY-INFEGPONPONYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF 121
                                                                                                                                                                                                       122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD 181
                                                                                                                                                                                                                                                                                                                                                          182 DVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTNV
                                                                               3 PNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASS
                                    Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 2.1e-169; 17; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
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PELASSIFCATION: 424
PELORATION: 424
PELORATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
PELORS: 19-DEC-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/08570311
              86.2%;
              Best Local Similarity 86.2
Matches 392; Conservative
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US-08-570-311-29
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TITLE OF INVENTION: IMMUNOEBNIC COMPOSITIONS COMPRISING
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS PROFEINS AND/OR PEPTIDES AND
TITLE OF INVENTION: METHODS
CORRESPONDENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       952 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS 1008
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                                                                                                                                                                                                                                                                                                                              WEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATORILIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,324
FILING DATE: 21-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,945
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
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86.2%; Pred. No. 2.6e-169;
iive 17; Mismatches 40;
                                                                                                                                                                                    ADDRESSEE: Greenlee, Winner and Sullivan, STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 33,878
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION: (303) 488.8080
                                     Travis, James
Genco, Caroline A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 1704 anino acids
TYPE: amino acids
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Best Local Similarity 86.2%
Matches 392; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , MOLECULE TYPE: protein US-08-822-324-6
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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GENERAL INFORMATION:
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STATE: CO
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ZIP: 80303
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                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/336,308A
FILING DATE: US-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
                                                                                                                                                                                        FILING DATE: 08-NOV-1994
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/119,361
FILING DATE: 10-SEP-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/265,441
FILING DATE: 24-UN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 3,878
REFERENCE/DOCKET NUMBER: 21-93C
TELEPHONE: (303) 499-8080
TELEPHONE: (303) 499-8080
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1704 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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DIOFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 421

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Sequence 6, Application US/08822324 Patent No. 6129917

US-08-822-324-6

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1307 DIQFTIMGGSPTPTDYTYTYRDGTKIKEGLIETTFEEDGVATGNHEYCVEVKYTAGVSPK 1366
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1127 EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNV 1186
                                                                                        1187 VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV 1246
                                                                                                                                                                                 1247 FEETPNGINKGGARFGLSTEANGAKPOSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD 1306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Reynolds, Eric C.

APPLICANT: Bhogal, Peter S.

APPLICANT: Bhogal, Peter S.

APPLICANT: Bhogal, Peter S.

APPLICANT: Bhogal, Peter S.

APPLICANT: Bhogal, Peter S.

APPLICANT: Bhogal, Peter S.

TILE REFERENCE: Reynolds

CURRENT PILING DATE: 1998-09-15

EARLIER FILING DATE: 1998-09-15

EARLIER FILING DATE: 1995-10-30

EARLIER FILING DATE: 1995-10-30

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                      FEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09066330A Patent No. 6511666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-066-330-10
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US-09-066-330-10
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                                                                                                                                                                            Sequence 10, Application US/09490931
Patent No. 6274718
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
TITLE OF INVENTION: Porphyromonas gingivalis
TITLE OF INVENTION: Arginine-specific Proteinase Coding Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                               84.0%; Score 2082; DB 3;
86.2%; Pred. No. 2.6e-169;
iive 17; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                     5: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
                       ECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
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APPLICATION NUMBER: US 08/265,441
FILING DATE: 24-UDN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 21-93C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/490,931
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RAIDA APPLICATION DATA:
APPLICATION NUMBER: 08/336,308
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1704 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 86.2³
Matches 392; Conservative
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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STREET: 53
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US-09-490-931-10
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688 LDDIQFIMGGSPTPIDYTYTVYRDGTKIKBGLTETTFEEDGVATGNHEYCVEVKYTAGVS 747
390 YSESFGLGGIGVLTPDNYLITPALDLANGGKLTFWVCAQDANYASEHYAVYASSTGNDAS 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tunwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 12
CORRESPONDENCE : Ted W. Whitlock
                                                                                                            240 NVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFT
                                                                                                                                                                                                                                                                                                                                                                                       568 NVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFT
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                                                                    120 NFANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWIN
                                                                                                                                                                                                      180 LDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGT
                                                                                                                                                                                                                                                     COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,485
FILING DATE: 09-DEC-1994
PRIOR APPLICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTONEY/AGENT INFORMATION:
NAME: WhitLock, Ted W:
NAME: WAITLOCK, Ted W:
REGISTRATION NUMBER: 36,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         748 PKVCVNVTINPTQFNPVKNLKAQPDGGDVVLKWEAPS 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
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2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: UF15.C2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08353485 Patent No. 5830710
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Tumwasorn, Somying
Lepine, Guylaine
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TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Progul
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   1309 DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 1368
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Progulske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Narilyn
APPLICANT: Han, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GTPNPNPNPNPNPGTTTLSESFENGIPASWKT1DADGDGNNWTTTPPPPGGTSFAGHNSAICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 2066; DB 2;
; Pred. No. 3.1e-168;
18; Mismatches 43;
                                                                                                                :||||||: |||||:|||
1369 KCVNVIVNSTQFNPVKNLKAQPDGGDVVLKWEAPS 1403
                                                                    422 ECVNVTVDPVQFNPVQNLTGSAVGOKVTLKWDAPN 456
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CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-UAN-1991
CLASSIFICATION ATA:
APPLICATION DATA:
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Patent No. 5824791
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MEDIUM TYPE: PIOPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 85.33
Matches 390; Conservative
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APPLICANT: Progul
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661 YSESFGLGGIGVLTPDNYLITPALDLANGGKLTFWVCAQDANYASEHYAVYASSTGNDAS 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 NFANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWIN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          899 VVFEETPNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLDYIL 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   839 NVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFT 898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               604 GTPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 LDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGT
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85.3%; Pred. No. 4.3e-168;
iive 18; Mismatches 43;
                                                                                                    PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-UBM-1991
CLASSIFFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY AGENT INFORMATION:
                      UMBER: US 08/353,485
09-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                        UF15.C3
                                                                                                                                                                                                                                                                                                                                                   NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFRENCE/DOCKET NUMBER: UF15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1358 amino acida
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Best Local Similarity 85.3
Matches 390; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-570-311-27
PRIOR APPLICATION DATA:
                         APPLICATION NUMBER:
FILING DATE: 09-DEC
CLASSIFICATION: 424
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APPLICANT: Progulske-Fox, Ann
APPLICANT: Tunwameorn, Somying
APPLICANT: Tunwameorn, Somying
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Han, Closeph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
                                                                                                                                                                                                                                                                                                                                                                                                                        SSASY-INFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDAS 119
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                                                                                                                                                                         Length 1087;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                         83.3%; Score 2066; DB 2;
85.3%; Pred. No. 3.1e-168;
tive 18; Mismatches 43;
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTY: USA
ZIP: 32606
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Patent No. 5824791
1087 amino acids
                                                                                                                                                                                                                                        Conservative
                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-485-8
                                                                                                                                                                                Query Match
Best Local Similarity
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   LENGTH:
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                                                                                                                                                                                                                                                   9; Gaps
                                                                                                                                                                                                                   Query Match 82.2%; Score 2039.5; DB 4; Length 1732; Best Local Similarity 84.5%; Pred. No. 1.2e-165; Matches 388; Conservative 18; Mismatches 44; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPKECVNVTVDPVQFNPVQNLTGSAV -- GQKVTLKWDAP 455
CURRENT APPLICATION NUMBER: US/09/066,330A;
CURRENT FILING DATE: 1998-09-15
EARLIER APPLICATION WUMBER: PN 6275
EARLIER APPLICATION WUMBER: PC/AU96/00673
EARLIER FILING DATE: 1995-10-30
NUMBER OF SEQ ID NOS: 15
NOWBER OF SEQ ID NOS: 15
SEQ ID NO 11
LENGTH: 1732
                                                                                                                                                      TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-066-330-11
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Search completed: May 18, 2004, 11:49:14 Job time: 15.0888 secs

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May 18, 2004, 11:42:50 ; Search time 35.3211 Seconds (without alignments) 3592.387 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
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| cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                        US-08-570-311-18
2480
                                                                                                                                - protein search,
                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description                   |                   | Sequence 11. Appl | 3,              | Sequence 5, Appli | 9               | 4               | 18,              | 21,              | Sequence 23, Appl | 24               | 26,              | 17,              | 5546                 |                  | 101,              |
|-----------|-------------------------------|-------------------|-------------------|-----------------|-------------------|-----------------|-----------------|------------------|------------------|-------------------|------------------|------------------|------------------|----------------------|------------------|-------------------|
| SUMMARIES | qī                            | TIS-10-229-066-10 | US-10-229-066-11  | US-10-174-695-3 | US-10-174-695-5   | US-10-174-695-6 | US-10-174-695-4 | US-10-387-977-18 | US-10-387-977-21 | US-10-387-977-23  | US-10-387-977-24 | US-10-387-977-26 | US-10-387-977-17 | US-10-282-122A-55467 | US-10-387-977-25 | US-10-387-977-101 |
|           |                               | 14                | 14                | 15              | 15                | 15              | 15              | 15               | 15               | 15                | 15               | 15               | 15               | 12                   | 15               | 15                |
|           | %<br>Query<br>Match Length DB | 1706              | 1732              | 419             | 419               | 231             | 196             | 29               | 29               | 29                | 29               | 29               | 29               | 872                  | 29               | 509               |
|           | %<br>Query<br>Match           | 83.5              | 82.2              | 29.3            | 28.6              | 15.5            | 9.4             | 6.2              | 6.2              | 6.2               | 6.2              | 6.2              | 5.9              | υ.<br>ο.             | 5.8              | 5.8               |
|           | Score                         | 2070              | 2039.5            | 726             | 710.5             | 385             | 232.5           | 153              | 153              | 153               | 153              | 153              | 147              | 147                  | 145              | 143               |
|           | Result<br>No.                 | 1                 | . (7)             | e               | 4                 | Ŋ               | 9               | 7                | 80               | 6                 | 10               | 11               | 12               | 13                   | 14               | 15                |

| Sequence 4. Appli | 4               | 'n        | 'n        | 20            | equence 77    | 80                        | Sequence 11, Appl | 12               | 13               | 14                  | Sequence 23473. A | 6                | Sequence 66335. A    | Sequence 4, Appli | Sequence 15. Appl | Sequence 81, Appl | equen         | Sequence 258, App |                   | equence           |                      |                 |                      | 83,              | 84               | 85.              | Н                   | 100,   | equenc            |
|-------------------|-----------------|-----------|-----------|---------------|---------------|---------------------------|-------------------|------------------|------------------|---------------------|-------------------|------------------|----------------------|-------------------|-------------------|-------------------|---------------|-------------------|-------------------|-------------------|----------------------|-----------------|----------------------|------------------|------------------|------------------|---------------------|--------|-------------------|
| US-10-175-282-4   | US-10-175-275-4 | -10-175-2 | -10-175-2 | -10 - 387 - 9 | -10 - 387 - 9 | $\stackrel{\sim}{\vdash}$ | US-10-387-977-11  | US-10-387-977-12 | US-10-387-977-13 | US-10-156-761-14592 | 93-234            | US-09-813-214A-9 | US-10-282-122A-66335 | vo                | 79                | .0-387            | .0-282-122A-6 | US-10-206-576-258 | US-10-206-576-262 | US-10-206-576-266 | US-10-282-122A-56997 | US-10-229-066-6 | US-10-282-122A-47453 | US-10-387-977-83 | US-10-387-977-84 | US-10-387-977-85 | US-10-369-493-18460 | 387-97 | US-10-206-576-264 |
| 14                | 14              | 14        | 14        | 15            | 15            | 15                        | 15                | 15               | 15               | 14                  | 15                | 6                | 12                   | 14                | 14                | 15                | 12            | 12                | 12                | 12                | 12                   | 14              | 12                   | 15               | 15               | 15               | 15                  | 15     | 12                |
| 1833              | 1833            | 1992      | 1992      | 29            | 25            | 25                        | 27                | 27               | 27               | 555                 | 169               | 2122             | 2468                 | 2468              | 960               | 25                | 1946          | 1638              | 1638              | 1638              | 1728                 | 24              | 2435                 | 25               | 25               | 25               | 4                   | 491    | 699               |
| 5.5               | 5.5             | 5.5       | 5.5       | 5.5           | 5.4           | 5.4                       | 5.4               | 5.4              | 5.4              | 5.3                 | 5.3               | 5.3              | 5.3                  | 5.3               | 5.3               | 5.2               | 5.2           | 5.2               | 5.2               | 5.2               | 5.2                  | 2.5             | 5.2                  | 5.1              | 5.1              | 5.1              | 5.1                 | 5.0    | 5.0               |
| 137               | 137             | 137       | 137       | 136           | 134           | 134                       | 134               | 134              | 134              | 132.5               | 132.5             | 131.5            | 131.5                | 131.5             | 131               | 130               | 130           | 129.5             | 129.5             | 129.5             | 129.5                | 129             | 129                  | 127              | 127              | 127              | 126                 | 123.5  | 123.5             |
| 16                | 17              | 18        | 19        | 20            | 21            | 22                        | 23                | 24               | 25               | 26                  | 27                | 28               | 29                   | 30                | 31                | 32                | 33            | 34                | 35                | 36                | 3,7                  | 38              | 39                   | 40               | 41               | 42               | 43                  | 44     | 45                |

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
           Sequence 10, Application US/10229066
Publication No US20030157637A1
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric C.
APPLICANT: Reynolds, Eric C.
APPLICANT: Blogal, Peter S.
APPLICANT: Blogal, Peter S.
APPLICANT: BLAKESKI, Nada
TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
CURRENT APPLICATION NUMBER: US/09/066,330
CURRENT PILION DATE: 1990-15
PRIOR APPLICATION NUMBER: US/09/066,330
PRIOR FILING DATE: 1995-10-30
PRIOR FILING DATE: 1995-10-30
PRIOR FILING DATE: 1995-10-30
PRIOR FILING DATE: 1995-10-30
SOFTWARE: PARCHICATION NUMBER: PCT/AU96/00673
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PARCHICH Ver. 2.0
SOFTWARE: PARCHICH Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PNPNPNPNPNPGTITLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1706;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.5%; Score 2070; DB 14;
85.7%; Pred. No. 3.9e-176;
cive 18; Mismatches 41;
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US-10-229-066-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.73
Matches 390; Conservative
US-10-229-066-10
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1324 LLDDIQFTWGGSPTPTDYTYTVYRDGTKIKEGLTETTFBEDGVATGNHEYCVEVKYTAGV 1383
    1204 SNVVSSFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDF 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 ASY-INFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 TNALLERIITAKG-VRSPEAIRG-RIQGIWRQKIVDLPAGIKXVAFRHFQSTDMFYIDLD 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 PNPNPNPPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGINSNGCVYŠ
                                                                                                                                   359 LLDDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGV
                                                    TVVFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYI
                                                                                      1264 TVVFEETPNGINKGGARFGLSTEANGAKPÔSVWIERTVDLPAGTKYVAFRHYNCSDLNYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 ESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reproducts, Eric Charles
APPLICANT: Slakeski, Nada
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
TITLE OF INVENTION: P. GINGTVALIS ANTIGENIC COMPOSITION
FILE REFERENCE: 52926200700
CURRENT APPLICATION NUMBER: US/10/174,695
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: PCT/AU00/01588
PRIOR PLILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PSELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/10174695
Publication No US20030232022A1
Publication No US2003023202A1
APPLICANT: Reymolds, Eric Charles
APPLICANT: Glakeski, Nada
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
APPLICANT: Han George
TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REFERENCE: 529282000700
                                                                                                                                                                                                                                                419 SPKECVNVTVDPVQFNPVQNLTGSAV--GQKVTLKWDAP 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10174695
Publication No. US20030232022A1
GENERAL INFORMATION:
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                      1129 EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLDWLTAHGGTNV 1188
                                                                                                                                                                                                                                                                                                                                                                                     1309 DIÒFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 1368
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                                                                                                                                                                     242 VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV 301
                                                                                                                                                                                                                                                         FEETPNGINKGGARFGLSTEADGAKPOSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD 361
                                                                                                                                                                                                                                                                                                                                               DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/10229066

Publication No. US20030157637A1

GENERAL INFORMATION:

APPLICANT: Reynolds, Eric C.

APPLICANT: Blogal, Peter S.

APPLICANT: Blogal, Peter S.

APPLICANT: Blogal, Peter S.

APPLICANT: Blogal, Peter S.

APPLICANT: Blogal, Peter S.

APPLICANT: Blogal, Peter S.

APPLICANT: Blogal, Peter S.

APPLICANT: Blogal, Peter S.

APPLICANT: Blogal, Peter S.

APPLICANT: Blogal, Peter S.

APPLICANT: Blogal, Peter S.

APPLICANT: Blogal, Peter S.

APPLICANT: Reynolds

CURRENT APPLICATION NUMBER: US/10/229,066

CURRENT FILING DATE: 1998-09-15

PRIOR FILING DATE: 1998-10-30

PRIOR PLILNG DATE: 1996-10-30

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
                                                                                 182 DVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 ECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 84.59 Matches 388; Conservative
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US-10-229-066-11
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291

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GENERAL INFORMATION:
APPLICANT: REYNOIDS, Exic Charles
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: Slakeski, Nada
ITILE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
ITILE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONITIS ASSOCIATED WITH
ITILE OF INVENTION: PORPHYROMONAS GINGIVALIS
FILE REFERENCE: 529282000301
CURRENT APPLICATION NUMBER: US/10/387, 977
CURRENT PAPLICATION NUMBER: US 09/423,056
PRIOR APPLICATION NUMBER: PCT/AU98/00311
PRIOR APPLICATION NUMBER: PCT/AU98/00311
PRIOR PILING DATE: 1998-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
                                                             389 EGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVNVTVD-PVQFNPVQNLTGSAVGQK 447
                                                                                      44 PNPNPNPNPRNPTILSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYL 100
                      ---DSPASYTYTVYRDGTKIK 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 ASYINFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 PNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAICASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15; Length 196;
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reynolds, Eric Charles
APPLICANT: Slakeski, Nada
APPLICANT: Slakeski, Nada
APPLICANT: Slakeski, Nada
APPLICANT: Chen, Chen, Chen George
TITLE CP INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REPERENCE: 52022000000
GURRENT APPLICATION NUMBER: US/10/174,695
CURRENT FILING DATE: 2002-06-18
PRIOR FILING DATE: 2000-12-21
PRIOR PLILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: AU PQ 4859
PRIOR PLILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FRAESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 9.4%; Score 232.5; DB 15; Similarity 39.1%; Pred, No. 1.5e-12; 61; Conservative 13; Mismatches 63;
                 92 RYDDFTFE--AGKKYTFTMRRAGMGDGTDMEVED--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10174695; Publication No. US20030232022A1; GENERAL INFORMATION:
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Publication No. US20040005276A1
                                                                                                                                                                                                202 VTLKWDAPN 210
                                                                                                                                                         448 VTLKWDAPN 456
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Best Local Similarity
Matches 61; Conserv
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                                                                                                                                                                                                                                                                                                                  DB 15; Length 419;
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                                                                                                                                                                                                                                                                                                           Query Match 28.6%; Score 710.5; DB 15; Length Best Local Similarity 73.6%; Pred. No. 5.6e-55; Matches 142; Conservative 12; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10174695
Fublication No. US2003023202A1
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Eric Charles
APPLICANT: Chen, Chao Guang
APPLICANT: Barx, lan George
TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REFERENCE: 529282000700
CURRENT APPLICATION NUMBER: US/10/174,695
CURRENT FILING DATE: 2002-06-18
PRIOR PRILING DATE: 2000-12-21
PRIOR PELING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE PEASERED FOR Windows Version 4.0
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15.5%; Score 385, DB 15;
Best Local Similarity 41.4%; Pred. No. 3.9e-26;
Matches 103; Conservative 31; Mismatches 69;
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: PCT/AU00/01588
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: AU PQ 4859
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTERO for Windows Version 4.0
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ORGANISM: Porphyromonas gingivalis
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ORGANISM: Porphyromonas gingivalis
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Best Local Similarity
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Gaps

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Length 29;

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Query Match
6.2%; Score 153; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 29; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                 1 DYTYTVYRDGTKIKEGLTETTFEEDGVAT 29
     PRIOR FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 105
SEQ ID NO 23
ERO ID NO 23
LENGTH: 29
                                                                                                                                              TYPE: PRT
ORGANISM: Porphyromonas gingivalis
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US-10-387-977-24
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| Publication No. US20040005276A1
| GENERAL INFORMATION:
| APPLICANT: Reynolds, Eric Charles
| APPLICANT: Reynolds, Eric Charles
| APPLICANT: C'Brien-Simpson, Neil Martin
| APPLICANT: C'Brien-Simpson, Neil Martin
| APPLICANT: O'Brien-Simpson, Neil Martin
| APPLICANT: O'Brien-Simpson, Neil Martin
| APPLICANT: O'Brien-Simpson, Neil Martin
| APPLICANT: O'Brien-Simpson, Neil Martin
| APPLICANT: O'Brien-Simpson, Neil Martin
| APPLICANT: O'Brien-Simpson, Neil Martin
| TITLE OF INVENTION: DIAGNOSIS AND TREATHENT OF PERIODARITIS ASSOCIATED WITH
| TITLE OF INVENTION: DIAGNOSIS AND TREATHENT OF PERIODARITIS ASSOCIATED WITH
| TITLE OF INVENTION: DIAGNOSIS AND TREATHENT OF PERIODARITIS ASSOCIATED WITH
| TITLE OF INVENTION NUMBER: US 09/423,056
| PRIOR PELLING DATE: 1998-04-30
| PRIOR FILING DATE: 1998-04-30
| PRIOR FILING DATE: 1998-04-30
| PRIOR FILING DATE: 1998-04-30
| NUMBER OF SEQ ID NOS: 105
| SEQ ID NOS: 105
| SEQ ID NOS: 105
| SEQ ID NOS: 105
| SEQ ID NOS: 106
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US-10-387-977-23

Sequence 23, Application US/10387977

Publication No. US20040005276A1

GENERAL INFORMATION:

APPLICANT: Reynolds, Eric Charles

APPLICANT: O'Exten-Simpson, Neil Martin

APPLICANT: O'Exten-Simpson, Neil Martin

APPLICANT: O'Exten-Simpson, Neil Martin

ITILE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE

TITLE OF INVENTION: DORPHYROWONAS GINGIVALIS

FILE REFERENCE: 529282000301

CURRENT FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: US 09/423,056

PRIOR PLILING DATE: 2000-03-22

PRIOR PILING DATE: 1998-04-30

PRIOR FILING DATE: 1998-04-30

PRIOR FILING DATE: 1998-04-30

PRIOR FILING DATE: 1998-04-30
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                                                                                                                                                                                                                         Length 29;
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100.0%; Pred. No. 1.3e-06;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                              Query Match 6.2%; Score 153; DB 15; Best Local Similarity 100.0%; Pred. No. 1.3e-06; Matches 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                           375 DYTYTVYRDGTKIKEGLTETTFEEDGVAT 403
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NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 29
                                                                                                 ; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-18
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US-10-387-977-21
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Best Local Similarity
Matches 29; Conserv
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US-10-387-977-21
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APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Bric Charles
APPLICANT: Reynolds, Neil Martin
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION NUMBER: US /10/387,977
CURRENT APPLICATION NUMBER: US /9/423,056
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: AU PO 6528
PRIOR PILING DATE: 1997-04-30
PRIOR FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FASTSEQ for Windows Version 4.0
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Publication No. US20040005276A1
GENERAL INFORMATION:
JAPPLICANT: Reynolds Eric Charles
APPLICANT: Reynolds Eric Charles
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANTON INTERNITON: PORPHYROMONAS GINGIVALIS
FILLE REFRENCE: S29282000101
FILLE REFRENCE: S29282000101
CURRENT PILLING DATE: 2003-07-18
FRIOR APPLICATION NUMBER: US 09/423,056
FRIOR FILLING DATE: 1998-04-30
FRIOR FILLING DATE: 1998-04-30
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100.0%; Pred. No. 1.3e-06;
tive 0; Mismatches 0;
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; Sequence 24, Application US/10387977; Publication No. US20040005276A1; GENERAL INFORMATION:
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US-10-387-977-26
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TYPE: PRT ORGANISM: Enterobacter cloacae
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Matches 112; Conservative
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Fublication No. US20040005276A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Reynolds, Eric Charles
APPLICANT: Slakeski, Nada
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: SYNTHETIC EPPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
CURRENT APPLICATION NUMBER: US/10/387,977
CURRENT APPLICATION NUMBER: US/9/423,056
FRIOR FILING DATE: 1998-04-30
FRIOR APPLICATION NUMBER: PCT/AU98/00311
FRIOR APPLICATION NUMBER: AU PO 6528
FRIOR APPLICATION NUMBER: AU PO 6528
FRIOR PILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 105
SOPTHARE: RESEEM OF WINDOWS 105
SOPTHARE: RESEEM OF WINDOWS 105
SOPTHARE: PASELSO for Windows Version 4.0
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                                                                                                                                                                            Score 153; DB 15;
Pred. No. 1.3e-06;
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Pred. No. 4.3e-06;
0; Mismatches 1;
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100.0%; Pred. No. 1...
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PRIOR APPLICATION NUMBER: AU PO 6528
PRIOR FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 55467, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                          ; ORGANISM: Porphyromonas gingivalis
US-10-387-977-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-17
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
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Best Local Similarity 96.6%;
Matches 28; Conservative
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                             Conservative
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Best Local Similarity
Matches 29; Conserv
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US-10-387-977-17
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                                                                                                          TYPE: PRT
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IITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 154;
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21.3%; Pred. No. 0.00064;
Live 56; Mismatches 205;
                                                    THIS REFERENCE BLITTAL U.344

CURRENT PELLING DATE: 2003-02-20

RIOR APPLICATION NUMBER: 06/191,078

RIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR PELLOATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,347

PRIOR PILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-10-23

PRIOR PELLOATION NUMBER: 60/242,578

PRIOR PILING DATE: 2000-10-23

PRIOR PELLOATION NUMBER: 60/242,578

PRIOR PILING DATE: 2000-12-27

PRIOR PELING DATE: 2000-12-27

PRIOR PILING DATE: 2000-12-27

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2000-12-22

PRIOR PILING DATE: 2001-12-22

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Sequence 101, Application US/10387977

Sequence 101, Application US/10387977

Sublication No. U52004000526A1

GENERAL INFORMATION:

APPLICANT: Stakeski, Nada

TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION NUMBER: US 103-07-18

PRIOR APPLICATION NUMBER: US 09/423,056

PRIOR PILING DATE: 1090-03-22

PRIOR PILING DATE: 1997-04-30

NUMBER OF SEQ ID NOS: 105

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 101

LEADTH: 509
                                                                      APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Eric Charles
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
ITILE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
TITLE OF INVENTION DATE: 2003-07-18
PRIOR PELING DATE: 2000-03-22
PRIOR PELING DATE: 1998-04-30
PRIOR PELING DATE: 1998-04-30
PRIOR PELING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FRASESQ for Windows Version 4.0
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Pred. No. 6.6e-06;
0; Mismatches 1; Indels
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Sequence 25, Application US/10387977
Publication No. US20040005276A1
GENERAL INFORMATION:
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; ORGANISM: Porphyromonas gingivalis
US-10-387-977-25
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Best Local Similarity 96.6
Matches 28; Conservative
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Best Local Similarity
Matches 94; Conserv
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380 PASLPQNQASYSIQASAGSYVAISKDGVLYGTGVANAS----GVATVSMTKQITENGNYD 435
SSTGNDASNFANALL---EEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQ--LPAGTKYVA 166
                                       123 ASSPEELTNIIDKVLMYEKATMPDKSYLEKVLLIAG--ADYSWNSQVGQPTIKYGMQYYY 180
                                                                                   FRHFGCTDFFWINLDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWL--C 224
                                                                                                                           181 NOEHGYTDVY------NYLKAPYTGCYSHLNTGVSFANYT---AHGSETAWADPL 226
                                                                                                                                                                                                                   227 LTTSQLKALTNKDKYFLAIGNCCITAQFDY----VQP----CFGEVITRVKEKGAYAYIG 278
                                                                                                                                                                                                                                                                  ---YAVMISKTGTNAGDFTVVF-EETPNGINKGGARFGLSTEA 322
                                                                                                                                                                                                                                                                                                                                                      323 DGAKPQSVWIERTVDLPAGT----KYVAFRHYNCSDLNYILLDDIQFTMGGSPTPTDYT- 377
                                                                                                                                                                                                                                                                                                                                                                                    225 LSSGQLGWLT-----AHGGTNVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  408 YCVEVKYTAGVSPKECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
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                                                                                                                                                                                                                                                                                                         279 SSPNSYWGEDYYWSVGANAVFGVOPTFEGTSMGSYDATFLEDSYNTVN-
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- protein search, using sw model OM protein

Run on:

May 18, 2004, 11:33:39 ; Search time 47.0287 Seconds (without alignments) 2739.638 Million cell updates/sec

US-08-570-311-20 Title: Perfect score:

2480 1 GTPNPNPNPNPNFGTTTLSESF.....QNLTGSAVGQKVTLKWDAPN 456 Sequence:

Gapop 10.0 , Gapext 0.5

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Scoring table:

1586107 Total number of hits satisfying chosen parameters: 1586107 seqs, 282547505 residues Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_29Jan04:\* geneseqp1980s:\* Database :

geneseqp2003as:\*geneseqp2003bs:\* geneseqp1990s:\* geneseqp2002s:\* geneseqp2001s:\* geneseqp2004s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Res

|   | Description    | 3 Aar96023 P. gingiv | 2 Aar96022 P. | Aaw69491 Hae | Aaw69490 | Aar96030 | B Aaw69488 Hae | 1 Aar96021 | 9 Aaw69489 Hae | Aar96024 | 2 Aaw69492 Hae | 3 Aar96033 | Aaw69495 Hae | Aar70188 | Aaw34843 | Aay67396 Arg | 8 Aau 08938 P. | Aaw24786 Prtf | 8 Aar96028 P. gingiv | Aaw69486 Hae | 2 Aar96032 P | Aaw69494 | 9 Aar96029 | 7 Aaw24787 PrtK anti | 7 Aaw69487 |  |
|---|----------------|----------------------|---------------|--------------|----------|----------|----------------|------------|----------------|----------|----------------|------------|--------------|----------|----------|--------------|----------------|---------------|----------------------|--------------|--------------|----------|------------|----------------------|------------|--|
|   | Н              | AAR9602              | AAR9602       | . AAW69491   | AAW69490 | AAR9603  | AAW6948        | AAR9602    | AAW6948        | AAR96024 | AAW6949        | AAR9603    | AAW69495     | AAR70188 | AAW3484  | AAY67396     | AAU0893        | AAW24786      | ·                    | AAW69486     | AAR9603      | AAW69494 | AAR9602    | AAW2478              | AAW6948    |  |
|   | Length DB      | 1                    |               | 26           | 456 2    | 628      | 28             |            | 20             | 6        | 439 2          | 1687 2     |              | 1704 2   | 1704 2   |              | 704            |               | 1087 2               |              | 358          | 358      |            | 32                   | 1732 2     |  |
| * | Query<br>Match | 100.0                | 100.0         | 100.0        | 100.0    | 100.0    | 100.0          | 98.2       |                | 94.8     | 94.8           | 84.0       | 84.0         | 84.0     | 84.0     | 84.0         | 84.0           |               | 83.3                 | •            | Э.           | ж.       |            | 82.0                 | 82.0       |  |
|   | Score          | 2480                 | 2480          | 2480         | 2480     | 2480     | 2480           | 2436       | 2436           | 2351     | 2351           | 2082       | 2082         | 2082     | 2082     | 2082         | 2082           | 2070          | 2066                 | 2066         | 2066         | 2066     | 034.       | 2034.5               | 034.       |  |
|   | Sult<br>No.    | П                    | 7             | m            | 4        | Ŋ        | 9              | 7          | 00             | σ        | 10             | 11         | 12           | 13       | 14       | 15           | 16             | 17            | 18                   | 19           | 20           | 21       | 22         | 23                   | 24         |  |

| Abp55081 Porphyrom Aau03574 P. gingiv Aay34522 Porphorym Aay34521 Porphorym Aay34329 Porphorym Aay34329 Porphorym Aay34392 Porphorym Aay3439 Porphorym Aay3438 Porphorym Aay3488 Porphorym Aar77458 Porphyrom Aau03575 P. gingiv Aar77458 Porphyrom Aav34885 Arg-speci Aay3488 Porphyrom Aaw34885 Arg-speci                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Ъ.       | Aaw34798 Arg-speci<br>Aaw83085 Peptide f |
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## ALIGNMENTS

AAR96023 standard; protein; 456 AA. (first entry) (revised) 16-OCT-2003 04-SEP-1996 AAR96023; AAR96023 

P. gingivalis haemagglutinin hagA HArep3 product.

Haemagglutinin; hagA; periodontal disease; vaccine; antibody; HArep3

Porphyromonas gingivalis; strain 381.

WO961.7936-A2

13-JUN-1996.

95WO-US016108 11-DEC-1995; 94US-00353485. 09-DEC-1994;

(UYFL ) UNIV FLORIDA

(UABR-) UAB RES FOUND

Patti Lantz M, Han N, Lepine G, Progulske-Fox A, Tumwasorn S,

Ŋ,

WPI; 1996-287181/29. N-PSDB; AAT30647.

Porphyromonas gingivalis genes and proteins – used in the detection and vaccination against periodontal disease.

Claim 4; Page 110-112; 153pp; English.

HArep3 (AAR96023) is the product of the HArep3 repeat unit (AAF30647) of the hagA gene (AAF30654) of P. gingivalis 318. It forms part of haemagglutinin hagA (see also AAF96030). HArep3 and other hagA repeat unit products (see also AAF9601-22 and AAF96024) can be obtd. from transformed host cells and used as vaccines to protect humans or animals against periodontal disease. Expression in Salmonella cells allows product live vaccine. HArep1-4 can also be used to detect the presence of anti-P. Gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-0CT-2003 to standardise OS field)

Sequence 456 AA;

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HAREP2 (AAR96022) is the product of the HAREP2 repeat unit (AAT30646) of the hagA gene (AAT30654) of P. gingivalis 318. It forms part of haemagglutinin hagA (see also AAR96030). HAREP2 and other hagA repeat unit products (see also AAR96031 and AAR96023-24) can be obtd. from transformed host cells and used as vaccines to protect humans or animals against periodontal disease. Expression in Salmonella cells allows product ive vaccine. HAREP1-4 can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)
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100.0%; Pred. No. 7.5e-191;
ive 0; Mismatches 0;
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100.0%; Score 2480; DB 2;
100.0%; Pred. No. 7.5e-191;
ive 0; Mismatches 0;
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ID AAR96022 standard; protein; 456
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N-PSDB; AAT30646.
                  Similarity
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100.0%; Pred. No. 7.5e-191;
ive 0; Mismatches 0;
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91US-00647119.
94US-00353485.
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UAB RES FOUND.
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Best Local Similarity
Matches 456; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 456 AA;
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                                                                      11-DEC-1995;
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100.0%; Pred. No. 7.5e-191;
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                                                 Han N, Lantz M,
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protease poly:peptide(s))
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Best Local Similarity 100.
Matches 456; Conservative
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                                                                                                                                                                                                                        100.0%; Score 2480; DB 2;
100.0%; Pred. No. 9e-190;
ive 0; Mismatches 0;
                                                                                                                                                                                             421 KECVNVŢVDPVQFNPVQNLTGSAVGQKVŢLKWDAPN
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91US-00647119.
94US-00353485.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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es 456; Conservative
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(UABR-) UAB RES FOUND
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N-PSDB; AAV58875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P. gingivalis 381 haemagglutinin hagA (AAR96030) was identified as the product of the hagA gene (AAT30654) isolated as an EcoRV fragment of genomic DNA. The haemagglutinin, or portions of it (see also AAR96021-24), can be obtd. from transformed host cells and used as a vaccine to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of a live vaccine. The haemagglutinin can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patti JM;
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                                                                                                                                                                            Haemagglutinin; hagA; periodontal disease; vaccine; antibody
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100.0%; Pred. No. 9e-190;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                      Porphyromonas gingivalis; strain 381
                                                                                                                                                                                                                                                                                                                   5. .21
/label= Sig_peptide
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    P. gingivalis haemagglutinin hagh.

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Les 456; Conservative
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(UABR-) UAB RES FOUND
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04-SEP-1996
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AAR96030;
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                                                                                                                                                                                                                                                                                                                                                                                                            VFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILL 360
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                                                                                                                                                                                                                                                                                                                                                            DDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSP 420
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                                         DDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTN
                                                                                                                      VVASFSWNGMAINPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTV
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protease poly:peptide(s)).
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91US-00647119.
94US-00353485.
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UAB RES FOUND.
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Query Match
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polypeptides are used to produce antibodies to organisms associated wing periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
                                                                                                                                                             EEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVBIK
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                                                                   Score 2436; DB 2;
Pred. No. 2.6e-187;
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    P. gingivalis haemagglutinin hagA HArep4 product.

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  - used in the detection
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 439,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2351; DB 2;
Pred. No. 1.7e-180;
3; Mismatches 5;
Porphyromonas gingivalis genes and proteins vaccination against periodontal disease.
                                                                    Claim 4; Page 114-115; 153pp; English.
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ses 431; Conserv
                                                                                                                                                                                                                                                                                                                                                                             Sequence 439 AA;
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20-0CT-1998

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P. gingivalis haemagglutinin hagE
                                                                                                                                                                                              Tumwasorn S,
                                                                                                                         95WO-US016108
                                                                                                                                             94US-00353485
 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    392; Conservative
                                                                                                                                                                (UYFL ) UNIV FLORIDA.
(UABR-) UAB RES FOUND.
                                                                                                                                                                                                                WPI; 1996-287181/29.
N-PSDB; AAT30656.
                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                             Progulske-Fox A,
                                                                                                                         11-DEC-1995;
                                                                                                                                             09-DEC-1994;
  04-SEP-1996
                                                                                                    13-JUN-1996
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                                                                                                                                                                                                    This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagA haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
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    encoding haemagglutinin and/or

                                                                                                    Lepine G;
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                                                                                                   Progulske-Fox A,
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                                                                                                                                                                                                                                                                                               Score 2351; DB 2;
Pred. No. 1.7e-180;
3; Mismatches 5;
                                                                                                   Tumwasorn S,
                                                                                                                                                     Isolated Porphyromonas gingivalis genes
                                                                                                                                                                                Claim 1; Col 139-144; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 1687 AA
                                     91US-00647119.
         95US-00570311
                            88US-00241640
                                                                                                                                                                                                                                                                                               94.8%;
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                                                                                                                                                              protease poly:peptide(s))
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Best Local Similarity 98.2
Matches 431; Conservative
                                                                              UAB RES FOUND
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                                                                                                                       1998-582627/49.
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                                    25-JAN-1991;
09-DEC-1994;
         11-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P. gingivalis 381 haemagglutinin hagE (AAR96033) was identified as the product of a gene (AAT30656) identified in P. gingivalis 318 genomic DNA. The haemagglutinin can be obtd. from transformed host cells and used as a vaccine to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. Of a live vaccine. The haemagglutinin can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)
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Haemagglutinin; hagE; pericdontal disease; vaccine; antibody
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86.2%; Pred. No. 5.2e-158;
live 17; Mismatches 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccination against periodontal disease
                                                  Porphyromonas gingivalis; strain FDC381
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1230 FEETPNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD 1289
                                                                                                     1290 DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A low mol.wt. arginine-specific gingipain (AG-1) and high mol.wt. AG (AG-2) were isolated from P. gingivalis strains H66 (ATCC 33277) and W50 (ATCC 53973). The sequences of the proteins were used to design PCR primers and probes to isolate AG DNA. Lambda DASH and lambda ZAP libraries were screened with a probe based on amino acids 11-22 of the AG protein to obtain DNA encoding AG-1 (AAQ03484) and AG-2 (AAQ03489). AG-2 correct PN field.)
                      FEETPNGINKGGARFGLSTEADGAKPOSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD 361
                                                                                    DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 421
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                                                                                                                                                                                                                                                                                                                                                                                                               Arg-gingipain-2; gingivalis; periodontal disease; vaccine; arginine-specific protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228. .719
/label= Protease
/note= "corresponds to Arg-gingipain-1"
                                                                                                                                                                    ECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barr PJ, Pavloff N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        720. .1091
/label= Hemagglutinin
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1430. .1704
/label= Hemagglutinin
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                                                                                                                                                                                                                                                               AAR70188 standard; protein; 1704
                                                                                                                                                                                                                                                                                                                                                                                 Arg-gingipain-2 prepolyprotein.
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                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                               (revised)
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                                                                                                                                                                                                                                                                                                                              25-MAR-2003
21-SEP-1995
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Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - encoding haemagglutinin and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagE haemagglutinin protein. I polypeptides are used to produce antibodies to organisms associated wiperiodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 DVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Progulske-Fox A,
                                                                                                                                                                                                                               Haemagglutinin protein; periodontal disease; vaccine; hagE.
Tumwasorn S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated Porphyromonas gingivalis genes
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                                                                                                AAW69495 standard; protein; 1687 AA
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91US-00647119.
94US-00353485.
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                                                                                                                                                                                             Haemagglutinin protein hagE
                                                                                                                                                               (first entry)
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Best Local Similarity
Matches 392; Conserv
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25-JAN-1991;
09-DEC-1994;
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Porphyromonas gingivalis Arg-specific gingipain protease peptide(s) -
useful for protecting animals and humans from gingivalis and periodontal
                                    Disclosure, Page 68-73; 95pp; English
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Best Local Similarity
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                                                             PNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS 1008
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                                                                                                                       122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD 181
                                                                                                                                                                                                                                                                            DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 421
                                             62
                                                                                             1127 EVETKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNV
                                             PNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASS
                                                                                  ASY-INFEGPONPONYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF
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                           Gaps
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                          9
      Length 1704;
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                          Indels
       Score 2082; DB 2;
Pred. No. 5.2e-158;
17; Mismatches 40;
                                                                                                                                                                                                                                                                                                                          ECVNVTINPIQFNPVKNLKAQPDGGDVVLKWEAPS 1401
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/note= "precursor protein"
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MOREHOUSE SCHOOL MEDICINE.
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       84.0%;
86.2%;
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                          Conservative
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N-PSDB; AAT93872.
                 Local Similarity
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                          Matches 392;
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        Query Match
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                                              POTDAYCOMODAS GINGIALS. THE COLOWING PERIODS OF THE PROCESSED OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      952 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1127 EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLDWLTAHGGTNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTNV
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The present sequence represents an arginine-specific protease of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1704;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
84.0%; Score 2082; DB 2;
Best Local Similarity 86.2%; Pred. No. 5.2e-158;
Matches 392; Conservative 17; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
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952 PNPNPNPNPGTITLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1069 TWALLEETITAKG-VRSPEAIRG-RIQCTWRQKTVULPAGTKYVAFRHFQSTDMFYIDLD 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1127 EVEIKANGKRADFTETFESSTHGEAPAEWITIDADGDGQGWLCLSSGQLDWLTAHGGTNV 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1187 VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1307 DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFBEDGVATGNHEYCVEVKYTAGVSPK 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a Porphyromonas gingivalis arginine-specific proteinase known as Arg-gingipain/gingipain-2 amino acid sequence. Gingipain-2 consists or a 50kD protease component non-covalently associated with a 44kD haemagglutinin component. The proteinase is stimulated by glycine containing peptides and glycine analogues. It is inhibited by cysteine protease group specific inhibitors. The protease inhibited by cysteine protease group specific inhibitors. The protease inflammatory response and tissue damage caused by P. gingivalis in periodontal disease. It can also be used to screen for agents that modulate Arg-gingipain proteinase activity inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASS 62
                                  229. .719 // Annino acids 229-719 are specifically claimed" /700: 1885 // 100te= "Amino acids 720-1185 are specifically claimed" // Anote= "Amino acids 720-1185 are specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 FEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             New Porphyromonas gingivalis arginine-specific protease preparation useful for preparing vaccines against periodontal disease and for screening for Arg-gingipain inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1704;
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84.0%; Score 2082; DB 3;
Best Local Similarity 86.2%; Pred. No. 5.2e-158;
Matches 392; Conservative 17; Mismatches 40;
                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                             (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Col 29-42; 55pp; English
                                                                                                                                                                                                                                                 93US-00119361
94US-00265441
                                                                                                                                                                                                            94US~00336308
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N-PSDB; AAZ60181.
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                                                                                                                                                                                                            38-NOV-1994;
                                                                                                                                                                                                                                                   10-SEP-1993;
                                                                                                                                                                                                                                                                       24-JUN-1994;
                                                                                                                                   US6017532-A
                                                                                                                                                                          25-JAN-2000
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Region
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Search completed: May 18, 2004, 11:42:43 Job time: 48.0287 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

May 18, 2004, 11:37:00 ; Search time 11.906 Seconds (without alignments) 3684.135 Million cell updates/sec Run on:

US-08-570-311-20 2480 I GTENPNPNPRPTTLSESF.....QNLTGSAVGQKVTLKWDAPN 456

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description           | hemagglutinin A - | gingipain R (EC 3. | gingipain R (EC 3. | Iysine-specific cy | arginyl endopeptid | conserved hypothet | hypothetical prote | hypothetical prote | Н      | autolysin [importe | hypothetical prote | amylase A-180 - al | hypothetical prote | prophage pil prote | hypothetical prote | tail-host specific | hypothetical prote | probable RTX famil | transferrin-like p | S-layer protein - | large repetitive p | cellulose 1,4-beta | hypothetical prote | hypothetical prote | alkaline serine pr | ein    | al pro | ы      | uncharacterized pr |
|-----------|-----------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------------------|
| SUMMARIES | αн                    | T28651            | A55426             | S49763             | 3083               | I40229             | AF2959             | H98323             | B75622             | A83412 | C89874             | AH2515             | S10789             | B75489             | A86685             | C86822             | T13256             | F90696             | B85547             | T10729             | A47023            | AD0835             | 859077             | AE2254             | T34416             | JC4908             | T30944 | 589    | T18213 | 703                |
|           | DB                    | 2                 | 7                  | N                  | 7                  | ~                  | N                  | 7                  | 7                  | 7      | 7                  | N                  | N                  | 7                  | 7                  | ~                  | 63                 | ~                  | N                  | 7                  | ~                 | N                  | 7                  | N                  | ~                  | ~                  | 0      | 7      | 7      | 7                  |
|           | Query<br>Match Length | 2628              | 1704               | 1526               | 73                 | 991                | 1052               | 34                 | 69                 | 2468   | 24                 | 93                 | 1684               | 713                | 44                 | 64                 | 1904               | 5291               | 5188               | 1274               | 465               | 3624               | 0                  | 90                 | α                  | -                  | 1873   | 92     | 1385   | 81                 |
| ok        | Query                 | 0                 | 4                  | 3                  | 82.0               | 0                  | 5.6                | 5.6                | 5.3                | 5.3    | 5.2                | 5.2                | 5.1                | 5.1                | 5.1                | 5.1                | 5.0                | 5.0                | 5.0                | 4.9                | 4.9               | 4.9                | 4.9                | 4.8                | 4.8                | 4.8                | 4.8    | 4.8    | 4.8    | 4.8                |
|           | Score                 | 2480              | 2082               | 2059               | 2034.5             | 266                | 139.5              | 139.5              | 132.5              | 131.5  | 128.5              | 128                | 127.5              | 127                | 126                | 126                | 124.5              | 124.5              | 123.5              | 122.5              | 121.5             | 121.5              | 121                | 120                | 120                | 119                | 119    | ٠      | 118.5  |                    |
|           | Result<br>No.         |                   | 7                  | ю                  | 4                  | Ŋ                  | 9                  | 7                  | 80                 | σ      | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19                 | 50                | 21                 | 22                 | 23                 | 24                 | 25                 | 26     | 27     | 28     | 29                 |

| hypothetical prote | hypothetical prote | hypothetical prote | beta-qalactosidase | hemolysin [importe | major surface prot | probable outer mem | protein-tyrosine-p | microbial collagen | probable S-layer p | probable secreted | outer membrane pro | hypothetical prote | cellulase - Cellul | hypothetical prote | internalin-like pr |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| S76412             | E90696             | A85547             | T30551             | AI0452             | 548753             | AF0472             | A49724             | JC4393             | D97316             | AD1507            | JC1340             | 876109             | S49541             | H90975             | AF1772             |
| 7                  | ۲                  | ~                  | ~                  | 7                  | 7                  | 7                  | гH                 | 7                  | N                  | 7                 | 7                  | 7                  | ~                  | ~                  | 7                  |
| 4199               | 1461               | 1461               | 1034               | 1635               | 702                | 875                | 1118               | 1282               | 1939               | 821               | 1651               | 3029               | 872                | 1345               | 938                |
| 4.8                | 4.8                | 4.8                | 4.7                | 4.7                | 4.7                | 4.7                | 4.7                | 4.7                | 4.7                | 4.6               | 4.6                | 4.6                | 4.6                | 4.6                | 4.5                |
| 118.5              | 118                | 118                | 117.5              | 116.5              | 115.5              | 115.5              | 115.5              | 115.5              | 115.5              | 115               | 115                | 115                | 114                | 113                | 112.5              |
| 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

RESULT 1

|   | hemagglutinin A - Porphyromonas gingivalis hemagglutinin A - Porphyromonas gingivalis C;Species: Porphyromonas gingivalis C;Species: Porphyromonas gingivalis C;Accession: T28651 R;Han, N.; Whitlock, J.; Progulske-Fox, A. C;Accession: T28651 R;Han, N.; Whitlock, J.; Progulske-Fox, A. R;Han, N.; Whitlock, J.; Progulske-Fox, A. R;Han, N.; Whitlock, J.; Progulske-Fox, A. R;Han, N.; Whitlock, J.; Progulske-Fox, A. R;Han, N.; Whitlock, J.; Progulske-Fox, A. R;Han, N.; Whitlock, J.; Progulske-Fox, A. R;Han, N.; Whitlock, J.; Progulske-Fox, A. R;Han, N.; Whitlock, J.; Progulske-Fox, A. R;Han, N.; Whitlock, J.; Progulske-Fox, A. R;Reference number: Z0494; MUID: 97047672; PMID: 8926061 A;Reference number: Z0494; MUID: 97047672; PMID: 8926061 A;Reference number: D1047672; PMID: 8926061 A;Residues: 1-2628 cHAN> A;Cross-references: EMBL: U41807; NID: 91552410; PID: 91469916; PIDN: AAB17128.1 C;Genetics: A;Genetics: |
|---|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| - | Query Match 100.0%; Score 2480; DB 2; Length 2628;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|   | TOTAL STRILL TO ON DARGE NO 1 AB. 160.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |

., 0; Gaps Best Local Similarity 100.0%; Pred. No. 1.4e-162;
Matches 456; Conservative 0; Mismatches 0; Indels

| λŏ | Ħ    | GTPNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNWWTTTPPPGGTSFAGHNSALCA 60  |
|----|------|--------------------------------------------------------------------|
| QQ | 950  | GTPNPNPNPNPNPGTTILSESFENGIPASWKTIDADGDGNNWTTPPPGGTSFAGHNSAICA 1009 |
| δý | 61   | SSASYINFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASN 120   |
| QC | 1010 | SSASYINFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHXAVYASSTGNDASN 1069  |
| λŏ | 121  | FANALLEEVLTAKTVVTAPEAIRGTRYQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINL 180   |
| q  | 1070 | FANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINL 1129  |
| ò  | 181  | DDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGHLCLSSGQLGWLTAHGGTN 240   |
| Op | 1130 | DDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGKLCLSSGQLGWLTAHGGTN 1189  |
| ò  | 241  | VVASFSWIGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTV 300   |
| Op | 1190 | VVASFSWIGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTV 1249  |
| ò  | 301  | VFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKKVVAFRHYNCSDLNYILL 360  |
| qq | 1250 | VEBETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILL 1309  |
| δ  | 361  | DDIQPTWGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSP 420   |
| qa | 1310 | DDIQFINGGSPTPTDYTYTVYRDGTKIKEGLIBITFEBBDGVAIGNHEYCVBVKYTAGVSP 1369 |

421 KECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456

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lysine-specific cysteine proteinase porphypain (EC 3.4.22.-) - Porphyromonas gingivalis N.Alternate names: lysine-specific cysteine proteinase 1, 60K (Species Drophyromonas gingivalis C.Species 22-Oct-1999 #corphyromonas gingivalis C.Accession: T30836; T30837; T30826; A53113 (Rattocy-Gallagher, G.A.; Han, N.; Patti, J.M.; Whitlock, J.; Progulske-Fox, A.; Lantz, J. Bacteriol. 178, 2734-2741, 1996 (A.Tile: Analysis of the prtP gene encoding porphypain, a cysteine proteinase of Porphymarkeesion: T30836 (A.Tile: Analysis of the prtP gene encoding porphypain, a cysteine proteinase of Porphymarkeesion: T30836 (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile: DNA) (A.Tile
C;Accession: S49763

R;Aduse-Opoku, J.; Muir, J.; Slaney, J.M.; Rangarajan, M.; Curtis, M.A.

submitted to the EMBL Data Library, November 1994

A;Description: Cloning, sequence analysis and expression in Escherichia coli of prpRl A;Reference number: S49763

A;Reference number: S49763

A;Status: preliminary

A;Molecule type: DNA

A;Molecule type: DNA

A;Cross-references: EMBL:X82680

C;Genetics:
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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C;Keywords: cysteine proteinase; hydrolase
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NAthernate names: 50K high molecular mass arginine-specific cysteine proteinase; HGP; R
C;Species: Porphyromonas gingivalis
C;Date: 10-Reb-1995 #sequence_revision 10-Reb-1995 #text_change 08-Oct-1999
C;Accession: A55466; D33133
R;PavJoff, N.; Potempa, J.; Pike, R.N.; Prochazka, V.; Kiefer, M.C.; Travis, J.; Barr, F
J. Biol. Chem. 270, 1007-1010, 1995
A;Title: Molecular cloning and structural characterization of the Arg-gingipain proteina
A;Accession: A55426
A;Accession: A55426
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A.Title: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolat A.Reference number: A53113; MUID:94103245; PMID:8276827
A.Accession: D53113
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C;Species: Porphyromonas gingivalis
C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 31-Mar-1997
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A,Residues: 1-1704 <PAV>
A,Cross-references: GB:U15282; NID:g557067; PIDN:AAA69539.1; PID:g557068
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A;Molecule type: protein
A;Residues: 228-249 -PIKS-
A;Residues: 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 0.00 - 
              KECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 1405
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ECVNVTINPIQFNPVKNLKAQPDGGDVVLKWEAPS 1401
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86.2%; Pred. No. 2.2e-135;
ive 17; Mismatches 40;
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Best Local Similarity 86.2%
Matches 392; Conservative
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-991 <RES>
A;Cross-references: GB:D26470; NID:g927644; PIDN:BAA05484.1; PID:g927645
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Best Local Similarity 20.99
Matches 123; Conservative
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Best Local Similarity
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A; Modecule type: DNA
A; Modecule type: DNA
A; Modecule type: DNA
A; Modecule type: DNA
A; Residues: 1-1350, NV, 1352-1363, YY, 1365-1447, 'H', 1449-1732 < LEW>
A; Cross-references: EMBL.AP017059; NID: 92738802; PID: 92738803; PIDN: AAC26523.1
S; Pike, R.; McGraw, W.; Potempa, J.; Travis, J.
J. Biol. Chem. 269, 406-411, 1994
A; Title: Lypsine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolat
A; Reference number: A53113; MUID: 94103245; PMID: 8276827
A; Reference protein
A; Residues: 229-249 < PIK>
A; Molecule type: protein
A; Residues: 229-249 < PIK>
A; Molecule type: protein
A; Residues: 229-249 < PIK>
A; Molecule type: protein
A; Residues: 229-249 < PIK>
A; Molecule type: protein
A; Residues: 229-249 < PIK>
A; Note: sequence extracted from NCBI backbone (NCBIP:141690)
C; Genetics:
A; Genetics:
A; Genetics: C; Keywords: cysteine proteinase; hydrolase
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Cispecies: Porphyromonas gingivalis
Cipate: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 08-Oct-1999
Ciacession: 140229
Riokamoto, K.; Misumi, Y.; Kadowaki, T.; Yoneda, M.; Yamamoto, K.; Ikehara, Y.
Arch. Biochem. Biophys. 316, 917-925, 1995
A;Title: Structural characterization of argingipain, a novel arginine-specific cysteine
A;Residues: 1-795,'I',797-1389,'N',1391-1478,'Y',1480-1732 <SLA>
A;Cross-references: EMBL:U75366; NID:g2182811; PID:g2182812; PIDN:AAB60809.1
A;Cross-references: EMBL:U75366; NID:g2182811; PID:g2182812; PIDN:AAB60809.1
Infect: Immun. 66, 3035-3042, 1998
A;Title: I5195, an insertion sequence-like element associated with protease genes in A;Reference number: Z20844; MUID:98298016; PMID:9632563
A;Reference number: T30326
A;Reference number: T30326
A;Reference number: T30326
A;Reference number: T30326
A;Reference number: T30326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.0%; Score 2034.5; DB 2
84.3%; Pred. No. 4.3e-132;
live 19; Mismatches 44;
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Cisperved hypothetical protein Atu3276 [imported] - Agrobacterium tumefaciens (strain C (Species: Agrobacterium tumefaciens C (Species: Agrobacterium tumefaciens C (Species: Agrobacterium tumefaciens C (Species: Agrobacterium tumefaciens C (Species: Agrobacterium tumefaciens C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Species) C (Spe
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                                                                                                            19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 QGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDV-EIKANGKRADFTETFESSTHGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 TIDADGDGNNWTTTPPPPGGTSFAGHNSAICASSASYINFEGPONPDNYLVTPELSLPNGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        680 TLKWDAPSTKINATTN-TARSVDGIRELVLLSVSDAPELLRSGQAEIVLEAHDVANDGS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      372 TPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVNVTVDPV
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                                                                                                                                                                                                                                                           Query Match
10.7%; Score 266; DB 2; Length 99:
Best Local Similarity 25.9%; Pred. No. 2e-10;
Matches 114; Conservative 50; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.6%; Score 139.5; DB 2; Length 1
20.9%; Pred. No. 0.12;
Live 67; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LTATT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLTLTV----VGYNKETVIKTINTNGEPNPYQPVSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 TTTLSESFENGIPASWKTIDADGDGNNWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432 QFNPVQN-LTGSAVGQKVTL 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADVTAQKPYTLTVVGKTITV 941
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A;Map position: linear chromosome
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Tue May 18 14:34:53 2004

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|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Db 287 VTAXVDNGTVNSGSVDVGFQGSGSLSVVNGGSLDAYLLYVGNALGSSGAVLVSGSVGSHVS 346  Qy 294NAGD                                                                                                                                          | 4 6 6 6                                   | :     :                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| Qy         379 TVPRDGTKIKEGLTETT                                                                                                                                                                                              | RESULT B75622 hypoth C;Spec C;Date C;Acce | etical protein - Deinococcus radiodurans (strain R1) ies: Deinococcus radiodurans : 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000 ssion: B75622 e, 0. Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| SULT 7  SULT 7  SULT 7  SULT 7  SULT 7  SULJ 1985 [imported] - Agrobacterium tumefaciens (strain C becies: Agrobacterium tumefaciens C by C 12-0ct-2014    Species: Agrobacterium tumefaciens                                 | 8, Cere<br>oldman,<br>1z, B.;<br>ium tum  | 7. Sinth, Work Wander J. J. J. Jam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mr. S.; Smith, Wo.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999 A,Title: Ganome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: B7562 A;Accession: B7562 A;Accession: B7562 A;Accession: B7562 A;Accession: B7562 A;Accession: B7562 A;Accession: B7562 A;Accession: B7562 A;Accession: B7562 A;Accession: B7562 A;Accession: B7622 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B7624 A;Accession: B76 |
| r chromosome                                                                                                                                                                                                                  | Query M<br>Best Lo<br>Matches             | Match 5.3%; Score 132.5; DB 2; Length 691; ocal Similarity 21.9%; Pred. No. 0.21; ss 111; Conservative 46; Mismatches 178; Indels 171                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| Db 341 TUTSESFENGIPASSETTTPPEGGTSFAGHNSAICASSAS 64  Db 341 TUTSESFENGIPASSETTTPPEGGTSFAGHNSAICASSAS 64  Db 341 TUTSGEAIIGRHSASEATVTGDGSKWTTGDLQVGGDTSDFGGLAGNGT388  Cy 65 YINFEGPQNPDNYLVTPELSLPNGGTLFWVCAQDANYASEHYAVXASSTGN | ò fi ò fi ò fi ò fi                       | 4 NPNPNPNGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSF 51  230 SPNPLPPTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |

| 239<br>492<br>299<br>523<br>342<br>581<br>641<br>01)                                                                                            | ickey, M.J.; Br  A; Experimental source: strain N315  C; Genetics: A; Gene: atl  Cuery Match  Cuery Match  Best Local Similarity 22.3%; Pred. No. 0.84;  Matches 105; Conservative 47; Mismatches 165; Indels 153; Gaps 2  Qy  3 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPP | 30; BB G 30; BB G 30 BB G 30 BB G 30 BB BB G 30 BB BB BB BB BB BB BB BB BB BB BB BB BB                                                                                                           | 189 Qy 264 TGATKVK 241 Db 924 TAPTAVKPTT 241 QY 308 GIN 986 Db 983 GQTWYYGKLS 292 RESULT 11 AH2515 Hypothetical protein alr C;Species: Nostoc sp. PC    |
|-------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------|
| HYALSGSTPIGPVKYYAINPDTDGDGGGWLCLSSGQ HYALSGSTPIGPVKYYAINPDTDGDGULSPAE  BDNYLISKDVTGAIKVXYYAVNDGFPGDHYAVMIS  BDNYLISKDVTGAIKVXYYAVNDGFPGDHYAVMIS | K.R.; Kas, Ssa PAO1, ar                                                                                                                                                                                                                                                       | A, Gene: PA1874  Query Match  Query Match  Best Local Similarity 22.2%; Pred. No. 1.3;  Matches 120; Conservative 47; Mismatches 184; Indels 189; Gaps  Qy  S PRINPADGTTTLSESFENGIPASWKTIDADGDGN | 130 LTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIKANG   130 LTAKTVVTAPEAIRVGGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIKANG   14 APAAPVNPSNGTTLSGT |

27;

Indels 149;

53; Mismatches 184;

DB 2;

Score 127.5; I Pred. No. 1.5;

5.1%;

81

----HNDIMNKDNEAAWANWGSD--

---NGMALNPDNYLISKDVTGATKVKYYYAVNDGFP 280

----FTAGTQGIILIENTAEPVT 604

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#97 QNV-LSHWQKLGQFRNNHIAIGAGAHQKLSDSPYTFARTYESDDIVDEVVVATGAGGTTA 555
                                                                                                                                                                                                                                                                                                                                                   140 BAIRGT-RVQGTWYQKTVQLPAGTKYVAFRHFGCTDFF--WINLDDVEIKANGKRADFTE 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  340 HVEIERWAELKNEAEVALÇTWRENNPÜKPGANW-----DDNFWMTAEVFGHGLGKSEYFD 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LIQAGTALLLPFGGVQVFYGDETARPLGDGG-----SDPEQGTRSSMNWANIN 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 DYTYTVYRDGTKIKEGLT--ETTFEEDGVAJGNHEYCVEVKYJAGVSPKECVNVTVDPVQ 432
                                                                                                                                                                                                                                                                                         281 PILRNKWNDQASGYEDWF-VPAAEPYRQDLNIAPKDYLIKWITSWVEEFGIDGFRVDTAK
                                                                                                                                                                                                                                                         82 ELSLPNGGILTFWVCAQD-ANYASEHYAVYASSTGNDASNFANALLEEVLTAKTV-VTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 TFESSTHGEAPAE----WITIDADGDGOGWLCLSSGOLGWLTA----HG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395 FGFDSVINFEFQNANFUNLEGLFSRYANSINTDPDFNMLSYVSSHDTKL---YSRDD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 GDHYAVMISKTGTN----AGDFTVVF-EETPNGINKGGARFGLSTEADGAKPQSVW--IE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 RIVDLPAGTKYVAFR-----HYNCSDLNYI-----LLDDIQFTMGGSPTPT
                                                                                                                                                         23 GIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAICA-SSASYINFEGPQNPDNYLVTP
            A;Cross-references: EMBL:X53373; NID:g48305; PIDN:CAA37453.1; PID:g48306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 GLPRDWTPNQA--QGQNWHT-
                                                                                                         Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GTNVVASFSW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433 FNPVQNLT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    605 NLPIVSAT 612
                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-713 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: B75489
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: DR0685
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             449
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                                                                      R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amylase A-180 - alkaliphilic eubacterium 163-26
C,Species: alkaliphilic eubacterium 163-26
C,Species: 1-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 15-Oct-1999
C,Accession: 510789
R,Candussio, A.; Schmid, G.; Boeck, A.
Eur. J. Biochem. 191, 177-185, 1990
A,Title: Biochemical and genetic analysis of a maltopentaose-producing amylase from an A,Reference number: $10789; MUID:90336627; PMID:1696201
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH2515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-----ITQSGGSTAVIEG-GNTDSYTLVLRTQPTADVTVTLNTGSQITTDKTTLTF 3257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
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                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-4936 «KUR»
A;Crosa-references: GB:BA000020; PIDN:BAB78388.1; PID:g17135842; GSPDB:GN00180
A;Experimental mource: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----WVCAQ------DANYASEHYAVYASSTGNDASNFANALLEEVLTAKTVVTAPEA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 IRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIKANGKRA--DFTETFE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------KGGARFGLSTEA----DGAKPQSVWIERTVDLPAG--TKYVAFRHYNCS 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GTPNPNPNPNPNPGT-----TTLSESFENGIPASWKTIDADGDGNNWTT-----TPPPGG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSFAGHNSAICASSASYINFEGPQNPDNYLV-----TPELSLP-NGG-----TLTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSTHGEAP--AEWITIDADGDGGGWLCLSSG-----QLGWLTAHGGTNV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                           5.2%; Score 128; DB 2; Length 4936;
20.4%; Pred. No. 5.5;
tive 60; Mismatches 171; Indels 190; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VASFSWNGMALN--PDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKT
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Best Local Similarity
                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                   A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 108;
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C.; M̃̃
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                                                                                                                                                                                                                                                                                             R1.
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Dee-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: B75489
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RA; Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.1%; Score 127; DB 2; Length 713; Best Local Similarity 21.6%; Pred. No. 0.51; Matches 129; Conservative 47; Mismatches 214; Indels 208;
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A,Status: preliminary A,Molecule type: DNA A,Residues: 1-1684 <CAN>

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| 281 GDHYAVMISKTGINAGDETVVEETENGINKGGARFGLSTEADGAKPGSVWIERT 335 402AVTVITTSQNDPTKSDITKDIIE'K'PGIAFGDPTPGLGGDFTPVGTPPT 451 336VDLPAGTKYVAFRHYNCSDLNYILLDDIQFTWGGSPF 372 452 GVPGNPGTPLTPGNPQTCTAPIRTYLPMBIANLGSQDDAFVVSGTAPVTVLNPDGTVNPT 511 373 PTDYTYTVYRDGTKIKBGLTETTFEEDGVATGNHEYCVEVKY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | RESULT 15 C86822 hypothetical protein yqbK [imported] Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: 056822 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehr] Genome Res. 11, 731-753, 2001 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis E A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Reference type: DNA A;Residues: 1-1649 cSTO> A;Cross-references: GB:AE005176; PID:g12724583; PIDN:AAK05677.1; GSPDB:GN00146 C;Genetics: A;Gene: yqbK |
| prophage pil protein 46, tail component [imported] - Lactococcus lactis subsp. lactis (species: Lactococcus lactis subsp. lactis (c) Species: Lactococcus lactis subsp. lactis (c) Lactococcus lactis subsp. lactis (c) Lactococcus lactis subsp. lactis (c) Lactococcus lactis subsp. lactis (c) Lactococcus lactis (c) Lactococcus lactis (c) Lactococcus lactic (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactococcus (c) Lactoco | Query Match Best Local S Matches 110 65 118 118 142                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Query Match         5.14; Score 126; DB 2; Length 1441;           Best Local Similarity 22.34; Pred. No. 1.5;         Length 1441;           Matches 98; Conservative 49; Mismatches 133; Indels 160; Gaps 26;           QY         30 TIDADGDGNNWTTTPPEGGTSPAGHNSAICASSASYINFEGPONPDNYLVTPELSL 85;           Db         602 TISSSGTVTPTGMS.           COASTLIFWVCAQDANYASEHYAV-YASSTGNQVPTLVKEQYL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 0y 184 EIRANGKRADFTETFESSTHGEAPAEWTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |

| 449 IGQALFIGGNAGIGASYAQAINSTIAAQGILYANIINYIKSAFITGIA 496 | 418VSPKECVNVTVDPVQFNPVQNLTGSANGQKVT 449 | 497 GAVYGIVGGNGHDSLKISPSQWGLGSQTGLDSAVGVT-DAKAYGQIPSTTVVSNAQKIT 554 |
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| TVXC   | <u>:</u> |
| GSAVGO |          |
| ONLTC  | <u></u>  |
| DFNPV  |          |
| VDPV   | _        |
| CVNV   | <u> </u> |
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| 418    |          |
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<sup>497</sup> GAVYGIVGGNGHDSLKISPSQWGLGSQTGLDSAVGVT-DAKAYGQIPSTTVVSNAQKIT 554

Search completed: May 18, 2004, 11:47:50 Job time : 12.906 secs

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P52081 staphylococ

Q62010 mus musculu

D50899 cellulomona

Q4576 bacillus th

P50401 cellulomona

Q8x8v7 escherichia

D52847 bacillus me

P46590 candida alb

Q49379 mycoplasma

D2851 archaeoglob

P25927 salmonella

P20533 bacillus ci

Q58789 methanocococ

Q45753 bacillus ci

Q58789 metranocococ

Q45753 bacillus ci

Q5536 trongyloce

D0653 router mem

P15921 rickettsia

Q9rem mycoplasma

P07897 rattus norv

P76347 escherichia

P07897 rattus norv

P76347 escherichia

P07897 rattus mem

P1591 rickettsia

Q9rem mycoplasma

P07897 rattus norv

P76347 escherichia

Q9148 serratia ma

P14914 rickettsia

Q53047 router mem

P6595 bacillus th
                                                              May 18, 2004, 11:35:14 ; Search time 8.3342 Seconds (without alignments) 2848.981 Million cell updates/sec
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1 GTPNPNPNPNPNPGTTTLSESF.....QNLTGSAVGQKVTLKWDAPN 456
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P46071
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Copyright (c) 1993 - 2004 Compugen Ltd.
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PRCHI PORGI
ATU STANU
GGP MOUSE
SIAĀ LACIR
GUKA CELFI
CSAA BACUD
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VEDJ ECCS7
BGAL BACNE
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|                | 34                     | 105                                     |                                         | 1045         | н.                                           | GUNB CELFI                                                                                                             | P26225 cellulomona                       |
|----------------|------------------------|-----------------------------------------|-----------------------------------------|--------------|----------------------------------------------|------------------------------------------------------------------------------------------------------------------------|------------------------------------------|
|                | 5 Y                    | 103 5                                   |                                         | 2182         | н -                                          | ZAN HUMAN                                                                                                              |                                          |
|                | 37                     | 103.5                                   | 1. 4.<br>3. C.                          | 1655         | ٦,                                           | AINZ CLUIM<br>OMPB RICCN                                                                                               | P10478 Clostridium<br>O9kka3 r outer mem |
|                | 38                     | 103.5                                   |                                         | 1861         |                                              | APU THETU                                                                                                              | t amvlor                                 |
|                | 39                     | 103                                     |                                         | 1157         |                                              |                                                                                                                        | 045704 bacillus th                       |
|                | 40                     | 102.5                                   |                                         | 282          |                                              | PRTA_ASPNG                                                                                                             |                                          |
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|                | 44                     | 101.5                                   |                                         | 1462         | + r-                                         | PTPE DROWE                                                                                                             |                                          |
|                | 45                     | 101.5                                   |                                         | 2132         | ı                                            | PGCA_MOUSE                                                                                                             |                                          |
|                |                        |                                         |                                         |              |                                              |                                                                                                                        |                                          |
|                |                        |                                         |                                         |              |                                              | ALIGNMENTS                                                                                                             |                                          |
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| T T            |                        | DODGT                                   |                                         | . חסגתואמדם  |                                              | AR OCAC . Had                                                                                                          |                                          |
| AC             | 0518                   | 14.                                     |                                         | , dans       |                                              |                                                                                                                        |                                          |
| DT             | 30-1                   | MAY-2000                                | (Rel.                                   | 39, Cre      | ate                                          | id >                                                                                                                   |                                          |
| TO             | 30-1                   | MAY-2000                                | (Rel.                                   | 39, Last seq | žť.                                          | sequence update)                                                                                                       |                                          |
| TO             | 10-(                   | 10-OCT-2003                             | (Rel.                                   | 42, Last     | ц                                            | annotation update)                                                                                                     |                                          |
| DE             | Hems                   | Hemagglutinin A precursor               | n A pr                                  | ecurso       |                                              | ı                                                                                                                      |                                          |
| N.             | HAGA                   |                                         |                                         |              |                                              |                                                                                                                        |                                          |
| S C            | Port                   | Porphyromonas<br>Bacteria: Dact         | is ging                                 | ivalis       | (Ba                                          | onas gingivalis (Bacteroides gingivalis).<br>Bacteroides Bacteroides Gingivalis).                                      |                                          |
| 35             | בו<br>מ<br>מ<br>מ<br>מ | Dorrhyromonadaceae: Dorrhyromonad       | dana dana                               | י ביים       | מו ל                                         | S<br>S                                                                                                                 | roldales;                                |
| ö              | NCBI                   | TaxID=837:                              | 37:                                     | 4704         | 7 7 7                                        | monab.                                                                                                                 |                                          |
| RN             | Ξ                      |                                         |                                         |              |                                              |                                                                                                                        |                                          |
| RP             | SEOU                   | SEQUENCE FROM N.A.                      | M N.A.                                  |              |                                              |                                                                                                                        |                                          |
| RC             | STR                    | AIN=381;                                |                                         |              |                                              |                                                                                                                        |                                          |
| ጟ              | MEDI                   | LINE=9704                               | 7672;                                   | PubMed=      | -892                                         | 6061;                                                                                                                  |                                          |
| RA             | Han                    | N., Whit                                | lock J                                  | ., Prog      | Jul 8                                        | Han N., Whitlock J., Progulske-Fox A.;                                                                                 |                                          |
| RT             | "The                   | hemaggl                                 | utinin                                  | gene A       | 2                                            | agA) of Porphyromonas g                                                                                                | ingivalis 381                            |
| RI             | cont                   | cains fou                               | r larg                                  | e, cont      | igu                                          | ous, direct repeats.";                                                                                                 |                                          |
| X (            | Int                    | ect. Immu                               | n. 64:                                  | 4000-40      | 004                                          | 1996).                                                                                                                 |                                          |
| ၁ ဗ            | 1                      | FUNCTION                                | - Agg1                                  | utinate      | 88                                           | rythrocytes.                                                                                                           |                                          |
| 3 5            |                        | SIMILAKI                                | IX: Be                                  | Tongs t      | 0                                            |                                                                                                                        |                                          |
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| 36             | Tul                    | SWISS-P                                 | KOI en                                  | cry 18       | S :                                          | Inls SWISS-PROT entry is copyright. It is produced through a between the cuit Institute of Bidisfermential and the man | collaboratio                             |
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| E E            | EMBI                   | U41807                                  | ; AAB1                                  | 7128.1;      | i                                            |                                                                                                                        |                                          |
| K i            | PIR;                   | ; T28651;                               | T28651                                  |              |                                              |                                                                                                                        |                                          |
| KW             | Heme                   | agglutini                               | n; Vir                                  | ulence;      | H                                            | Hemagglutinin; Virulence; Hydrolase; Thiol protease;                                                                   | ; Signal; Repeat.                        |
| <br>           | SIGNA                  | T AT                                    |                                         | 4, 6         |                                              | POTENTIAL.                                                                                                             |                                          |
| T E            | DOMAIN                 |                                         | 2 2                                     | 539          |                                              | HEMAGGLOTININ A.<br>PEPTIDASE C25-1.TKE 1                                                                              |                                          |
| FT             | DOMAIN                 |                                         |                                         | 900          |                                              |                                                                                                                        |                                          |
| FF             | DOMAIN                 |                                         |                                         | 1451         |                                              | C25-LIKE 3                                                                                                             |                                          |
| FT             | DOMAIN                 |                                         |                                         | 1907         |                                              | C25-LIKE 4                                                                                                             |                                          |
| FT             | DOMAIN                 |                                         |                                         | 2628         |                                              | C25-LIKE 5                                                                                                             |                                          |
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Length 2628; Indels

2628 AA; 283324 MW; 61C4DE32540C99DA CRC64;

SEQUENCE

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Query Match Best Local Similarity 100.0 Matches 456; Conservative

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Matches 449; Conserv
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                                   1190 VVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTV 1249
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Dewhirst F.E., Fraser C.M.;
Porphyromonas gingivalis strain W83.";
Porphyromonas gingivalis strain W83.";
J. Bacteriol. 185:5591-5604 (2003).
-i. FUNCTION: Agglutinates erythrocytes (By similarity).
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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PEPTIDASE C25-LIKE 1.
PEPTIDASE C25-LIKE 2.
PEPTIDASE C25-LIKE 3.
M; 6DFAB22832586C63 CRC64;
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2164 AA;
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Fletcher Immun. 62:5707-5707 (1994).

-1- FUNCTION: CLEAVES HUMAN COMPLEMENT COMPONENT C3. MAY ENABLE
F.GINGTIVALIS TO EVADE COMPLEMENT-MEDIATED KILLING DURING THE
IMMUNE RESPONSE. PLAYS AN IMPORTANT ROLE IN SOFT TISSUE INFECTIONS
AND IS A VIRULENCE PACTOR.

-1- SUBCELLULAR LOCATION: In membrane vesicles.
-1- SIMILARITY: Belongs to peptidase family C25.
                                                                                                                                                                                                                     ASYINFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFA
                                                                                                                                                                                                                                                                                    123 NALLEEVLTAKTVVTAPBAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDD
                                                                                                                            196 PNGTPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGSSFAGHNSAICVSS
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
Pred. No. 6.2e-161;
2; Mismatches 3; Indels
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01-NCV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protease prtH (BC 3.4.22.-).
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Infect. Immun. 62:4279-4286(1994)
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 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                          209
                                                                                                                                                                                                                                                                                                                                                                                            270 IPIDYTYTVYRDGTKIKEGLIETTFEEDGVATGNHEYCVEVKYTAGVSPKKCVNVTVNST 329
                                                                                                                                                                                             191
                                                                                                                                                                                                                                        251
                                                                                                                                                                                                                                                               149
                                                                                                                                                                                                                                                                                                                                                                              TPIDYTYTVYRDGTKIKEGLIETTFEEDGWATGNHEYCWEWKYTAGWSPKECWNWTWDPW 431
                                                                                                                                                                                                                                                                                     LNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINK 311
                                                                                                                                                                                                                                                                                                                                 GGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSP 371
                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                      90 ADFTETFESSTHGEAPAEWITIDADGDGQGWLCLSSGQLDWLTAHGGTNVVSSFSWNGWA
                                                                                                                                                                                                                                                                                                  136 VTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFG----CTDFFWINLDDVEIKANGKR
                                                                                                                                                                                                                                                                                                                                                    210 GGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSP
                                                                                                                                                                                                                 34 VRSPEAIRG-RIQGTWRQKTVDLPAGTEICCFPSLPKAPICSTSTLMRL----RSKTNAKR
                                                                                                                                                                                                                                        192 ADFIETFESSTHGEAPAEWITIDADGDGQGWLCLSSGQLGWLTAHGGTNVVASFSWNGMA
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen Z., Potempa J., Polanowski A., Wikstrom M., Travis J., "Purification and characterization of a 50-kDa cysteine proteinase (gingipain) from Porphyromonas gingivalis.";
                                                                                                                                                Length 989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arginine-specific cysteine proteinase as a major periodontal
pathogenic factor from Porphyromonas gingivalis.";
Arch. Biochem. Biophys. 316:917-925(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okamoto K., Misumi Y., Kadowaki T., Yoneda M., Yamamoto K.,
                                                                                                                                                                    30; Indels
                                                                                                                          989 AA; 110238 MW; FA85FE8A3AC8944C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 228-290 AND 517-541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structural characterization of argingipain, a novel
                                                                                                                                                58.6%; Score 1453; DB 1;
84.9%; Pred. No. 5.7e-93;
ive 11; Mismatches 30;
                                                   MESOPS, C25.001; -. InterPro; IPR002376; formyl transf.
Pfam; PF00551; formyl transf; 1.
Hydrolase; Thiol protease; Repeat; Virulence.
           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                         OFNPVQNLTGSAVGOKVTLKWDAPN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                      330 QFNPVKNLKAQPDGGDVVLKWEAPS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95168884; PubMed=7864651;
                                 EMBL; L27483; AAA51298.1; -.
HSSP; P23882; IFMT.
                                                                                                                                                                     Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 228-270.
                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGPA OR RGP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=381;
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                                                                                                                          SEQUENCE
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680 TLKWDAPSTKTNATIN-TARSVDGIRELVLLSVSDAPBLLRSGQAEIVLEAHDVWNDGS-

ADGAKPQS---VWI-----ERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSP 371 ---AAPQANAKIWIAGQGPTKEDDYVFEAGKKY----HFLMKKMGSGDGTELTISEGGG- 863 TPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVNVTVDPV 431 

DVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLSTE 321

262

812

795 DGTASVNI------PAGTY------DFAI----

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LINES 637
                                                                                                                                                        complement C3 and C5.

CATALYTIC ACTIVITY: Cleavage of proteins, including collagens and immunoglobulins, with a preference for Arg in P1, and hydrophobic residues in P2 and P3.

ENZYME REGULATION: Requires cysteine for activation and Ca(2+) and/or Mg(2+) for stabilization. It is stimulated by glycine-containing dipoptides. It is resistant to inhibition by proteinase inhuman plasma.
Biol. Chem. 267:18896-18901(1992).
- FUNCTION: Thiol protease which is believed to participate in intracellular degradation and turnover of proteins. Its proteolytic activity is a major factor in both periodontal tissue destruction and in bacterial host defense mechanisms. Activates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 TIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASYINFEGPQNPDNYLVTPELSLPNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MERCYS; C25.001; ...
InterPro; IPR007110; Ig-like.
InterPro; IPR007159; Peptidase C25.
InterPro; IPR005536; Peptidase C25.
InterPro; IPR005536; Peptidase C25.
Pfam; PF01364; Peptidase C25, I.
Pfam; PF03785; Peptidase C25. C; I.
Virulence; Hydrolase, Thiol protease; Calcium; Signal; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50; Mismatches 164; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 PROTON DONOR (BY SIMILARITY).
171 NUCLEOPHILE (BY SIMILARITY).
155 RT -> TK (IN REF 2).
108782 NW, 03EE3F43CBBE2544 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVNVSCDYNGAIATISANGKMF --- GSAVVENGTATINLTG-
                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Belongs to peptidase family C25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.7%; Score 266; DB 1; 25.9%; Pred. No. 8.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GINGIPAIN R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D26470; BAA05484.1; -.
PIR; 140229; 140229.
HSSP; P95493; 1CVR.
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991
438
471
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ACT_SITE
CONFLICT
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                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-SE-FEB-2003 (Rel. 41, Last annotation update)
Bifunctional autolysin precursor [Includes: N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28); Mannosyl-glycoprotein endo-beta-N-acetylglucosamidase (EC 3.2.1.96)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foster S.J.; Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: ENDOHYDROIVSIS OF THE DI-N-ACETYLCHITOBIOSYL UNIT IN HIGH-MANNOSE GLYCOPEPTIDES AND GLYCOPROTEINS CONTAINING THE -[(MAN) S (GLCNAC)2] ASN STRUCTURE. ONE N-ACETYL-D-GLUCOSAMINE RESIDUE REMAINS ATTACHED TO THE PROTEIN; THE REST OF THE OLIGOSACCHARIDE IS RELEASED INTRAT.
-!-CATALYTIC ACTIVITY: Hydrolyzes the link between N-acetylmuramoyl residues and L-amino acid residues in certain bacterial cell-wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATALYTIC ACTIVITY: Endohydrolysis of the di-N-acetylchitobiosyl unit in high-mannose glycopeptides and glycoproteins containing the -[Man(GloMAc)2]Ann-structure. One N-acetyl-D-cultining residue remains attached to the protein; the rest of the oligosaccharide is released intact.

SUBCELULAR LOCATION: Secreted.

FIM: UNDERGOES PROTEOLYTIC PROCESSING TO GENERATE THE TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR LYTIC ENZYMES.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE N-ACETYLMURAMOYL-L-ALANINE AMIDASE FAMILY 2.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 73 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A Staphylococcus aureus autolygin that has an N-acetylmuramoyl-L-alanine amidase domain and an endo-beta-N-acetylglucosaminidase domain: cloning, sequence analygis, and characterization."; Proc. Natl. Acad. Sci. U.S.A. 92:285-289(1995).
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InterPro; IPR002901; Amidase_4.
Fram, PF01210; Amidase_2; 1.
SMART; SM00644; Ami_2; 1.
SMART; SM00047; LYZ2; 1.
CELl wall; Hydrolase; Signal; Multifunctional enzyme; Repeat.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95116542; PubMed=7816834;
Oshida T., Sugai M., Komatsuzawa H., Hong Y.-M., Suginaka H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 205-214 AND 776-792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria, Firmicutes, Bacillales, Staphylococcus
NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                          922 ADVTAČKPYÍLTVVČKTIÝV 941
   432 OFNPVQN-LIGSAVGQKVTL
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                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=RN450;
                                                                                                                                                                                                           ATL_STAAU
P52081;
01-OCT-1996
01-OCT-1996
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594 PTPTPTPKPSTPTTNNKLTVSSLNGV----AQINAKNNGLFTTVYDKTGKPTKEVQKTFA 649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       766 AVAQPKTAVKAYTVIKPQTIQIVSKIAQVKPNNTGIRASVYEKTAK--NGAKY-ADRTFY 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 WITIDADGDGQGWLCLSSGQLGWLTAHGGTNVVASFSWN-----GMALNPDNYLISKDV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 IGAIKVK------YYYAVNDGFPGDHYAVMISKIGT-----NAGDFTVVFEETPN 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          650 VIKEASLGGNKFYLVKDYNSPTLIGWVKQGDVIÝNNAKSÞVNVMQTÝTVKPGTKLYSVÞW 709
                                                                                                                                                                                                                                                                                                                                                                                       G-----GTLIFWVCAQDANYASEHYAVYASSTGNDASNFAN------ALLE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 EVLTAKT-----VVTAPEAIR------GTRVQGTWYQKTVQLPAGTKYVAFRHFG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --DFFWINLDDVEIKANGKRADFTE--TFESSTHGEAPAE 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 823 VIKERAHGNETYVLINNTSHNIPLGWFNVKDLNVQNLGKEVKTTQKYTVNKSNNGLSMVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           883 WGT-----KNQVILIGNNI----AQGTFNATKQVSVGKDVYLYGTINNRTGWVNAKDL
                                                                                                                                                                                                                                                                                                              47 -----GGTSF---AGHNSA----ICASSASYINFEGPON-PDNYLVTPE---LSLPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                      N-ACETYLMURAMOYL-L-ALANINE AMIDASE.
ENDO-BETA-N-ACETYLGLUCOSAMIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      991 GQTWYYGKLSNGKLAWIKST--DLAKELIKYNQTGMTLNOVAOIQAGLOY 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Oviduct-specific glycoprotein precursor (Oviductal glycoprotein)
(Oviductin) (Bstrogen-dependent oviduct protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 G-----INKGGARFGLSTEADGAK-----POSVWIERTVDLPAGTKY 344
                                                                                                                                                          DB 1; Length 1256;
                                                                                                                                                                                                                                3 PNPNPNPNPNPGTTT----LSESFENGIPASWKTIDADGDG---NNWTTTPPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ICR; TISSUE=Oviduct;
MEDLINE=96115001; PubMed=7492680;
Sendal Y., Komlya H., Suzuki K., Onuma T., Kikuchi M., Hoshi
                                                                                                                                                      Similarity 22.3%; Score 131.5; DB 1; Length 1 Similarity 22.3%; Pred. No. 0.24; 15; Conservative 47; Mismatches 165; Indels
                                                                                                                  137384 MW; 2BB76CAA292FDD20 CRC64;
      BIFUNCTIONAL AUTOLYSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                721 AA
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  30 125
199 77
776 125
425 58
596 75
770 93
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                                                                                                                                                  Query Match
Best Local Simil
Matches 105; (
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Q62010;
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                                                                                                                  SEQUENCE
CHAIN
DOMAIN
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                             EGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALLEE
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21 X 7 AA TANDEM REPEATS OF S-K-T-T-[TAP]-G-[IV].

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                         185; Indels 202;
                                                                                                                                                                                                                                                                                                                5.1%; Score 126; DB 1; Length 721;
18.9%; Pred. No. 0.28;
tive 55; Mismatches 185; Indels 20
                                                                                                                                                                                                                                                                              469 N-LINKED (GLCNAC. . .) (PC 78807 MW; 37246C8F01665652 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             R MGD; MGI:106661; Ovgpl.
R InterPro; 1PR001223; Glyco hydro 18.
InterPro; 1PR001223; Glyco hydro 18.
R Pfam; PR000044; Glyco hydro 18; 1.
ProDom; P000041; Glyco hydro 18; 1.
R PROSITE; RM00636; Glyco hydro 18; 1.
PROSITE; P801095; CHITINASE 18; FALSE NEG.
Glycoprotein; Fertilization; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                FAGHNSAICA----SSASYINF---
                                                                                                  EMBL; D32137; BAA06863.1; -.
                                                                                                                                                                                                                                                                                                                                         Matches 103; Conservative
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RESULT 7

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TSTDGTKAGSKVSDKAADQTALEAYINANKPSGYTVTNPNAA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               382 RDGTKIKEGLIETTFE-------EDGVATGNHEYCVEV-----KYTAGVSFK 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 TITLSESFEN-GIPASWKTIDA----DGDGNNWTTTPPPGGTSFAGHNSAICASSASYIN
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                                                                                                                                                                                                                                                                                                                                                             STRAIN=ATCC 8287 / DSM 20556;
MEDLINE=930451388; PubMed=1429463;
MEDLINE=930451389; PubMed=1429463;
Widgren G., Palva J., Pakkanen K., Lounatmaa K., Palva A.;
"S-layer protein gene of Lactobacillus brevis: cloning by polymerase chain reaction and determination of the nucleotide sequence.";
J. Bacteriol. 174:7419-7427(1992).
-I. FUNCTION: The S-layer is a paracrystalline mono-layered assembly of proteins which coat the surface of bacteria.
-I. SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-layer with tetragonal symmetry.
-I. SIMILARITY: SOME, TO THE S-LAYER PROTEIN OF L.ACIDOPHILUS.
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                                                                                                                                                                                                                                   Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
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                                                                                                                                                                       S-layer protein precursor (Surface layer protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.9%; Score 121.5; DB 1;
19.8%; Pred. No. 0.32;
ive 48; Mismatches 201;
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                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-LAYER PROTEIN.
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      465 AA
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   STANDARD;
                                                                                                                                                                                                       Lactobacillus brevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 99; Conserv
                                                                                                                                                                                                                                                           Lactobacillus.
NCBI_TaxID=1580;
SLAP LACBR
Q05044;
01-JUN-1994 (
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 CenE, a member of a new family of beta-1,4-glucanases.";
Biochem. Biophys. Res. Commun. 199:1223-1228(1934).
-! FUNCTION: Hydrolyze cellohexaose to a mixture of cellotetraose,
cellotriose and cellobiose, with only a trace of glucose. It
hydrolyzed cellopentaose to cellotriose and cellobiose, and
cellotetraose to cellobiose, but it did not hydrolyze cellotriose.
Has also weak endoglucanase activity. Hydrolyzes glucosidic bonds
with inversion of anomeric configuration.
-!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
in celliblose and cellotetraose, releasing cellobiose from the non-
reducing ends of the chains of the chains.
-!- SIMILARITY: Contains 1 fibronectin type III domains.
-!- SIMILARITY: Contains 1 bacterial-type cellulose-binding (CBD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93209933; PubMed=8458833; Miller R.C. Jr., Warren R.A.J.; Meinke A., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.; "Cellulose-binding polypeptides from Cellulomonas fimi: endoglucanase D (CenD), a family A beta-1.4-glucanase."; J. Bacteriol. 175:1910-1918(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO CELLULASE FAMILY L (FAMILY 48 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                     Shen H., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.; "Cellobiohydrolase B, a second exo-cellobiohydrolase from the cellulolytic bacterium Cellulomonas fimi."; blochem. J. 311:67-74(1955).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shen H., Tomme P., Meinke A., Gilkes N.R., Kilburn D.G.,
Warren R.A.J., Miller R.C. Jr.,
"Stereochemical course of hydrolysis catalysed by Cellulomonas fimi
                                                                                                                                                                                                                                          m
                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Excollucanase B precursor (EC 3.2.1.91) (Exocellobiohydrolase (1,4-beta-cellobiohydrolase B) (CBP120).
                                                                                                                                                                                                                                                                                                         Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Micrococcineae, Cellulomonadaceae, Cellulomonas.
                                                                                                                                                              PRT; 1090 AA.
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 456-461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S59077; S59077.
HSSP; P07986; LBXG.
InterPro; IPR001919; Bac celose-bind.
InterPro; IPR001955; CelIul bind.
                                            ECVNVTVDPVQFNPVQNLTGS 442
                                                                          429 ASSNAS---TOFG--SNVTGT 444
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96003898; PubMed=7575482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94197708; PubMed=8147863;
                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
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                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 54-75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 54-78
                                                                                                                                                                                                                                                                                        Cellulomonas fimi
                                                                                                                                                                                                                                                                                                                                      NCBI TaxID=1708;
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 484;
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GUXB CELFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 VTAPEAIRGTRVQG------TWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             620 IYIPSGWTGTMPNGDVIKPGVSFLDIRSFYKKD---PNWSKVQTFLDGGABPQFRYHRFW 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 VEIKANGKRADFTETFESSTHGEAPAEWŢŢIDADGDGQGWLCLSSGQLGWLTAHGGŢNVV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              677 AQTAVAGALADYARLFDDGT-----TTPDTTAP-----TVPTG----LQAGVVTSTE 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVRAFDAAGNVSAPSAALTVTTKATPSDTTAP-----SVPAITS----SSSTA 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 NYILLDDIOFTMGGSPTPTDYT-----YTVYRDGTKIKEGLIETTFEEDGV-ATGNHE 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein crySAa (Insecticidal delta-endotoxin
CryVA(a)) (Crystaline entomocidal protoxin) (152 kDa crystal protein).
CRYSAA OR CRYVA(A) OR CRYVA.
Bacillus thuringiensis (subsp. darmstadiensis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         720 ATISWT--ASTDDTRVTGYDVYRGATKV-----GTATTTSFTDTGLTASTAYAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 ASWKT---IDADGDGNNWTTTPPPPGG-----TSPAGHNSAICASSASYINFEGPONPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 ASFSWNGMALNPDNYLISKDY-TGATKVKYYAVNDGFPGDHYAVMISKTGTNAGD---F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVVFEETPNGINKGGARFGLSTEA---DGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                811 NSV-----TIGWSAS-TDNAGGSGLAGYDVYRGATRVAQ-TTALTFTDTGLTASTAYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               574 TASRDKAKALLD----AIWANNODP-----LGVSAVETRGDYKRFDDTYVAN----GDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408 YCVEVKYTAG--VSPKECVNVTV-----DPVQFNPVQNLTGSAVGQ-KVTLKWDA 454
R InterPro; IPR008957; FN III-like.
R InterPro; IPR008951; FN III-like.
R InterPro; IPR008956; Glyco_hydro 48.
R InterPro; IPR008958; Glyco_hydro 48.
R InterPro; IPR008958; Glyco_hydro 48.
R Pfam; PF00151; Glyco_hydro 48; 1.
R Pfam; PF0011; Glyco_hydro 48; 1.
R PRINTS; PR00844; Glyco_hydro 48; 1.
R PRODIS; PR00644; Glyco_hydro 48; 1.
R PRODIS; PR00650; FN3; 3.
R PROSITE; PR00561; CBD_BACTERIAL; 1.
SMART; SM00060; FN3; 3.
R R CATRIPATION:
W Gellulose degradation; Hydrolase; Glycosidase; Repeat; Signal.
SIGNAL
T PROPEP
T CHAIN
S 4 199 EXOGLUCANASE B.
T CHAIN
T DOMAIN 700 788 FIBRONECTIN TYPE-III 1.
T DOMAIN 700 788 FIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC (BY SIMILARITY).
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
CELLULOSE-BINDING (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53; Mismatches 197; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.9%; Score 121; DB 1; Length 1090; 22.3%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 BY SIMILARITY.
114829 MW; 046BB9D956F2F399 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1385 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                              53
1090
699
785
884
978
1090
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794
891
989
513
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Q45760;
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DOMAIN
ACT SITE
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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MEDIANS=3320933; PubMed=8458833;

MEDIANS=33209933; PubMed=8458833;

Meinke A., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;

Meinke A., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;

"Callulose-binding polypeptides from Cellulomonas fimi: endoglucanase

"To Cennol, a family A beta-1,4-glucanase.";

"I D. Bacteriol. 175:1910-1918(193).

"I J. Bacteriol. 175:1910-1918(193).

"I J. Bacteriol. 175:1910-1918(193).

"I J. Bacteriol. 175:1910-1918(193).

"I J. Bacteriol. 175:1910-1918(193).

"I J. Bacteriol. Inkages of cellulose and barley beta-glucosidic linkages of microcrystalline cellulose and barley beta-glucan. Has also weak endoglucanase activity. Hydrolyses glucosidic bonds with inversion of anomeric configuration of 1,4-beta-D-glucosidic linkages

"I J. Bacteriol Service and barley beta-glucosidic linkages in cellulose and cellotetraose, releasing cellobiose from the non-reducing ends of the chains.

"I SIMILARITY: Contains 1 bacterial-type cellulose-binding (CBD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
         821 VQGNYTYTGTPVLILNAYRNNTVVSSIPVYSPFDITIQTEADSLELELQPRYGFATVNGT 880
                                                                                                      -!- SIMILARITY: Belongs to cellulase family B (family 6 of glycosyl
                                                                   408 YCVE---VKYTAGVS-PKECVNVT--VDPVQFNPVQNLTGSAVG----QKVTLKWDA
                                                                                                                                                                                                                                                                                                                                         01-0cT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Excelucanase A precursor (EC 3.2.1.91) (Exocellobiohydrolase A) (1,4-beta-cellobiohydrolase A) (CBP95).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cellobiohydrolase A (CbhA) from the cellulolytic bacterium Cellulomonas fimi is a beta-1,4-exocellobiohydrolase analogous Trichoderma reesei CBH II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meinke A., Gilkes N.R., Kwan E., Kilburn D.G., Warren R.A.J.,
Miller R.C. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Cellulomonadaceae; Cellulomonas.
NCBI_TaxID=1708;
                                                                                                                                                                                                                                                                                         872 AA
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                                                                                                                                                                                                                                                                                      PRT;
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InterPro; IPR003962; FWIII subd.
InterPro; IPR001362; FWIII subd.
InterPro; IPR001524; GJYco_hydro_6.
Pfam; PP000641; fm3, 3.
Pfam; PP001041; fm3, 3.
PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94344030; PubMed=8065260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Microbiol, 12:413-422(1994)
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                                                                                                                                                                                                                                                                                      STANDARD:
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InterPro; IPR001919;
InterPro; IPR008965;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cellulomonas fimi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 41-58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413 PAVDPQAĞPNYVSIDSSNPİIQINMDTWKİPPQGASĞ--WNİNLMRĞSVSGLSFLQRDGT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          471 RLSAGMGGGFADTIYSLPATHYLSYLYGTPYQTSDNYSGHVGALVGVSTPQEATLPNIG 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---NYASEHYAVYAS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 STGNDASNF-----ANALLEEVLTAKTVVTAPEAIRGTRVQG------TWYQ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 591 YASNDYINVFFNVDTGGANPIFQQINFASTV-----DNNTGVQGANGVYVVKSIATTDN 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 KTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIKANGKRADFTETFESSTHGEAPAEWTTI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             645 SPTEIPAKTINVHLTNQGSSDVF---LDRIEFIPFSLPLIYHGSYNTSS-GADDVLW--- 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 DADGDGQGWLCLSSGQLGWLTAHGGTNVVASFSWNGMALNPDNYLISK------DVTGA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------SSSNMNYY-----DIIVNGQANSSSIASSMHLLNKGKVIKTIDIPGH 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 TKVKY-YYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLSTEADGA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---DYTYT-----GVARDGTKIKEGLTETTF-----EED------GVATGNHE 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
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                                                                                                                                                                                                                                                                         FUNCTION: ENDOTOXIN WITH NEWATICIDAL ACTIVITY.

DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 PNPNPNPGTTTLSESFENGI----PASWKTIDADGDGNNWTTTPPPG---GTSF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----AGHNSAICASSA----SYINFEGPQNPDNY------LVTP-ELSLPN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             531 OPDEQGNVSTMGFPFEKASYGGTVVKEWLNGANAMKLSPGQSIGIPITNVTSGEYQIRCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                  the spore coat. MISCELLANEOUS: Toxic segment of the protein is located in the N- \ensuremath{\mathsf{MISCELLANEOUS}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66; Mismatches 192; Indels 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.8%; Score 118.5; DB 1; Length 1385; 20.1%; Pred. No. 2.2;
                                                                                                                   STRAIN=NRRL B-18243 / PS17;
Sick A.J., Schwab G.E., Payne J.M.;
Genes encoding nematode-active toxins cloned from Bacillus thuringiensis isolate P817.";
Patent number US5281530, 25-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 KPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSPTPT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1385 AA; 152439 MW; E29FF11FC799DE95 CRC64;
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the delta endotoxin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR, T18213; T18213.
InterPro; IPR005639; endotoxin C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal bind like.
Fram; PP03944; endotoxin C; 1.
Fram; PP03945; endotoxin N; 1.
Toxin; Sporulation.
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                                   NCBI_TaxID=132264;
                                                                                   FROM N.A.
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                                                                                         SEQUENCE
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A Committee

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PRINTS; PR01369; ĬNTIMIN.
SMART; SM00634; BID_1; 16.
SMART; SM00089; PKD; 8.
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DOMAIN 738 834
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        583 LTAGTTTTTTVPLSWTASTDNAGGSGVAGYEVLRGTTVVGTTTATSYTVT-GLTAGTTY- 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTNV--VASFSWNGMALNPDN----YLIS 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 KDVTG-----ATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINK-G 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNPDNYLVTPELSLPNGGTLTFWVCAQDA--NYASEHYAVYASSTGNDASNFANALLEEV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 GTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASYINFEGP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLTWT---ASTDNAG----GSGVAGYEVFNGTTRVATVTSTSYTVTGLAADTAYSFTVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              745 KDVAGNVSAASAAVSARTQAATSGG-----CTVKYSASSWNTG-FTGTVEVKNNGTAALN
                                                                                                                                                                                                                                                                                                                                                                                                                           24.3%; Pred. No. 2.4;
tive 29; Mismatches 146; Indels 112; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli 0157:H7.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                     FIBRONECTIN TYPE-III 3.
CELLUICOSE-BINDING (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
                                                                  PROSITE; PS00561; CBD BACTERIAL; 1.
PROSITE; PS00655; GLYGOSYL HYDROL F6 1; 1.
PROSITE; PS00656; GLYCOSYL HYDROL F6 2; 1.
Cellulose degradation; Hydrolase; Glycosidase; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                            Score 114; DB 1; Length 872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTTAT----SVPLSW---TASTDNVAVTGYDVYRGTTLVGTTAA
                                                                                                                                                                                                                                                                                                                                                                         7883B407F995533B CRC64;
                                                                                                                                                                                  CATALYTIC.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YEEJ ECO57 STANDARD; PRT; 2660 AA. 08X807; Q8X2B9; Q8X2C0; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) Hypothetical protein yeeJ. 23135 OR ECS2775/ECS2776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 AFRHFGCTDFFWINLDDVEIKANGKRADFTETFE--
                                                                                                                                                               EXOGLUCANASE A.
                 α.
           Probom; PD003733; Glyco hydro 6;
SMART; SM00637; CBD II; 1.
SMART; SM00060; FN3; 3.
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PRINTS; PR00733; GLHYDRLASE6
                                                                                                                                                                                                                                                                                                                                                                                                            4.68;
                                                                                                                                                                                                                                                                                                                                                                         89300
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DISULFID
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                                                                                                                                                                                                                                                                                                                              STRAIN=0157:H7 / RIMD 0509952;
MEDLINE21156231; PUMPdd=11258796;
Hayashi T. . Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Saeakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTLSESFE---NGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASYINFE
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grocbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Gelowe sequence of enterohaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533(2011).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0157.H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
1- SIMILARITY: Contains 16 Big-1 domains.
-!- SIMILARITY: Belongs to the intimin/invasin family.
-!- CAUTION: Ref. 2 sequence differs from that shown due to a frameshift in position 1315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58; Mismatches 199; Indels 106;
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EMBL; AP002559; BAB36198.1; ALT_FRAME.
EMBL; AP002559; BAB36199.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003344, Big.1.
InterPro; IPR003355; Intimin.
InterPro; IPR008964; Invasin_intimin.
InterPro; IPR000601; PKD.
Pfam; PF02369; Big.1; 16.
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BIG-1
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us-08-570-311-20.rsp

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4.5%;
                                                                                                                         19.9%;
                                                                                       Query Match
Best Local Similarity 19.99
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
       481
                                                   1034 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 LNPD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5476;
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    ACT_SITE
ACT_SITE
SEQUENCE
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P46590;
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                                                                                                                                                                                                                   1781 TATVADTEGNAIANSEVTFTLPEDVRANFTLG--------DGGKVVTDTEGKAK 1826
                                                                                                                                                                                                                                                                                                                                                                            TKYVAFRHYNC---SDLNYILLDDIQ--FTMGGSPTPTDYTYTVYRDGTKI---KEGLTE 393
                                                                                                                                                                                      241 V---VASFSWNG------MALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISK
                                                                                                                                                                                                                                                                                291 TGTNAGDFTVV-----FEETPNGI-NKGGARFGLSTEADGAKPQSVWIERTVDLPAG
                                                                                                                                                                                                                                                                                                             1727 TATKAGVYQVTATLENGDSMQQTVTVVPNVANAEISLAASKDPV-----IANNNDLTTL
122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD
                                                                                                                                        1625 SIE---SGARPD---TVEASLENGSSTLSTSINVNADASTAHLTLLQALFDTVSAGDTTN
                                                                                            182 DVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGO-GWLCLSSGQLGWLTAHGGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: Hydrolygis of terminal, non-reducing beta-D-galactose residues in beta-D-galactosides.
-!- SIMILARITY: Belongs to family 2 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 TIFEEDGVATGNHEYCVEVKYTAGVSPKECVNVTVDPVQFNPVQNLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus megaterium.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strey J.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Beta galactosidase (EC 3.2.1.23) (Lactase).
BGAM.
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PROSITE; PSO7019; GLYCOSYL HYDROL F2 1; 1.
PROSITE; PS0608; GLYCOSYL HYDROL F2 2; 1.
Hydrolase; Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR008999; Gal bind like.
InterPro; IPR006101; Glyco hydro_2.
InterPro; IPR006101; Glyco hydro_21g.
InterPro; IPR006104; Glyco hydro_21g.
InterPro; IPR006104; Glyco hydro_22B.
InterPro; IPR004200; Glyco hydro_42C.
InterPro; IPR004199; Glyco hydro_42C.
InterPro; IPR004199; Glyco hydro_42C.
Pfam; PF02990; Bgal_small_C; 1.
Pfam; PP02929; Bgal_small_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00703; Glyco hydro 2; 1.
Pfam; PF02836; Glyco hydro 2 C; 1.
Pfam; PF02837; Glyco hydro 2 N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ000733; CAA04267.1; -.
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                                                                                                                                                                                                                                                                                       487
                                                                                                                                                                                                                                                                                                                                                                                                    --TMYVKPADV----ERYAL 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            537 MNPKKPYILCEYSHAMGNSCGNLYKYWELFDQY------PILQGGFIWDWK 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 QKTVQLPA--GTKYVAF-RHFGCT----DFFWINLDDVEIKANGKRADFTETFESSTHGE 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----DLNYILLDDIQFTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    796 RP-NFW-RAVTDNDLGNKL----HERCQTWRQASLEQHVKKVTVQPQVDFVII-SVELAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 GT-TILSESFENGIPAS----WK--TIDA-----DGDGNN-----WTTTPPPGGTSFAGHN
                                                                                                                                                                                                                                                                                  432 GTWTYLOEGEOKAVPGSKPEWKENVLDRCRSMYERDKNHPSIIIWSL----GNESFGGEN
                                                                                                                                                                                                                                                                                                                                       56 SAIC-----ASSASYINFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----YASSTGNDASNFAN--ALLEEVLTAKTVVTAPEAIRGTRVOG----TWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 582 DQALQATAEDGTSYLAYGGDFGDTPNDGNFCGNGLIFADGTASPKIAEVKKCYQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      636 -PVKWTAVDP-----AKGKFAVQNKHLFTNLNAYDFVWTVEKNGELVEKHASLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   685 VAPDGTDELTLSYPLYEQENETDEFVLTLSLRLSKDTAWASAGYEVAYEQFVLPAKAAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 -YYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLSTE-----ADGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              745 SVKAAHPALTVDQNEQTLTVTGTN---FTAIFDK-----RKGQFISYNYERTELLASGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hoyer L.L., Scherer S., Shatzman A.R., Livi G.P.,
"Candida albicans ALS1: domains related to a Saccharomyces cerevisiae
sexual agglutinin separated by a repeating motif.";
Mol. Microbiol. 15:39-54(1995).
-!- FUNCTION: MAY PLAY A ROLE IN ADHESION AND PATHOGENESIS.
-!- PTM: N-glycosylated and O-glycosylated (Potential).
-!- SIMILARITY: TO YEAST SAGI.
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, mitosporic Saccharomycetales, Candida.
                                                                                                                                                                       221;
                                                                                                                  Length 1034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --NYLISKDVTGAT---KVKY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 APAEWITIDADGDGQGWLCLSSGQLGWLTAHGGTNVVA-SFSW----NG
81 PROTON DONOR (BY SIMILARITY).
47 NUCLEOPHILE (BY SIMILARITY).
118673 MW; 38644C9A649415E9 CRC64;
                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 GGSPTPTDYTYTVYRDG-TKIKEGL--TETTFE-----
                                                                                                             ; Score 112.5; DB 1;
; Pred. No. 3.9;
70; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                             488 FQHMYTFFKEKDSTRLVHYEGIFHHRDYDASDIES----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           909 YWDRKTGAKLALHKGSVKEQVTPYLRPQECGNKT 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 ----EDGVATGNHEYCVEVKYTAGVSPKECVNVT 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 KPQSVWIERTVDLPAGTKYVAFRHYNCS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1260
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MEDLINE=95272392; PubMed=7752895;
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Mycoplasma gallisepticum
                                                                   ::| ||
594 TTTTVTAPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S6;
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DOMAIN
CONFLICT
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              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSPNPTVSTTEYWSQSF----ATTTTVTAPPGGTDTVIIREPPNHTVTTTEYWSQSFAT 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 TLTFWV-----CAQDANYASEHYAVYASSTGNDASNFANALLEEVLTAKTVVTAPEAIR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --TTTPPPGGTSFAGHNSAICASSASYINFEGPONP-----DNYLVTPELSLPNGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X 26 AA APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             763D1063A2354C24 CRC64;
                                                                                                                                                                                                                                       Repeat; Signal.
POTENTIAL.
AGGLUTININ-LIKE PROTEIN 1.
10 X 36 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Similarity 19.5%; Score 112.5; DB 1; Similarity 19.5%; Pred. No. 5; SB; Conservative 30; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 PNPNPNPGTTTL-SESFENGIPASWKTIDADGDGNN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDSVIIREPPNPTVTTTEYWSQSYA
                                                                                                                                                                              EMBL; L25902; AAC41649.2; -.
InterPro.; IPRO0840; Candida ALS.
Pfam; PPO5792; Candida ALS; I.
Cell adhesion; Glycoprotein; Repea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1260 AA; 132641 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68; Conservative
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599
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671
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404
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Best Local S:
Matches 68
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CARBOHYD
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CARBOHYD
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 --SQSYA 593
                                  200 SSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTNVVASFSWNGMALNPDNYLI 259
                                                                       ----GGTDTV-----IIREPPNHTV 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Keeler C.L. Jr., Hnatow L.L., Whetzel P.L., Dohms J.E.;
Cloning and characterization of a putative cytadhesin gene (mgcl)
from Mycoplasma gallisepticum:
Infect. Immun. 64:1541-1647(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=S6;
MEDLINE=93371270; PubMed=8363503;
Dohms J.E., Hnatow L.L., Whetzel P., Morgan R., Keeler C.L. Jr.;
Indentification of the putative cytadhesin gene of Mycoplasma
gallisepticum and its use as a DNA probe.";
Avian Dis. 37:380-388(1993).
                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma
                                                                                                          260 SKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPN 307
                                                                                                                                              ----SQSFATTTVTGPPSGTDTVIIREPPN 651

    CAUTION: Ref.4 sequence differs from that shown due to a
frameshift in position 159 to 213.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goh M.S., Geary S.J.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Could be involved in cytadherence.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable)
-!- SIMILARITY: Belongs to the adhesin P1 family.
                                                                                                                                                                                                                                     ADP1_MYCGA STANDARD; PRT; 1122 AA.
049379; 049437; 053351;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
Adhesin Ply Rel. 37, Last annotation update)
Adhesin Pl precursor (Cytadhesin Pl) (Attachment protein)
GAPA OR MGCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hnatow L.L., Keeler C.L. Jr., Tessmer L., Dohms J.E.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-ILE.
DM -> IW (IN REF. 4).
Y -> F (IN REF. 3).
--PGGTDSVIIREPPNHTVTTTEYW--
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ADHESIN P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U34842; AAB02987.1; -.
EMBL; U4404; AACB3385.1; ALT_FRAME.
PIR; T18346; T18346.
Cytadherence; Signal; Transmembrane.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96201559; PubMed=8613358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 159-1122 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 378-570 FROM N.A.
                                                                                                                                                -----TTTEYW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-12 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30
1122
1021
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1002
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---NGLALAPALGÓDVG 479
                                                                                                                                                                                                                                                                                                                                                                       --VYASST---GNDASNFAN-----ALLEEVLTAKTV 135
                                                                                                                                                                                                                                                                                                                                                                                                                     480 Y---HFVPRLAVGGVSSPRGANGNIFLGSAITWGTNGGNFLDTKWHSPAVIEDAPTTFIT 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTAPEAIRGTRVQGTWYQKTVQLP--AGTKYVAFRHFGCTDFFWINLDDVEIK---ANGK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            537 VNSSGVLQNS---GSQQSTSTPMPNSNGNESIPYRWTNSYDYNSVRFAALISKPAGGNTK 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAD--FIETFESSTHGEAPAEWITID-----ADGDGQGWLCLSSGQLGWLTAHGGTNVV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TGATKVKYYYAV 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ND------GFPGDHYAVMISKTGTNAGDFTVVFEETPNGINK-GGARFGLSTEADG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          710 GGAITTWPEVQVNYKISANITYYNLIRTDFGSTTPATQDANTVSSKLNGAYLSSTGDQQG 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 AKPQSVWIERTVDLPAGTKYV--AFRHYNCSDLNYILLDDIQFTMGGSPTPTDYTYTVYR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               819 DDDTV-FSVSKIPPEKEITAAVNVRSLDSYYVQLNGETSVNTVARVSPDSSA-LTLNPKR 876
                                                                                                                                                                                                                                                                TTPPPGGTSFAGHNSAICASSASYINFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDAN 101
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Burotiales, Trichocomaceae, mitosporic Trichocomaceae, Aspergillus.
NCBI_TaxID=5053;
                                                                                                                                                                                                             Indels 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pectinesterase precursor (EC 3.1.1.11) (Pectin methylesterase)
                                                                                                                                                    4.5%; Score 110.5; DB 1; Length 1122; 19.0%; Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I -> T (IN REF. 3).
R -> G (IN REF. 3).
T -> A (IN REF. 3).
DIL -> VYT (IN REF. 4).
MW; 155C34DA2D6C3C65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----KDV-
                                                                                                                                                                                                             77; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 AA
                                                                                                                                                                                                                                                                                              437 TABAPGNTKTVGYPYGILLSA---ISFDATR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- GMALNPDNYLIS---
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01-NOV-1997 (Rel. 35, Last seq
28-FEB-2003 (Rel. 41, Last ann
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                                                                                                            121305
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570
695
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                                                                                                      1122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 ASFSWN----
                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                       YASEHYA--
                                                                                                                                                                                                                94;
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  CONFLICT
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                   42
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                                                                                                                                                            Query Match
                                                                                                                                                                                          Local
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PROSITE; PS00800; PECTINESTERASE 1; 1.
PROSITE; PS00503; PECTINESTERASE 2; 1.
Hydrolase; Aspartyl esterase; CeIl wall; Signal.
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SEQUENCE 331 AA; 35681 MW; IFIC81BF1E32174F CRC
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22.5%; Pred. No. 1.4;
tive 33; Mismatches
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description                   | Itorodatiosad | P72197 porphyromon | Q9r9b7 porphyromon | Q51816 porphyromon | P72194 porphyromon | P96967 porphyromon | Q51839 porphyromon | O51838 porphyromon | Ogznb5 porphyromon | P72196 porphyromon | 007442 porphyromon | Q51817 porphyromon |        | 09f4j0 porphyromon |        |        | Q8p377 xanthomonas |
|-----------|-------------------------------|---------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------|--------|--------------------|
| SUMMARIES | Ę                             | 77            | P72197             | Q9R9B7             | 051816             | P72194             | P96967             | 051839             | Q51838             | Q9ZNB5             | P72196             | 007442             | 051817             | 052050 | Q9F4J0             | Q9KIB3 | 608X6Q | Q8P377             |
|           | E E                           | 1             | 7                  | ~                  | 7                  | C)                 | 7                  | ~                  | 7                  | N                  | ~                  | 7                  | 7                  | ~      | ~                  | ~      | 7      | 16                 |
|           | %<br>Query<br>Match Length DR | 117677        | 1723               | 1687               | 1704               | 1723               | 1358               | 1706               | 1706               | 1223               | 1097               | 1732               | 1732               | 1732   | 925                | 312    | 293    | 1742               |
|           | %<br>Query<br>Match           | 11000         | 84.4               | 84.0               | 84.0               | 83.8               | 83.5               | 83.5               | 83.0               | 82.8               | 82.2               | 82.2               | 82.0               | 81.5   | 27.5               | 22.6   | 9.4    | 6.1                |
|           | S. C.C.S.                     |               | 2094               | 2082               | 2082               | 2079               | 2071               | 2070               | 2059               | 2054.5             | 2039.5             | 2039.5             | 2034.5             | 2020.5 | 682                | 561.5  | 233    | 152.5              |
|           | Result                        |               | н                  | 7                  | m                  | 41                 | ស                  | 9                  | 7                  | α                  | 6                  | 10                 | 11                 | 12     | 13                 | 14     | 15     | 16                 |

| Q7wn54 bordetella | Q8uaul agrobacteri | Q7wbn0 bordetella | Q8tpz1 methanosarc |        |        | Ω.     | Q88rq2 pseudomonas | Q52644 ruminococcu | O8eka6 shewanella | Q826wl streptomyce |        | Q9hd43 homo sapien | Q8nx96 staphylococ |        | Q9i2m3 pseudomonas |        | Q9rmb8 arthrobacte |        | Q8ti72 methanosarc | Q858b6 enterobacte | Q82yw8 enterococcu | Q7uwz8 rhodopirell |        | Q7wtc6 staphylococ |        | O8y366 ralstonia s | Q8ykj3 anabaena sp | unidentifi |
|-------------------|--------------------|-------------------|--------------------|--------|--------|--------|--------------------|--------------------|-------------------|--------------------|--------|--------------------|--------------------|--------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------|--------------------|--------------------|------------|
| Q7WN54            | QBUAU1             | O1WBN0            | Q8TPZ1             | 08E9G6 | 97UQJ9 | Q9L948 | Q88RG2             | 052644             | QBEKA6            | Q826W1             | Q9RZS7 | Q9HD43             | 96XX8Q             | Q8THC8 | Q912M3             | 61M88Q | Q9RMB8             | Q8TQ91 | Q8TI72             | Q858B6             | Q82YW8             | Q7UMZ8             | Q99V41 | Q7WTC6             | Q9GNU3 | O8X366             | QBYKJ3             | Q03658     |
| 16                | 16                 | 16                | 17                 | 16     | 16     | 7      | 16                 | 8                  | 16                | 16                 | 16     | 4                  | 16                 | 17     | 16                 | 16     | ~                  | 17     | 17                 | 0                  | 16                 | 16                 | 16     | ~1                 | Ŋ      | 16                 | 16                 | 0          |
| 3346              | 1341               | 2215              | 3988               | 2768   | 1541   | 1800   | 8682               | 680                | 2522              | 522                | 691    | 1115               | 1256               | 1357   | 2468               | 2219   | 880                | 955    | 1386               | 756                | 1744               | 7716               | 1248   | 1255               | 2656   | 1672               | m                  | 1684       |
| 5.8               | 5.6                | 5.6               | 5.4                | 5.4    | 5.4    | 5.4    | 5.4                | 5.4                | 5.4               | 5.3                | 5.3    | 5.3                | 5.3                | 5.3    | 5.3                | 5.3    | 5.3                | 5.3    | 5.2                | 5.2                | 5.2                | 5.5                | •      | 5.2                |        | 5.2                | 5.2                | 5.1        |
| 144               | 139.5              | 139               | 135                | 134.5  | 134    | 134    | 134                | 133,5              | 133               | 132.5              | 132.5  | 132,5              | 131.5              | 131.5  | 131.5              | 131    | 130.5              | 130.5  | 130                | 129.5              | 129.5              | 129                | 128.5  | 128.5              | 128.5  | 128                | 128                | 127.5      |
| 11                | 18                 | 13                | 20                 | 21     | 22     | 23     | 24                 | 25                 | 56                | 27                 | 28     | 59                 | 30                 | 31     | 32                 | 33     | 34                 | 32     | 36                 | 37                 | 38                 | 39                 | 40     | 41                 | 42     | 43                 | 44                 | 45         |
|                   |                    |                   |                    |        |        |        |                    |                    |                   |                    |        |                    |                    |        |                    |        |                    |        |                    |                    |                    |                    |        |                    |        |                    |                    |            |

## ALIGNMENTS

| RESULT         | UT 1                                                                                                           |
|----------------|----------------------------------------------------------------------------------------------------------------|
| P72197<br>ID P | 97<br>P72197 PRELIMINARY; PRT; 1723 AA.<br>P72197:                                                             |
| 122            | 1997 (TrEMBLrel. 02, Creat<br>1997 (TrEMBLrel. 02, Last                                                        |
| O DE           | in.                                                                                                            |
| 88             | Porphyromonas gingivalis (Bacteroides gingivalis).                                                             |
| 38             | <pre>bacteria; bacterolderes; bacteroldes (class); bacteroldales;<br/>Porphyromonadaceae; Porphyromonas.</pre> |
| × ×            | NCBI_TaxID=837;<br>[1]                                                                                         |
| RP             | SEQUENCE FROM N.A.                                                                                             |
| R R            | Pavloti N., Pemberton P.A., Potempa J., Chen WC.A., Pike R.N.,<br>Prochazka V. Kiefer M.C. Travis J. Barr D.J. |
| R.             | "Molecular cloning and characterization of Porphyromonas gingivalis                                            |
| RT             | Lys-gingipain.";                                                                                               |
| E.             | Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.                                                       |
| אם ב           | EMBL; U54691; AAA99810.1;<br>MREODS: C2E 003.                                                                  |
| 4 E            | MBNOES; (25:002;<br>GO: GO:0005524: F:ATP hinding: TRA                                                         |
| H<br>H         | GO, GO:0008234; F:cysteine-type peptidase activity; IEA.                                                       |
| B.             | F:DNA ligase (ATP) activity; IEA.                                                                              |
| K 5            | GO; GO:0006310; P:DNA recombination; IEA.                                                                      |
| <u> </u>       | GO; GO:0006281; P:DNA repair; IEA.                                                                             |
| i ii           | GO; GO:0006508; P:proteolysis and peptidolysis; IEA.                                                           |
| DR             | 0977; DNA ligase.                                                                                              |
| DR<br>DR       | Interbro; IPR001769; Peptidase_C25.<br>Interpro: IPR005536: Dentidase_C25.                                     |
| <b>西</b>       | Pfam, PF01364; Peptidase C25; 1.                                                                               |
| ¥ 2            | Pram; Pro3/85; Peptidase C25 C; 1.<br>PROSTTR: PRO0697: DNa 1.1Gase a1. 1                                      |
| g              | SEQUENCE 1723 AA; 186831 MW; 4508A7E50197CEBD CRC64;                                                           |
| 9e<br>Be       | Query Match<br>Best Local Similarity 86.2%; Pred. No. 6.8e-128;                                                |

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1170 VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV 1229
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                                                                                                                                                935 PNPNPNPOTITISESFENGIPASWKIIDADGDGHGWKPGNAPG---IAGYNSNGCVXS 991
                                                                                                                                                                                                                                                                                   122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV 301
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                                                                                                                                                                                                 63 ASY-INFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF
                                                                                                                 3 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASS
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AMEDILINE=95138080; PubMed=7836351;
AMEDILINE=95138080; PubMed=7836351;
AMEDILINE=95138080; PubMed=7836351;
ATRAVIS J., Barr P.J.;
ATRAVIS J., Barr P.J.;
ATRAVIS J., Barr P.J.;
AMOLECULar cloning and structural characterization of the Argingingin proteinase of Porphyromonas gingivalis. Biosynthesis as a proteinase-adhesin polyprotein.";
AMOLECULAR AAA69339.1;
AMA69339.1;
AMA69339.1;
AMA69339.1;
AMA69339.1;
BMENDE; AS5426;
AS5426;
AS5426;
AS5426;
AS5426;
ASSP; P95493; ICVR.
BMENDE; COS.001;
AMEROPS; COS.001;
AMEROPS; COS.001;
AMEROPS; COS.001;
AMEROPS; COS.001;
AMEROPS; PRAIP binding; IEA.
BMENDE; COS.000310; PRAM recombination; IEA.
BMENDE; COS.0003281; PRAM repair; IEA.
BMENDE; COS.0006281; PRAM repair; IEA.
BMENDE; PRROMOST; DAM repair; IEA.
BMENDE; PRROMOST; DAM repair; IEA.
BMENDE; IPRO0110; IG-like.
BMENDES; IPRO0110; IG-like.
BMENDES; IPRO0110; IG-like.
                                                                           Gaps
                            84.0%; Score 2082; DB 2; Length 1687;
86.2%; Pred. No. 4e-127;
ive 17; Mismatches 40; Indels 6
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Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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NCBL_TaxID=837;
                                                                       Conservative
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                                              al Similarity
392; Conserv
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01-NOV-1996
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01-OCT-2003
                            Query Match
Best Local S:
Matches 392
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                                                                                                                            61 SSASY-INFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDAS 119
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                                          1 GIPNPNPNPNPNPGTITLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICA 60
                                                                                                                                                                    1026 YSESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDAS
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      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
      Indels
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WRRADES, C25.001; -.

GO; GO:0008234; F:Prim binding; IEA.

GO; GO:0008234; F:Prim binding; IEA.

GO; GO:000310; F:NNA ligase (ATP) activity; IEA.

GO; GO:0006281; P:NNA recombination; IEA.

GO; GO:0006281; P:NNA repair; IEA.

GO; GO:0006281; P:NNA replication; IEA.

GO; GO:0006289; P:Prim replication; IEA.

GO; GO:0006589; P:Prim replication; IEA.

GO; GO:0006589; P:Prim repair; IEA.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
      40;
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  Mismatches
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InterPro; IPR007110; Ig-like.
InterPro; IPR001769; Peptidase C25.
InterPro; IPR005536; Peptidase C25.
Ffam; PF01364; Peptidase C25: I.
Pfam; PF03785; Peptidase C25: I.
Pfam; PF03785; Peptidase C25: I.
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NCBI_TaxID=837;
    17;
    Conservative
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STRAIN=381;
Matches 394;
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Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, 168468; AAB49691.1; -
GO; GO:0005524; F:ATP binding, IEA.
GO; GO:000334; F:Cysteine-type peptidase activity; IEA.
GO; GO:0003910; F:DNA ligase (ATP) activity; IEA.
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                                                                                                                                                                                                                                                       Length 1723;
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
               GO; GO:0006310; P:DNA recombination; IEA.

GO; GO:0006261; P:DNA repair; IEA.

GO; GO:0006568; P:DNA replication; IEA.

GO; GO:0006568; P:DNA replication; IEA.

R InterPro; IPR001769; Peptidase.

R InterPro; IPR001769; Peptidase.

R InterPro; IPR001536; Peptidase.

R PF01364; Peptidase.

R Pfam; PF01364; Peptidase.

R Pfam; PF01364; Peptidase.

R Pfam; PF01364; Peptidase.

R PR0SITE; PS006697; DNA LIGASE AI; 1.

R PROSITE; PS006697; DNA LIGASE AI; 1.
                                                                                                                                                                                                                                                   83.8%; Score 2079; DB 2; Length 1
85.8%; Pred. No. 6.4e-127;
ive 17; Mismatches 42; Indels
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Porphyromonadaceae; Porphyromonas.
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01-MAX-1997 (TrEMBLrel, 03,
01-MAX-1997 (TrEMBLrel, 03,
01-OCT-2003 (TrEMBLrel, 25,
                                                                                                                                                                                                                                                                       Best_Local Similarity 85.8
Matches 392, Conservative
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SEGURNORE RROM N.A.
SERGURNORE RROM N.A.
STRAIN=381,
MEDLINE=97044756; PubMed=8889827;
Okamoro K., Kadowaki T., Nakayama K., Yamamoto K.;
Cloning and sequencing of the gene encoding a novel lysine-specific cystaine proteinase [Lys-qingipain] in Porphyromonas gingivalis: structural relationship with the arginine-specific cysteine proteinase
                                                                                                                                                                                                                                                                                                                                              FEETPINGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD
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                                                                                                                                                                                                                                                                                                                         63 ASY-INFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF
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                                                                                                                                                                                                             Gaps
InterPro, IPR005536; Peptidase_~__

Fram; PR01364; Peptidase_C25; 1.

Pfam; PR03708; Peptidase_C25_C; 1.

PR08ITE; PS00697; DNA_LIGASE_A1; 1.

PR1N 228 719

GINGIPAIN

GINGIPAIN.
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                                                                                                                                                                         Length 1704;
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                           40; Indels
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GO; GO:0008234; F:cysteine-type peptidase activity; IEA.
GO; GO:0003910; F:DNA ligase (ATP) activity; IEA.
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Last annotation update)
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                                                                                                                                                                         DB 2;
                                                                                                                                                               84.0%; Score 2002; 17;
86.2%; Pred. No. 4e-127;
rive 17; Mismatches 4
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J. Biochem. 120:398-406(1996)
EMBL; D83258; BAA11870.1; -.
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                                                                                                                                                                                       Best Local Similarity 86.2³
Matches 392; Conservative
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1309 DIQFTWGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 1368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 421
                                                                      MEDILINE=56311339; PubMed=8713096; Slakeski N., Cleal S.M., Reynolds E.C.; Characterization of a Porphyromonas gingivalis gene prtR that encodes an arginine-specific thiol proteinase and multiple adhesins."; Biochem. Biophys. Res. Commun. 224:605-610(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 DVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGOGWLCLSSGOLGWLTAHGGTNV
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                                                                                                                                                                                                               Reynolds E.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                   GO; GO: 000524; F: ATP binding; IEA.
GO; GO: 000524; F: Cysteine-type peptidase activity; IEA.
GO; GO: 0003310; F: DNA ligase (ATP) activity; IEA.
GO; GO: 00053110; P: DNA recombination; IEA.
GO; GO: 0006281; P: DNA repair; IEA.
GO; GO: 0006280; P: DNA replication; IEA.
GO; GO: 0006280; P: DNA replication; IEA.
INTEXPO: IPRO0110; IG-Tike.
INTEXPO: IPRO0110; IG-Tike.
INTEXPO: IPRO01769; Peptidase C25.
INTEXPO: IPRO01769; Peptidase C25.
Fram: PF01364; Peptidase C25.
Fram: PF01364; Peptidase C25.
Fram: PF01364; Peptidase C25.
Fram: PF01364; Peptidase C25.
Fram: PF01364; Peptidase C25.
Fram: PF01364; Peptidase C25.
         Biochem. Biophys. Res. Commun. 207:424-431(1995).
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85.7%; Pred. No. 2.5e-126;
ive 18; Mismatches 41;
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Slakeski N.;
Submitted (NOV-1995) to the
EMBL; LE6441; AAC18876.1; --
HSSP; P95493; ICVR.
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Les 390; Conservative
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                                       SEQUENCE FROM N.A.
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95160709; PubMed=7857299; Kirszbaum L., Sotiropoulos C., Jackson C., Cleal S., Slakeski N., Reynolds E.C.; "Complete nucleotide sequence of a gene prtR of Porphyromonas gingivalis W50 encoding a 132 kba protein that contains an arginine-specific thiol endopeptidase domain and a haemagglutinin domain.";
                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                               Length 1358;
R GO; GO:0006310; P:DNA recombination; IEA.

GO; GO:0006281; P:DNA replication; IEA.

GO; GO:0006280; P:DNA replication; IEA.

GO; GO:0006500; P:DNA replication; IEA.

R InterPro; IPR001977; DNA_ligase.

R InterPro; IPR00179; PEPtidase_C25.

R InterPro; IPR001789; Peptidase_C25.

R InterPro; IPR00184; Peptidase_C25.

R Pfam; PF01364; Peptidase_C25; I.

R Pfam; PF03785; Peptidase_C25; I.

R PRMST; SW0060; PN3; I.

R PROSITE; PS000607; DNA_LIGASE_A1; 1.

R PROSITE; PS000607; DNA_LIGASE_A1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                   43: Indels
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Last annotation update)
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                                                                                                                                                                                                                                             83.5%; Score 2071; DB 2;
85.6%; Pred. No. 1.6e-126;
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                                                                                                                                                                                                                                                                                  17; Mismatches
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01-NOV-1996 (TrEMELrel. 01, Created)
01-NOV-1996 (TrEMELrel. 01, Last sequence v
01-OCT-2003 (TrEMELrel. 25, Last annotation
Arginine-specific thiol protease precursor.
                                                                                                                                                                                                                                                                              Matches 391; Conservative
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Best Local Similarity
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SEQUENCE FROM N.A.
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1249 FEETPNGINKGGARFGLSTEADGAKPOSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD 1308
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                                                                                                                                                                                                                                                             DIQFTMGGSPTPTDYTYTVYRDGTKIKEGL/TETTFEEDGVATGNHEYCVEVKYTAGVSEK 421
                                                                          VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=381;
MEDLINE=99143166; PubMed=9988746;
Shibata Y., Hayakawa M., Takiguchi H., Shiroza T., Abiko Y.;
"Determination and characterization of the hemagglutinin-associated short motifs found in Porphyromonas gingivalis multiple gene
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1223 AA
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J. Biol. Cl
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rangarajan M., Aduse-Opoku J., Slaney J.M., Young K.A., Curtis M.A., "The prpR1 and the prR2 arginine-specific protease genes of Porphyromonas gingivalis M50 produce five biochemically distinct
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of a protease
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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BETA-ADHESIN.
W; 0E56DCD87FDA8CDD CRC64;
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MEDLINE=56071894; PubMed=7591131;
Aduse-Opoku J., Muir J., Slaney J.M., Rangarajan M., Cu "Characterization, genetic analysis, and expression of antigen (PrpRI) of Porphyromonas gingivalis WSO.";
Infect. Immun. 63:4744-4754(1995).
                                                                                                                                                                                                          Last sequence update)
Last annotation update)
43;
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83.0%; Score 2059; DB 2;
Best Local Similarity 85.5%; Pred. No. 1.3e-125;
Matches 389; Conservative 17; Mismatches 43;
                                                                                                                                         1706 AA
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EMBL, X82680; CAA57997.1; -.
HSSP, P95493; ICVR.
MEROPS; C25:001; -.
                                                                                                                                                                                     UL-NUV-1996 (TrEMBLrel. 01,
01-MAY-1997 (TrEMBLrel. 03,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                           Protease precursor
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01-MAY-1997
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969 GTPNPNPNPNPNPGTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGC 1025
                                                       SNFANALLEEVLIAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWI 178
                                                                                 391 VYSESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDA 450
                                                                                                                                                                179 NLDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGG 238
                                                                                                                                                                                                                     DLDEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGG 568
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Slakeski N., Cleal S.M., Bhcgal P.S., Reynolds E.C.;
"Characterization of a Porphyromonas gingivalis gene prtK that encodes
a lysine-specific cysteine proteinase and three sequence-related
adhesins.";
                                                                                                                                                                                                                                                                                239 INVVASFSWNGMALNPDNYLISKDVTGATKVKYYXAVNDGFPGDHYAVMISKTGTNAGDF
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Bacteria, Bacteroidetes; Bacteroides (class); Bacteroidales;
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84.5%; Pred. No. 2.4e-124;
ive 18; Mismatches 44; Indels
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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EMBL; U75366; AAB60809.1; -.
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Best Local Similarity 84.5³
Matches 388, Conservative
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                                                                                                                                                                                                                                                                                                                                                         LLDDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGV 418
                                                                                                                                                                                                                                                                                                                                                                                      694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GIPNPNPNPNPGT-TILSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAIC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The tia gene of Porphyromonas gingivalis W50: a homologue of the arginine-specific protease precursor (PrpRI) which shares sequence and interpretate to TonB-linked receptors.";

J. Bacteriol. 179:4778-4788 (1997).

EMBL, Y07618; CAA68897.1; -...

BMBL, Y07618; CAA68897.1; -...

GO; GO:0019867; C:outer membrane; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0005215; F:RTP binding; IEA.

GO; GO:0005215; F:receptor activity; IEA.

RO; GO:0006210; P:DNA recombination; IEA.

RO; GO:0006281; P:DNA replication; IEA.

RO; GO:0006281; P:DNA replication; IEA.

RO; GO:0006281; P:DNA replication; IEA.

RO; GO:0006281; P:DNA replication; IEA.

RO; GO:0006281; P:DNA replication; IEA.

RO; GO:0006281; P:RONA replication; IEA.

RO; GO:000631; TonB boxc.

RILEFPC: IPRO00531; TonB boxc.

REPOSTE; PS00697; DNA LIGASE A1; 1.

REPOSTE; PS00697; DNA LIGASE A1; 1.

REPOSTE; PS00697; DNA LIGASE A1; 1.

REPOSTER: RECEPTOR MEMBRANE RECEPTOR RECEPTOR REPOSTER: RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEPTOR RECEP
                                                       NLDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLGWLTAHGG
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                                                                                                                                TNVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDF
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Aduse-Opoku J., Slaney J.M., Young K.A., Muir J., Rangarajan M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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01-FEB-1997
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969 GTPNPNPNPNPNPNPNPSGTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGC 1025
                                                                      1086 SNFTWALLEETITAKG-VRSPKAIRG-RIQGTWRQKIVDLPAGTKYVAFRHFQSTDMFYI 1143
                                                                                                                                                                                             1144 DLDEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLDWLTAHGG 1203
  GTPNPNPNPNPGT-TTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAIC 59
                                                                                                                                                                   NLDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLGWLTAHGG
                                                                                                                                                                                                                                        SINVSSFSWIGWALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVWISKTGTNAGDF
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                                                      60 ASSASY-INFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDA
                                                                                                             SNFANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWI
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| SPKKCVDVTVNSTQFNPVQNLTAEQAPNSMDAILKWNAP 1422
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PROSITE; PS00697; DNA_LIGASE_A1; 1
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MEDLINE=98298016; PubMed=9632563;
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                                                                                                          179 NLDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barkocy-Gallagher G.A., Han N., Patti J.M., Whitlock J., Progulake-Fox A., Han N., Patti J.M., Whitlock J., Progulake-Fox A., Lantz M.S. N. Analysis of the prtP gene encoding porphypain, a cysteine proteinase of Porphyromonas gingivalis."; Bacteriol. 178:2734-2741(1996).

EMBL: U42210; AAB06565.1; -.
                                                                                                                                                                239 TNVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDF
                                                                                                                                                                                  60 ASSASY-INFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDA
                                                                                                                                                                                                                       TVVFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYI
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                                                     SNFANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWI
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Bacteria, Bacteroidetes, Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           READPS, C25.002; —.
READPS, C25.002; —.
RGO, GO:0005524; F:ATP binding; IEA.
GO; GO:000310; F:DNB ligase (ArP) activity; IEA.
RGO; GO:000310; F:DNB ligase (ArP) activity; IEA.
RGO; GO:0006310; P:DNB recombination; IEA.
RGO; GO:0006281; P:DNB repair; IEA.
DR GO; GO:0006508; P:DNB replication; IEA.
DR GO; GO:0006508; P:DNB replication; IEA.
DR GO; GO:0006508; P:Proteolypsis and peptidolysis; IEA.
DR InterPro; IPR001769; Peptidase_C25.
DR InterPro; IPR001769; Peptidase_C25.
DR InterPro; IPR00536; Peptidase_C25.
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Last annotation update)
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; Pred. No. 5.2e-124;
19; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1732 AA
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NCBL_TaxID=837;
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Best Local Similarity 84.3
Matches 387; Conservative
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01-OCT-2003
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Lewis J.P., Macrina F.L.; "18195, an insertion sequence-like element associated with protease
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                                                    01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Lysine specific cysteine protease
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroideles; Bacteroides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes in Porphyromona Squalus is infect. Immun. 66:3035-3042(1998).

Enfect. Immun. 66:3035-3042(1998).

R BMEACPS C25.002;

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000534; F:ATP binding; IEA.

GO; GO:0003310; F:DNA ligase (ATP) activity; IEA.

GO; GO:000528; P:DNA recombination; IEA.

GO; GO:0006281; P:DNA repair; IEA.

GO; GO:0006281; P:DNA replication; IEA.

GO; GO:0006282; P:DNA replication; IEA.

R GO; GO:0006583; P:DNA replication; IEA.

R InterPro; IPR001769; Peptidase. C25.

InterPro; IPR001769; Peptidase. C25.

R Dfam; PF01364; Peptidase. C25.
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PRT; 1732
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588 IPEGWLLIDADGDNVNW-----DYYPWTWYGHDSEKCIASPSYLPMIGVLTPDNYLVTPR 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALLEE 128
                                                                                                                                                                                                      ----GAWYERTINLPEGTKYIAWRHYNCTDIYFLKLDDITVFGT 467
                                                                                                                                                                                                                                                                                                   468 PASEPEPVTDFVVSLIENNKGRLKWNYPNGYEPDKTDDKDPLQLAGYNIYANGSLLVHIQ 527
                                                                                                                                                                                                                                                                                                                                                                                      528 DPTVLEYIDETYSSRDDQVEVEYCVTAVYNDNIESQSVCDKLIYDSQSDIILYEGFEAGS 587
                                                                                                                                                                                                                                                                                                                                                                                                                              206 APAEWITIDADGDGGGWLCLSSGQLGW-LTAHGGTNVVASFSWNGM--ALNPDNYLISKD 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 VIGAIKVKYYYAVNDG-FPGDHYAVMISKIGINAGDFTVVFEETPNGINKGGARFGLSTE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----QFTMGGSPTPTD-----YTYTVYRDGT------KIKEGLTETTF 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 SLIENNKGRLKWNYPNGYEPDKTDDKKPLQLTGYNIYANGSLLVHIQDPTVLEYIDETYS 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROSS B.C.; "Genomic analysis of Porphyromonas gingivalis for vaccine discovery."; "Genomic analysis of Porphyromonas gingivalis for vaccine discovery."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF237555; AAF81413.1; SEQUENCE 312 AA; 34592 MW; OD5792C9643A25F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYI LLDDI --------
                                                                                                                                                                       VLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDV----
                                                                                                                             364 IGPVTPDNYLITPKVE--GAKRVKYWVSTQDANWAAEHYAVMASTTGTAVGDFV-ILPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.6%; Score 561.5; DB 2; Length 312; 32.8%; Pred. No. 7e-29; ive 23; Mismatches 73; Indels 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical outer membrane protein PG27.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397 EEDGVATGNHEYCVEVKYTAGV-SPKEC--VNVTV---DPVQ 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            806 SRDGQV--EMEYCVTAVYNDNIESQSVCDKLNYTITSLDNIQ 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and nucleic acids.";
EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : || || : : || || : : || || 643 LEGAKLVKYWVSAQDAVYSAEHYAVMVSTIGTAVEDFVLLFEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ross B., Barr I., Patterson M., Agius C., Rothel L.,
Hocking D., Webb B.;
"P. gingivalis polypeptides and nucleic acids.";
Submitted (FBB-2000) to the EMBL/GenBank/DDBJ databas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphyromonadaceae; Porphyromonas. NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                             ------KRADFTET-
                                                                                                                                                                                                                 421 TMTAKPT-----
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Best Local Similarity 32.8[†]
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                    SNFANALLEEVLIAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWI 178
                                                                                                                                                                                                                                                                                                                                          238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 LLDDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGV 418
                                                                                                                                                                                                                                                                          1086 SNFTNALLEETITAKG-VRSPKAIRG-RIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYI
                                                                                                                                                                                                                                                                                                                                    179 NLDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGG
                                                                                                                                                                                                                                                                                                                                                                              1144 DLDEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1204 SNVVSSFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDF
                                                                                                                                                                                                                                                                                                                                                                                                                        TNVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDF
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Patterson M., Agius C., Camuglia S., Reynolds E., Barr I.G.;
"Identification of vaccine candidates from genomic analysis of
                                                                                 1 GTPNPNPNPNPNPGT-TTLSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAIC
                                                                                                                                                                   60 ASSASY-INFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVVFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYI
                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 4e-36;
62; Mismatches 132; Indels 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria, Bacteroidetes, Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.5%; Score 682; DB 2; Length 925; 30.2%; Pred. No. 4e-36;
                                         46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hocking D., Webb E., "P. gingivalis polypeptides and nucleic acids."; submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porphyromonas gingivalis.";
Submitted (ARR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AX007522; AAG24228.1;
InterPro; IRR003961; FN III.
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         925 AA; 103632 MW; SFF2198D6914DAE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPKECVNVTVDPVQFNPVQNLTGSAV--GQKVTLKWDAP 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4.2e-123;
9; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Porphyromonadaceae; Porphyromonae.
NCBI_TaxID=837;
Matches 385; Conservative
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Matches 176; Conserv
                   Best Local Similarity
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SEQUENCE FROM N.A.
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73; Indels 183;

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75

16 LSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASYINFEGPQNPD

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68

16 LSESFENG-IPASWKTIDADGDGNNWTTTPPPGG-----TSFAGHNSAICASSASYINF

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182
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                                                                    58 NYLITPELKLPTDALVEIIYWVCTQDLTAPSEHYAVYSSSTGNNAADFVNLLYEETLTAK 117
                                                                                                                 134 TVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIKANGKRAD 193
                                                                                                                                                                                                                                                    254 PDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGG 313
                                                                                                                                                                                                                                                                                     ------YTP----- 172
                                                                                                                                                                                                                                                                                                                    314 ARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSPTP 373
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                                                                                                                                                                                   194 FIETFESSTHGEAPAEWTTIDADGDGGWLCLSSGQLGWLTAHGGTNVVASFSWNGMALN 253
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-WESO,
ROSS B., Barr I., Patterson M., Agius C., Rothel L., Margetts M.,
Roksing D., Webb E.;
"P. gingivalis polypeptides and nucleic acids.";
"P. gingivalis polypeptides and nucleic acids.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AR155351; AAD38410.1;
SEQUENCE 293 AA; 32272 MW; CC03BAC241F7F6F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Immunoreactive 32 kDa antigen PG25.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.4%; Score 233; DB 2; Length 293; Best Local Similarity 59.0%; Pred. No. 1.7e-07; Matches 46; Conservative 7; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                       ---LP-----RRAPC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 AA
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completed: May 18, 2004, 11:46:39

Search completed: May 18 Job time: 34.3368 secs

135 VTNLTGTASNDEVSLDWD 152

436 VONLTGSAVGQKVTLKWD 453

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NAME: Whitlock, Ted W. REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
TELEFAX: (904) 375-8100
INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Appl Sequence 20, Appl Sequence 14, Appl Sequence 12, Appl Sequence 22, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 11, Appl Sequence 11, Appl Sequence 10, Appl Sequence 11, Appl Sequence 12, Appli Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli 
                                                                                                                                                                                 May 18, 2004, 11:38:40 ; Search time 14.0888 Seconds (without alignments) 1670.936 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                     US-08-570-311-20
2480
I GTENPNPNPRTTTLSESF.....QNLTGSAVGQKVTLKWDAPN 456
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
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US-08-570-311-14

US-08-570-311-14

US-08-570-311-12

US-08-570-311-22

US-08-570-311-22

US-08-322-324-6

US-08-922-324-6

US-08-922-324-6

US-08-920-311-10

US-08-920-311-10

US-08-570-311-27

US-08-570-311-27

US-08-570-311-27

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US-08-621-944A-4

US-08-621-944A-4

US-08-621-944A-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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No.
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APPLICANT: Progulske-Fox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Han, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUMTRY: USA
ZIP: 32606
                                            Sequence 5434, Appliagemence 2, Appliagemence 4, Appliagemence 4, Appliagemence 10, Appliagemence 10, Appliagemence 258, Appliagemence 266, Appliagemence 266, Appliagemence 5999, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence 19, Appliagemence
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                  US-08-119-361-5
US-08-336-308A-4
US-08-32-324-4
US-09-490-931-4
US-09-071-035-258
US-09-071-035-266
US-09-071-035-266
US-09-10-035-266
US-09-10-000-5999
US-09-10-000-5999
US-09-10-000-5999
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US-09-00-10-035-264
US-09-268-347-36
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US-09-268-347-36
US-09-268-347-36
US-09-268-347-36
    US-09-252-991A-30227
                                            -09-543-681A-5434
-09-482-500A-2
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CLASSIPTCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
APPLICATION NUMBER: US 07/241,640
FILING DATE: US 07/241,640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18, Application US/08570311; Patent No. 5824791; GENERAL INFORMATION:
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                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 08-SEP-1968
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTAATION NUMBER: 36-965
REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
PRIOR APPLICATION DATA:
                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
US-08-570-311-14
; Sequence 14, Application US/08570311
; Batent No. 5824791
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              INFORMATION: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 456 amin
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Tumwasorn, Somying
Lepine, Guylaine
Han, Naiming
Lantz, Marilyn
                                          APPLICATION NUMBER: US 08
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 456; Conservative
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MOLECULE TYPE: protein
US-08-570-311-20
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Programs
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                             GTPNPNPNPNPNPSTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICA
                                                                                                                                                                                                                                                                                                                         61 SSASYINFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASN
                                                                                                                                                                                                                                                                                                                                                    SSASYINFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASN
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                                                                                                                                                                                            Gaps
                                                                                                                                                                                            0;
                                                                                                                                               100.0%; Score 2480; DB 2; Length 456; 100.0%; Pred. No. 2.8e-204; cive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
WORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 20, Application US/08570311; Patent No. 5824791
                    amino acid
                                                                                                                                                                     Best_Local Similarity 100.
Matches 456; Conservative
                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                       ; MOLECULE 111
US-08-570-311-18
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                                                                                                                                                 Query Match
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361 DDIOFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSP 420
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APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Datti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 PNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASSASYI
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                                                                                                                                     1370 KECVINTYDPVQFNPVQNLTGSAVGQKVTLKWDAPN 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                             421 KECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 98.2%; Score 2436; DB 2; Best Local Similarity 99.8%; Pred. No. 1.6e-200; Matches 449; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION NUMBER: US 07/647,119
FILING DATE: 25-UAN-1991
CLASSIFICATION NUMBER: US 07/647,119
FILING DATE: 25-UAN-1991
CLASSIFICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY AGENT INFORMATION:
NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UF15.C3
                                                                                                                                                                                                                                                     US-08-570-311-16; Sequence 16, Application US/08570311; Patent No. 5824791; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Whitlock, Ted W.
REGISTATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.
TELECOMMUNICATION INPORMATION:
TELEFAX: (904) 375-8100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
TOPOLOGY: limito
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
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APPLICANT: Parti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINL
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Best Local Similarity 100.0%; Score 2480; DB 2; Length 2628;
Best Local Similarity 100.0%; Pred. No. 3.8e-203;
Matches 456; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                               ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRICE APPLICATION PATA:

APPLICATION NUMBER: US 07/241,640
FILIND DATE: 08-SEP-1988
ATTORNEY AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: UF15.C3
REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-GAM-1991
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2628 amino acids
                                                                                                                                                                                                                                 ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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Sequence 1, Application US/09482500A;
Sequence 1, Application US/09482500A;
Patent No. 6621193
GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Travis, James
APPLICANT: Protempa, Jan
TITLE OF INVENTION: MAD
FILE REFERENCE: 235.00160101
CURRENT APPLICATION NUMBER: US/09/482,500A
CURRENT APPLICATION NUMBER: US/09/482,500A
CURRENT FILING DATE: 1999-01-13
PRIOR FILING DATE: 1999-01-13
NUMBER OF SEQ ID NOS: 4
SOUTWARE: PATENTIN VERSION 3.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SSASYINFEGPONPONYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 DDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 VVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTV 300
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                                                                                                                                                                                                                                                                                                  Score 2351, DB 2; Length 439;
Pred. No. 3e-193;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
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            REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
TELEPRONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 439 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 KECVNVTVDPVQFNPVQNL 439
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36,965
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98.2%;
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                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.2
Matches 431; Conservative
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REGISTRATION NUMBER:
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                                                                                                                                                                                                          TOPOLOGY:
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US-09-482-500A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 MGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVNV 420
                                                                    120
                                                                                                                                          247 WNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVNV 426
                        NFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALL 126
                                                                                                                EBVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                         181 ANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASFS
                                                        61 NFEGEQNDDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALL
                                                                                                                                                                                                            187 ANGKRADFIEIFESSTHGEAPAEWITIDADGDGQGWLCLSSGQLGWLTAHGGINVVASFS
                                                                                                                                                                                                                                                                                                                                                                                                   307 NGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFT
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
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PRIOR APPLICATION DATA:
PRUCK APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/08570311
Patent No. 5824791
GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Progulske-Fox, Ann APPLICANT: Tumwasorn, Somying APPLICANT: Lepine, Guylaine APPLICANT: Han, Naiming APPLICANT: Lantz, Marilyn APPLICANT: Patti, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 PNPNPNPNPGTITLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASS
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APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Parloff, Vadine
TITLE OF INVENTION: Porphyromonas gingivalis
TITLE OF SEQUENCES: A
NUMBER OF SEQUENCES: 16
APPLICANTS OF SEQUENCES: 16
APPLICANTS OF SEQUENCES: 16
APPLICANTS OF SEQUENCES: 16
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84.0%; Score 2082; DB 2;
Best Local Similarity 86.2%; Pred. No. 2.5e-169;
Matches 392; Conservative 17; Mismatches 40;
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|350 ECVNVTINPTQFNPVKNLKAQPDGGDVVLKWEAPS 1384
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                                                      US 07/241,640
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APPLICANT: Travis, James
                               PRIOR APPLICATION DATA,

APPLICATION NUMBER: US 07/241,

FILING DATE: US 08-2EP-1988

ATTORNEY/AGENT INFORMATION:

NAME: Whitlock, Ted W.

REGISTRATION NUMBER: 36,965

REFERENCE/DOCKET NUMBER: UFIS.

TELEPHONE: (904) 375-8100

TELEPHONE: (904) 375-800

INYORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENTH: 1687 amino acids
                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: line
                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-570-311-29
                 CLASSIFICATION:
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STATE: Colorad
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US-08-336-308A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application US/08570311
Patent No. 5824791
GENERAL INFORMATION
APPLICANT: Progulske-Fox, Ann
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marillyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
NITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
                                                 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASS
                                                                                                                   63 ASY-INFEGPQNPDNYLVTPELSLPNGGTLTFWYCAQDANYASEHYAVYASSTGNDASNF
                              Gaps
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                          Indels
   86.2%; Pred. No. 2.1e-169; ive 17; Mismatches 40;
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1140 ECVNVTINPTQFNPVKNLKAQPDGGDVVLKWEAPS 1174
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Ted W. Whitlock
: 2421 N.W. 41st Street, Suite A-1
Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION DATE: 08 08/353,465
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Best Local Similarity 86.2
Matches 392; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Wh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: PatentII
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US-08-570-311-29
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IMMUNOGENIC COMPOSITIONS COMPRISING PORPHYROMONAS GINGIVALIS PROTEINS AND/OR PEPTIDES AND METHODS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN RElease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,324
FILING DATE: 21-MAR-1997
CLASSIFICATION: 536
PRICK APPLICATION NUMBER: US 60/013,945
FILING DATE: 22-MAR-1996
ATTONEY/AGENT INFORMATION:
APPLICATION NUMBER: US 60/013,945
FILING DATE: 22-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.0%; Score 2082; DB 3;
86.2%; Pred. No. 2.6e-169;
tive 17; Mismatches 40;
                                                                                                                                                                       5: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ferber, Donna M.
REGISTATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 103-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 498-8080
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                         Caroline A.
GENERAL INFORMATION:
APPLICANT: Potempa, Jan S.
APPLICANT: Travis, James
APPLICANT: Genco, Carcoline
TITLE OF INVENTION: PORPHY
TITLE OF INVENTION: METHOD
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                     Potempa, Jan S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 86.23
Matches 392; Conservative
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                                                                                                               OURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/336,308A

FILING DATE: 08-NOV-1994

CLASSIFICATION NUMBER: US/08/336,308A

PRICATION NUMBER: US/08/36,308A

PRICATION NUMBER: US/08/36,308A

PRICASSIFICATION DATA:

APPLICATION NUMBER: US/08/119,361

FILING DATE: 10-SEP-1993

PRICAS APPLICATION NUMBER: US/08/265,441

FILING DATE: 24-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: FEEDER: DOING M.

REGISTRATION NUMBER: 33,878

REGISTRATION NUMBER: 33,878

REGISTRATION NUMBER: 31-93C

TELEFAK: (303) 499-8080

TELEFAK: (303) 499-8080

TELEFAK: (303) 499-8080

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TELEFAK: (303) 499-8080
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ECVNVTINPTQFNPVKNLKAQPDGGDVVLKWEAPS 1401
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; Pred. No. 2.6e-169;
17; Mismatches 40;
                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.0%;
86.2%;
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Best Local Similarity 86.2%
Matches 392; Conservative
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TYPE: amino acid
TOPOLOGY: linear
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                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-336-308A-10
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US-08-822-324-6; Sequence 6, Application US/08822324; Patent No. 6129917

RESULT 9

1068 181 301 421 122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD DVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGTNV 1127 EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGMLCLSSGQLDWLTAHGGTNV 242 VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV 362 DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFBEDGVATGNHEYCVEVKYTAGVSPK PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS 302 FEETPNGINKGGARFGLSTEADGAKPOSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD 3 PNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAICASS 63 ASY-INFEGPONPONYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF Gaps 9 Length 1704; ö

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187 VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV 1246
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EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNV 1186
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APPLICANT: Reynolds, Eric C.
APPLICANT: Bhogal, Peter S.
APPLICANT: Blakeshi, Nada
TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
FILE REFERENCE: Reynolds
FILE REFERENCE: Reynolds
CURRENT APPLICATION NUMBER: US/09/066,330A
CURRENT APPLICATION NUMBER: W6275
EARLIER PELING DATE: 1998-09-15
EARLIER FILING DATE: 1995-10-30
EARLIER FILING DATE: 1996-10-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PARCHAIN Ver. 2.0
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Best Local Similarity 85.7%; Pred. No. 2.7e-168;
Matches 390; Conservative 18; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 10, Application US/09066330A; Patent No. 6511666
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                                                                                                                                                                                                                                                                                                     Porphyromonas gingivalis
Arginine-specific Proteinase Coding Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,931
                                          ECVNVTINPTQFNPVKNLKAQPDGGDVVLKWEAPS 1401
                                                                                                                                                                                                                                                                                                                                                                                     3: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.0%; Score 2082; DB 3;
86.2%; Pred. No. 2.6e-169;
ive 17; Mismatches 40;
                       ECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/265,441
FILLING DATE: 24-UNI-1994
ATTORNEY/AGENT INFORMATION:
NAME: Perber, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                         Sequence 10, Application US/09490931
Patent No. 6274718
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/336,308
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 21.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33,878
                                                                                                                                                                                                                       APPLICANT: Travis, James APPLICANT: Travis, James APPLICANT: Barr, Philip J. APPLICANT: Pavloff, Nadine TITLE OF INVENTION: Porphyron TITLE OF INVENTION: Arginine NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ferber, Donna M. REGISTRATION NUMBER: 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boulder
STATE: Colorad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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US-09-490-931-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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Best Local S
Matches 392
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TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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STATE: FL
COUNTRY: USA
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1309 DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 1368
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                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Progulske-Fox, Ann
APPLICANT: Tunwasorn, Somyling
APPLICANT: Tunwasorn, Somyling
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Han, Somyling
APPLICANT: Han, Somyling
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 GTPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                    83.3%; Score 2066; DB 2;
85.3%; Pred. No. 3.1e-168;
tive 18; Mismatches 43;
                                                             422 ECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
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STREET: 2421 N.W. 41st Street, Suite A-1
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CIASSIRICATION: 124
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIPICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
REGISTATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
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Patent No. 5824791
GENERAL INFORMATION:
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IBM PC compatible
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Best Local Similarity 85.33
Matches 390; Conservative
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MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
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390 YSESFGLGGIGVLTPDNYLITTPALDLANGGKLTFWVCAQDANYASEHYAVYASSTGNDAS 449
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APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
                                                                                                                                                                        LDEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQDWLCLSSGQLDWLTAHGGT
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                                                                                                                                          LDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGT
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ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: WhitLock, Ted W.
REGISTRALION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08353485
Patent No. 5830710
GENERAL INFORMATION:
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Tumwasorn, Somying
Lepine, Guylaine
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Patent No. 5824791
GENERAL INFORMATION
APPLICANT: Progulske-Fox, Ann
APPLICANT: Han, Waining
APPLICANT: Han, Waining
APPLICANT: Han, Waining
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Waining
APPLICANT: Han, Waining
APPLICANT: Lapta, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                     390 YSESFGLGGIGULTPDNYLITPALDLANGGKLTFWVCAQDANYASEHYAVYASSTGNDAS 449
                                                                                                                                                                                                                                                                                                                                   120 NFANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWIN 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 LDDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFBEDGVATGNHBYCVEVKYTAGVS 419
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                                                                                                                                                                                                                                                                    61 SSASY-INFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDAS
                                                                                                                                                                                                                                                                                                                                                                                                    180 LDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGT
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                                                                                                                             Length 1087;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 424
                                                                                                                                 83.3%; Score 2066; DB 2; 85.3%; Pred. No. 3.1e-168;
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: 2421 N.W. 41st Street, Suite A-1
Gainesville
                                                                                                                                                  Pred. No. 3.1e
18; Mismatches
TYPE: amino acide TOPOLOGY: ling
                                                                                                                                               Best Local Similarity 85.3 Matches 390; Conservative
                                                                                MOLECULE TYPE: protein
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US-08-570-311-27
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US-08-353-485-8
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959 LDDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVS 1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 NFANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 LDDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLGWLTAHGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVS
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APPLICANT: Bhogal, Peter S.
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.3%; Score 2066; DB 2;
85.3%; Pred. No. 4.3e-168;
cive 18; Mismatches 43;
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-UAN-1991
CLASSIFICATION DATA:
APPLICATION UNDERS: US 07/241,640
APPLICATION UNDERS: US 07/241,640
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence II, Application US/09066330A; Patent No. 6511666; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REPERENCE/DOCKET NUMBER: UFI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (904) 372-5800 INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 85.3
Matches 390; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: Reynolds
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119

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239 838 868

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1263
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                                                                                                                                                                                                                                                                                                    238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVVFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYI 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLDDIQFTWGGSPTFTDYTYTVYRDGTKIKEGLTFTFEEDGVATGNEEXCVEVKYTAGV 418
                                                                                                                                                                                                                                                                                      60 ASSASY-INFEGPONPONYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDA 118
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                                                                                                                                                                                                                                    1 GIPNPNPNPNPGT-TTLSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAIC
                                                                                                                                                                                                            9;
                                                                                                                                                                                 82.2%; Score 2039.5; DB 4; Length 1732; 84.5%; Pred. No. 1.2e-165; cive 18; Mismatches 44; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPKECVNVTVDPVQFNPVQNLTGSAV--GOKVTLKWDAP 455
CURRENT APPLICATION NUMBER: US/09/066,330A;
CURRENT FILING DATE: 1998-09-15
EARLIER APPLICATION NUMBER: PN 6275;
RARLIER FILING DATE: 1995-10-30
EARLIER FILING DATE: 1996-10-30
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 11
                                                                                                                                 ; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-066-330-11
                                                                                                                                                                                   Query Match
Best Local Similarity 84.5%
Matches 388; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           179
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Search completed: May 18, 2004, 11:49:16 Job time : 16.0888 secs

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May 18, 2004, 11:42:50 ; Search time 35.3211 Seconds (without alignments) 3592.387 Million cell updates/sec
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1 GTENPNPNPNPGTTTLSESF.....QNLTGSAVGQKVTLKWDAPN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: /cgn2 6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_BUBGOMB.pep:*
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7: /cgn2_6/ptodata/1/pubpaa/US106_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters: 🕆
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1145568 seqs, 278261457 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listing first 45 summaries
                                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB sed length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                     US-08-570-311-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|        |        |       |        |     | SUMMARIES            |                   |
|--------|--------|-------|--------|-----|----------------------|-------------------|
|        |        | æ     |        |     |                      |                   |
| Result | ·      | Query | Query  | 6   | f                    |                   |
| ON     | Score  | March | rengen | n : | TD                   | Description       |
| П      | 2070   | 83.5  | 1706   | 14  | US-10-229-066-10     | Sequence 10, Appl |
| 7      | 2039.5 | 82.2  | 1732   | 14  | US-10-229-066-11     | Sequence 11, Appl |
| m      | 726    | 29.3  | 419    | 15  | US-10-174-695-3      | Sequence 3, Appli |
| 4      | 710.5  | 28.6  | 419    | 15  | US-10-174-695-5      | Sequence 5, Appli |
| Ŋ      | 385    | 15.5  | 231    | 15  | US-10-174-695-6      | Sequence 6, Appli |
| 9      | 232.5  | 9.4   | 196    | 15  | US-10-174-695-4      | Sequence 4, Appli |
| 7      | 153    | 6.2   | 29     | 15  | US-10-387-977-18     | Sequence 18, Appl |
| 60     | 153    | 6.2   | 29     | 15  | US-10-387-977-21     | Sequence 21, Appl |
| σv     | 153    | 6.2   | 29     | 15  | US-10-387-977-23     |                   |
| 10     | 153    | 6.2   | 29     | 15  | US-10-387-977-24     | Sequence 24, Appl |
| 11     | 153    | 6.2   | 29     | 15  | US-10-387-977-26     | Sequence 26, Appl |
| 12     | 147    | 5.9   | 29     | 15  | US-10-387-977-17     | Sequence 17, Appl |
| 13     | 147    | 5.9   | 872    | 12  | US-10-282-122A-55467 | Sequence 55467, A |
| 14     | 145    | 5.8   | 29     | 15  | US-10-387-977-25     | Sequence 25, Appl |
| 15     | 143    | 5.8   | 509    | 15  | US-10-387-977-101    | Segmence 101, App |

| Sequence 4, Appli<br>Sequence 4, Appli | equence 3,     | ñ             | Sequence 20,    | e 77,           | Sequence 80,    | Sequence 11,    | 12,             | Seque           | 592 Seque       | 73 Segue        | Sequence 9, Appli | 66335 Seguence 66335, | Seguence 4, Appl | Sedne           | 1 Sequence 81, Appl | 62947 Seque     | 58 Seque        | 62          | 66 Sequence 266 | 997 Sequence 569 | ednence 6,     | 7453 Sequence 47 | ednence         | Sequence 84     | Sequence 85     | 460 Seguence 18 | 0 Sequence 10   | 4 Sequence 2    |  |
|----------------------------------------|----------------|---------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-------------------|-----------------------|------------------|-----------------|---------------------|-----------------|-----------------|-------------|-----------------|------------------|----------------|------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|--|
| 10-175-28                              | US-10-175-282- | US-10-175-275 | US-10-387-977-2 | US-10-387-977-7 | US-10-387-977-8 | US-10-387-977-1 | US-10-387-977-1 | US-10-387-977-1 | US-10-156-761-1 | US-10-369-493-2 | 813-214A-         | US-10-282-122A-       | US-10-246-330-   | US-10-311-879-1 | US-10-387-977-8     | US-10-282-122A- | US-10-206-576-2 | 0-206-576-2 | US-10-206-576-2 | US-10-282-122A-  | US-10-229-066- | US-10-282-122A-  | US-10-387-977-8 | US-10-387-977-8 | US-10-387-977-8 | US-10-369-493-1 | US-10-387-977-1 | US-10-206-576-2 |  |
| 1833 1                                 | 992 1          | 992 1         | 9               | 5 1             | .u              | 7               | 7 1             | 7 1             | 5               | 1               | 122               | 8                     | 468 1            | 1 0             | 7.                  | 9               | 638 1           | 8           | 638 1           | 728 1            | 4              | 77               | r.              | 7               | 2               | 9               | 1               | 9               |  |
|                                        |                |               | •               |                 |                 |                 |                 |                 |                 |                 |                   |                       |                  |                 | ٠                   | ٠               |                 | •           |                 |                  |                | •                | •               | •               |                 | •               |                 |                 |  |
| നന                                     | 137            | m             | m               | m               | m               | 3               | m               | m               | 32.             | 32.             | •                 | 31.                   | 31.              | m               | m                   | L)              |                 |             |                 | _'               | N              | N                | N               | N               | N               | N               | 23.             | •               |  |
| 16                                     | 18             | 19            | 20              | 21              | 22              | 23              | 24              | 25              | 26              | 27              | 28                | 29                    | 30               | 31              | 32                  | 33              | 34              | 35          | 36              | 37               | 38             | 39               | 40              | 41              | 42              | 43              | 44              | 45              |  |

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 ASY-INFEGPQNPDNYLVTPELSLFNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
US-10-229-066-10

Sequence 10, Application US/10229066

Publication No. US20303157637A1

GENERAL INFORMATION:
APPLICANT: Brogal, Peter S.
APPLICANT: Brogal, Peter S.
APPLICANT: Brogal, Peter S.
APPLICANT: Slakeski, Nada

TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
CURRENT FILING DATE: 1002-08-28

PRIOR PELICATION NUMBER: US/10/229,066
CURRENT FILING DATE: 1998-09-15

PRIOR PILING DATE: 1998-09-15

PRIOR PILING DATE: 1998-09-15

PRIOR PILING DATE: 1998-10-30

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PATCH PATCH IN VET: 2.0

SEQ ID NO 10

LUMBER OF SEQ ID NOS: 15

LUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 954 PNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 PNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAICASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 83.5%; Score 2070; DB 14;
Best Local Similarity 85.7%; Pred. No. 3.9e-176;
Matches 390; Conservative 18; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-229-066-10
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1204 SNVVSSFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDF 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 TNALLEETITAKG-VRSPEAIRG-RIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYIDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 PNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 ASY-INFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASBHYAVYASSTGNDASNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235 PNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS
                                                                                 1264 TVVFEETPNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYI
                                                                                                                          LLDDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGV
                                           TVVFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL LINEARMATION:

APPLICANT: Reynolds, Eric Charles
APPLICANT: Slakeski, Nada
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REPRENCE: 529282000700
CURRENT APPLICATION NUMBER: VCT/AU00/01588
PRIOR PILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: PCT/AU00/01588
PRIOR APPLICATION NUMBER: AD 4859
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASTERE for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/10174695
Publication No. US20030232022A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chen, Chao Guang
APPLICANT: Barr, Ian George
IIILE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REFERENCE: 529282000700
CURRENT APPLICATION NUMBER: US/10/174,695
                                                                                                                                                                                                                                      SPKECVNVTVDPVQFNPVQNLTGSAV--GQKVTLKWDAP 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.3%; Score 726; DB 15;
ilarity 75.3%; Pred. No. 2.3e-56;
Conservative 11; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Porphyromonas gingivalis US-10-174-695-3
                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10174695; Publication No. US20030232022A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVEIKANGKR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVEIKANGKR 419
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Matches 143;
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                                                                                                                               1188
                                                                                                                                                                                                TNVVASFSWNGMALNDDNYLLSKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDF 298
                            119 SNFANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWI 178
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APPLICANT: Bhogal, Peter S.
APPLICANT: Bhogal, Peter S.
APPLICANT: Slakeski, Mada
TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
FILE REFERENCE: Reynolds
CURRENT PEPLICATION NUMBER: 0202-08-28
PRIOR PAPLICATION NUMBER: US/09/066,330
PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1995-10-30
PRIOR PLING DATE: 1995-10-30
PRIOR PLING DATE: 1996-10-30
PRIOR PLING DATE: 1996-10-30
PRIOR PLING DATE: 1996-10-30
PRIOR PLING DATE: 1996-10-30
PRIOR PLING DATE: 1995-11-30
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                                                                                                                               1129 EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLDWLTAHGGTNV
        122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD
                                                                                                                                                                        VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Gaps
                                                                                         182 DVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLGWLTAHGGTNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
82.2%; Score 2039.5; DB 1
Best Local Similarity 84.5%; Pred. No. 2.2e-173;
Matches 388; Conservative 18; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                422 ECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
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Publication No. US20030157637A1
GENERAL INFORMATION:
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US-10-229-066-11
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GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 KYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLSTEADGAKPQS 329
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                                                                                                                                                                                                                                                                                                                                                                                                                        289 VYSESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDA 348
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                                                                                                                                                                                                                                            Length 419;
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APPLICANT: Ghen, Chao Guang
APPLICANT: Chen, Chao Guang
APPLICANT: Barr, Lan George
TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REPERENCE: 52282000700
CURRENT APPLICATION NUMBER: 101/1/4,695
CURRENT FILING DATE: 2002-06-18
FRICR APPLICATION NUMBER: AU PQ 4859
FRICR APLICATION NUMBER: AU PQ 4859
FRICR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69; Indels
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41.4%; Pred. No. 3.9e-26;
iive 31; Mismatches 69;
                                                                                                                                                                                                                                        ; Score 710.5; DB 15;
; Pred. No. 5.6e-55;
12; Mismatches 32;
CURRENT FILING DATE: 2002-06-18

PRIOR APPLICATION NUMBER: PCT/AU00/01588

PRIOR FILING DATE: 2000-12-21

PRIOR APPLICATION NUMBER: AU PQ 4859

PRIOR FILING DATE: 1999-12-24

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 419
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ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                            ; ORGANISM: Porphyromonas gingivalis US-10-174-695-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10174695
Publication No. US20030232022A1
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric Charles
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ilarity 73.6%;
Conservative 12
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Best Local Similarity
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KESULT 7
US-10-387-977-18
Sequence 18, Application US/10387977
PUBLICATION 10 US20040005276A1
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric Charles
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
CURRENT APPLICATION NUMBER: US/10/387,977
CURRENT APPLICATION NUMBER: US 09/423,056
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-04-30
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-- DSPASYTYTVYRDGTKIK 141
                                                                                                                 142 EGLTATTFEEDGVAAGNHEYCVEVKYTAGVSPKVCKDVTVEGSNEFAPVQNLTGSSVGQK 201
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APPLICANT: Slakeski, Nada
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REFERENCE: 529282000700
CURRENT APPLICATION NUMBER: US/10/174,695
CURRENT APPLICATION NUMBER: PCT/AU00/01588
PRIOR APPLICATION NUMBER: PCT/AU00/01588
PRIOR APPLICATION NUMBER: AU PQ 4859
PRIOR FILING DATE: 1999-12-24
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   92 RYDDFTFE--AGKKYTFTMRRAGMGDGTDMEVED-
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SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-387-977-26
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GENERAL INFORMATION:

APPLICANT: Reynolds, Exic Charles

APPLICANT: Reynolds, Exic Charles

APPLICANT: Slakeski, Nada

TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION WIMBER: US/10/387,977

CURRENT PILING DATE: 2000-03-22

PRIOR FILING DATE: 1998-04-30

PRIOR FILING DATE: 1998-04-30

PRIOR FILING DATE: 1998-04-30

NUMBER OF SEQ ID NOS: 105

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SEQ ID NOS: 105
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APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Eric Charles
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: PORPHYROWOMAS GINGIVALIS
FILE REFERENCE: 529282000301
CURRENT APPLICATION NUMBER: US /10/387, 977
CURRENT PILING DATE: 2003-07-18
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: W PO 6528
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100.0%; Pred. No. 1.3e-06;
ative 0; Mismatches 0;
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100.0%; Pred. No. 1.3e-06;
iive 0; Mismatches 0;
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NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 29
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US-10-387-977-21
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                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-387-977-21; Sequence 21, Application US/10387977; Publication No. US20040005276A1
                                                                                                              ) ORGANISM: Porphyromonas gingivalis US-10-387-977-18
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Best Local Similarity
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                                                                                              TYPE: PRT
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Best Local
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GENERAL INFORMATION:

APPLICANT: Reynolds, Eric Charles

APPLICANT: Reynolds, Eric Charles

APPLICANT: 80 Staten-Simpson, Neil Martin

APPLICANT: 0'Brien-Simpson, Neil Martin

APPLICANT: 0'Brien-Simpson, Neil Martin

APPLICANT: 0'Brien-Simpson, Neil Martin

TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

TITLE OF INVENTION: DIAGNOSIS

CURRENT FILING DATE: 2003-07-18

FRIOR PELICATION NUMBER: US 09/423,056

PRIOR PELICATION NUMBER: PCT/AU98/00311

FRIOR APPLICATION NUMBER: AU PO 6528

FRIOR APPLICATION NUMBER: AU PO 6528

FRIOR FILING DATE: 1997-04-30

PRIOR FILING DATE: 1997-04-30

NUMBER OF SEQ ID NOS: 105

SOFTWARE: FASTESQ for Windows Version 4.0

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APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DORPHYROMONAS GINGIVALIS
FILE REFERENCE: 5292000301
CURRENT APPLICATION NUMBER: US 09/423,056
PRIOR APPLICATION NUMBER: US 09/423,056
PRIOR FILING DATE: 2000-3-22
PRIOR FILING DATE: 1998-04-30
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Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                   Ouery Match
6.2%; Score 153; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 29; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO. 23
LENGTH: 29
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Publication No. US20040005276A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-387-977-24; Sequence 24, Application US/10387977; Publication No. US20040005276A1; GENERAL INFORMATION:
                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-23
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70 GPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASST---GNDASNFANALL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 G----KNYAATTAAD----GTWSLTVPAADLAGLGDHYTLSATATNGVGNSVSNTANLLV 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 EBVLTAKT------VVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 NTVTVTIGGN----SYTATVQSDLTWSVNVPESVLTALGNGD--LTVSATV---TNGHGN 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 T----NVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGT 293
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                                  CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/230,335
PRIOR PELICATION NUMBER: 60/230,347
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
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PRIOR PELING DATE: 2000-12-226
PRIOR PELING DATE: 2000-12-26
PRIOR PELING DATE: 2001-02-99
PRIOR PELING DATE: 2001-02-96
PRIOR PELING DATE: 2001-02-16
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Identification of Essential Genes in Microorganisms
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21.3%; Pred. No. 0.00064;
tive 56; Mismatches 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 21.3
Matches 112; Conservative
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APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Neil Martin
APPLICANT: Slakeski, Nada
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
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FILE REFERENCE: 529282000301
CURRENT APPLICATION NUMBER: US/10/387,977
CURRENT APPLICATION NUMBER: US/09/423,056
PRIOR APPLICATION NUMBER: PSCT/AU98/00311
PRIOR APPLICATION NUMBER: AU PO 6528
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1997-04-30
PRIOR FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 105
SEQ ID NO 17
LENGTH: 29
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Pred. No. 4.3e-06;
                                                                                                                                                                                                                                                                                                         Length 29;
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                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                   Query Match
6.2%; Score 153; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 29; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   375 DYTYTVYRDGTKIKEGLTETTFEEDGVAT 403
                                                                                                                                                                                                                                                                                                                                                                                                                             DYTYTVYRDGTKIKEGLTETTFEEDGVAT 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYTYTVYRDGTKIKEGLTETTFEEDGVAT 29
   PRIOR APPLICATION NUMBER: AU PO 6528
PRIOR FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 55467, Application US/10282122A; Publication No. US20040029129A1
                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-10-387-977-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 17, Application US/10387977; Publication No. US20040005276A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Obleen, Kari
APPLICANT: Cyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.9%;
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Forsyth, R.
Xu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wall, Daniel
Trawick, John
Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-10-282-122A-55467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-10-387-977-17
                                                                                                                       SEQ ID NO 26
LENGTH: 29
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 25, Application US/10387977

Sequence 25, Application Wo. US20040005276A1

Jennstal INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

JEDICANT: Reynolds, Eric Charles

APPLICANT: Reynolds, Eric Charles

APPLICANT: Slakeski, Nada

TITLE OF INVENTION: SVATHEFIC PEPTIDE CONSTRUCTS FOR THE

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

FILLE REFERENCE: 52928200301

CURRENT APPLICATION NUMBER: US/10/387,977

CURRENT APPLICATION NUMBER: US/10/387,977

CURRENT FILING DATE: 2003-07-18

PRIOR FILING DATE: 1997-04-30

PRIOR FILING DATE: 1997-04-30

NUMBER OF SEQ ID NOS: 105

SEQ ID NO 25

LENGTH: 29

LENGTH: 29

LENGTH: 29

LENGTH: 29

LENGTH: 29

LENGTH: 29

LENGTH: 29

LENGTH: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reynolds, Exic Charles
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: Slakeski, Nada
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: SYNTHEMIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
CURRENT APPLICATION NUMBER: US/10/387,977
CURRENT PILING DATE: 2000-03-22
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1997-04-30
PRIOR FILING DATE: 1997-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.8%; Score 145; DB 15; Length 29;
larity 96.6%; Pred. No. 6.6e-06;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                375 DYTYTVYRDGTKIKEGLTETTFEEDGVAT 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DYTYTVYRDGTKIKWGLTETTFEEDGVAT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 101
LENGTH: 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 101, Application US/10387977
Publication No. US20040005276A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Porphyromonas gingivalis US-10-387-977-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-387-977-101
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380 PASLPQNQASYSIQASAGSYVAISKDGVLYĞTGVANAS----GVATVSMTKQITENGNYD 435
                                ----YAVMISKTGTNAGDFTVVF-EETPNGINKGGARFGLSTEA 322
112 SSTGNDASNFANALL---EEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQ--LPAGTKYVA 166
                                                                                                            167 FRHFGCTDFFWINLDDVEIKANGKRADFTETFESSTHGBAPAEWTTIDADGDGGGWL--C 224
                                                                                                                                                                                                                                                                                227 LTTSQLKALTNKDKYFLAIGNCCITAQFDY----VQP----CFGEVITRVKEKGAYAKIG
                                                                                                                                                                                                                         225 LSSGQLGWLT-----AHGGTNVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVND
                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 DGAKPQSVWIERTVDLPAGT----KYVAFRHYNCSDLNYILLDDIQFTMGGSPTPTDYT-
                                                                                                                                                                    -----NYLKAPYTGCYSHLNTGVSFANYT---AHGSETAWADPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              408 YCVEVKYTAGVSPKECVNVTVDPVQFNPVQNLTGSAVGQKVTLKWDAPN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---YTVYRDGTKIKEGLTETTFEEDGVAT--
                                                                                                                                                                       181 NQEHGYTDVY-----
                                                                                                                                                                                                                                                                                                                                           278 GFPGDH----
```

Search completed: May 18, 2004, 11:52:21 Job time : 36.3211 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

- protein search, using sw model OM protein May 18, 2004, 11:33:39 ; Search time 45.2755 Seconds (without alignments) 2739.638 Million cell updates/sec Run on:

US-08-570-311-22 2388 1 GTPNPNPNPNPGTTTLSESF......PKVCVNVTINPTQFNPVQNL 439

score: Sequence: Title: Perfect E

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched: 1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A Geneseq 29Jan04:\*

1. geneseqp1980s:\*
2. geneseqp2000s:\*
3. geneseqp2001s:\*
5. geneseqp2001s:\*
6. geneseqp2003s:\*
6. geneseqp2003bs:\*
8. geneseqp2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|            |        | æ     |        |    | SUMMAKIES |                    |
|------------|--------|-------|--------|----|-----------|--------------------|
| ult<br>No. | Scor   |       | Length | DB | αı        | Description        |
| i          | 2388   | 100.0 | 439    | 2  | AAR96024  | Aar96024 P. gingiv |
| 7          | 2388   | 100.0 | 439    | 7  | AAW69492  | 2 Hae              |
| m          | 2388   | 100.0 | 2628   | ~  | AAR96030  |                    |
| 4          | 2388   | 100.0 | 2628   | 7  | AAW69488  | Aaw69488 Haemagglu |
| ស          | 2351   | 98.5  | 456    | 7  | AAR96023  | Aar96023 P. gingiv |
| 9          | 2351   | 98.5  | 456    | N  | AAR96022  | <u>п</u>           |
| 7          | 2351   | 98.5  | 456    | 7  | AAW69491  | _                  |
| 80         | 2351   | 98.5  | 456    | ~  | AAW69490  | Hae                |
| σ          | 2321   | 97.2  | 450    | N  | AAR96021  | Aar96021 P. gingiv |
| 10         | 2321   | 97.2  | 450    | 7  | AAW69489  | Aaw69489 Haemagglu |
|            | 2058   | 86.2  | 1687   | 7  | AAR96033  |                    |
| 12         | 2058   | 86.2  | 1687   | N  | AAW69495  |                    |
| 13         | 2058   | 86.2  | 1704   | N  | AAR70188  | 00                 |
| 14         | 2058   | 86.2  | 1704   | 7  | AAW34843  | 3 Arg-ging         |
| 15         | 2058   | 86.2  | 1704   | ٣  | AAY67396  | Aay67396 Arg-gingi |
| 16         | 2058   | 86.2  | 1704   | 4  | AAU08938  | о<br>Б             |
|            | 2055   | 86.1  | 1087   | 7  | AAR96028  | 8<br>P.            |
| 18         | 2055   | 86.1  | 1087   | 7  | AAW69486  | 6 Hae              |
|            | 2055   | 86.1  | 1358   | ~  | AAR96032  | Aar96032 P. gingiv |
| 20         | 2055   | 86.1  | 1358   |    | AAW69494  | Aaw69494 Haemagglu |
| 21         | 2048   | 85.8  | 1706   |    | AAW24786  | Aaw24786 PrtR anti |
| 22         | 2025.5 | 84.8  | 1732   | ~  | AAR96029  | Aar96029 P. gingiv |
| 23         | 2025.5 | 84.8  | 1732   | 7  | AAW24787  | Aaw24787 PrtK anti |
| 24         | 2025.5 | 84.8  | 1732   | 7  | AAW69487  | Aaw69487 Haemagglu |
| 25         | 727    | 30.4  | 135    | 9  | ABP55081  | Abp55081 Porphyrom |

| Aau03572 P. gingiv | Aau03574 P. gingiv | Aab49217 Peptide u | Aay34522 Porphorym | Aay34521 Porphorym | Aay34520 Porphorym |          | Aay34359 Porphorym | Aay34484 Porphorym | Aar96025 P. gingiv | Aaw69483 Haemagglu | Aar72458 Porphyrom | Aau03575 P. gingiv | Aar77313 Porphyrom | Aaw34805 Arg-speci |          | Aay34483 Porphorym | Aay34358 Porphorym | Aaw34798 Arg-speci | Aaw83085 Peptide f |  |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|--|
| AAU03572           | AAU03574           | AAB49217           | AAY34522           | AAY34521           | AAY34520           | AAY34392 | AAY34359           | AAY34484           | AAR96025           | AAW69483           | AAR72458           | AAU03575           | AAR77313           | AAW34805           | AAU03573 | AAY34483           | AAY34358           | AAW34798           | AAW83085           |  |
| 4                  | 4                  | 4                  | 7                  | 7                  | 7                  | 7        | 7                  | N                  | 7                  | ~                  | N                  | 4                  | 7                  | ~1                 | 4        | ~                  | ~                  | 7                  | (7)                |  |
| 419                | 419                | 134                | 921                | 922                | 925                | 938      | 377                | 312                | 497                | 497                | 970                | 231                | 991                | 49                 | 196      | 293                | 299                | 46                 | 29                 |  |
| 30.4               | 29.8               | 29.8               | 29.0               | 29.0               | 29.0               | 29.0     | 24.1               | 23.9               | 19.2               | 19.2               | 13.6               | 12.7               | 10.6               | 10.1               | 9.6      | 8.3                | 8.3                | 8.2                | 6.4                |  |
| 727                | 711.5              | 711                | 691.5              | 691.5              | 691.5              | 691.5    | 575.5              | 571.5              | 458.5              | 458.5              | 325                | 303                | 252.5              | 242                | 233.5    | 199                | 199                | 195                | 153                |  |
| 26                 | 27                 | 28                 | 29                 | 30                 | 31                 | 32       | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41       | 42                 | 43                 | 44                 | 45                 |  |

## ALIGNMENTS

AAR96024 standard; protein; 439 AA. RESULT 1 AAR96024

AAR96024;

16-OCT-2003 04-SEP-1996

(revised)
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P. gingivalis haemagglutinin hagA HArep4 product.

Haemagglutinin; hagA; periodontal disease; vaccine; antibody; HArep4.

Porphyromonas gingivalis; strain 381.

WO9617936-A2.

13-JUN-1996.

95WO-US016108 11-DEC-1995; 94US-00353485 09-DEC-1994;

(UYFL ) UNIV FLORIDA. (UABR-) UAB RES FOUND

Patti JM; Lantz M, Han N, Lepine G. Progulske-Fox A, Tumwasorn S,

WPI; 1996-287181/29. N-PSDB; AAT30648.

Porphyromonas gingivalis genes and proteins - used in the detection and vaccination against periodontal disease.

Claim 4; Page 114-115; 153pp; English.

HARP94 (AAR96024) is the product of the HArep4 repeat unit (AAT30648) of the hagA gene (AAT30654) of P. gingivalis 318. It forms part of haemagglutinin hagA (see also AAR96030). HArep4 and other hagA repeat unit products (see also AAR96021-23) can be obtd. from transformed host cells and used as vaccines to protect humans or animals against periodontal disease. Expression in Salmonnella cells allows prodn. of live vaccine. HArep1-4 can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-0CT-2003 to standardise OS field)

Sequence 439 AA;

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Gaps

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Query Match

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361 DDIOPTWGGSPTPTDYTYTVYRDGTKIKEGLIETTFEBDGVATGNHEYCVEVKYTAGVSP 420
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    This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the hagA haemagglutinin protein. I polypeptides are used to produce antibodies to organisms associated wi periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
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; Score 2388; DB 2;
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Porphyromonas

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AAW69492

AAW69492

US5824791-A. 20-0CT-1998 25-JAN-1991; 09-DEC-1994;

Patti JM,

Claim 1;

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Haemagglutinin protein; periodontal disease; vaccine; hagA.

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AAW69488 standard; protein; 2628 AA

AAW69488

Haemagglutinin protein hagA

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    encoding haemagglutinin and/or

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91US-00647119.
94US-00353485.
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Porphyromonas gingivalis.
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UAB RES FOUND
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(UABR-) UAB R
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HARPEQ2 (AAR96022) is the product of the HARPEQ2 repeat unit (AAT30646) of the hagA gene (AAT30654) of P. gingivalis 318. It forms part of the hagA (see also AAR96030). HARPEQ2 and other hagA repeat unit productin (see also AAR9601301 and AAR96023-24) can be obtd. from transformed host cells and used as vaccines to protect humans or animals against periodontal disease. Expression in Salmonella cells allows product live avaccine. HARPEL-4 can also be used to detect the presence of antio-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)
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98.5%; Score 2351; DB 2;

Best Local Similarity 98.2%; Pred. No. 1.3e-182;

Matches 431; Conservative 3; Mismatches 5;
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                                                     AAR96023 standard; protein; 456 AA
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Best Local Similarity 98.2
Matches 431; Conservative
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UAB RES FOUND
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N-PSDB; AAT30647
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KECVNVTVDPVQFNPVQNL 439
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protease poly:peptide(s)).
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                                                                                                                HAREPI (AAR96021) is the product of the HAREPI repeat unit (AAT30645) of the hagA gene (AAT30654) of P. gingivalis 318. It forms part of haemagglutinin hagA (see also AAR96030). HAREPI and other hagA repeat unit products (see also AAR96030). Harepi and other hagA repeat cells and used as vaccines to protect humans or animals against periodontal disease. Expression in Salmonella cells allows produ. of live vaccine. HAREPI-4 can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)
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                                 in the detection and
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                                                                                                                                                                                                                                                                                                                      97.2%; Score 2321; DB 2;
98.4%; Pred. No. 3.4e-180;
iive 3; Mismatches 4;
                                 Porphyromonas gingivalis genes and proteins vaccination against periodontal disease.
                                                                                  Claim 4; Page 103-104; 153pp; English
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1110 EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGOGWLCLSSGOLDWLTAHGGTNV 1169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        P. gingivalis 381 haemagglutinin hagE (AAR96033) was identified as the product of a gene (AAT30656) identified in P. gingivalis 318 genomic DNA. The haemagglutinin can be obtd. from transformed host cells and used as evaccine to protect humans or animals against periodontal disease. Expression in Salmonella cells allows prodn. of a live vaccine. The haemagglutinin can also be used to detect the presence of anti-P. gingivalis antibodies and to raise monoclonal antibodies for diagnostic appln. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            992 ESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASNF
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                                                              Haemagglutinin; hagE; periodontal disease; vaccine; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.2%; Score 2058; DB 2;
88.8%; Pred. No. 5.8e-158;
cive 12; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                              Porphyromonas gingivalis genes and proteins vaccination against periodontal disease.
                                                                                                                                                                                                                                                                                                    Lepine G,
                                                                                            Porphyromonas gingivalis; strain FDC381
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                               P. gingivalis haemagglutinin hagE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDEVEIK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASFS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGINKGGARFGLSTBADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKVCVNV 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGGSPTPTDYTYTVYRDGTKIXEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVWV 420
                                                                                                                                                                                                                                                                                                           This sequence is encoded by a Porphyromonas gingivalis gene of the invention. This sequence represents the haga haemagglutinin protein. The polypeptides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease
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    encoding haemagglutinin and/or

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 450;
                                                                                                                                                        Progulske-Fox A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2321; DB 2;
Pred. No. 3.4e-180;
3; Mismatches 4;
                                                                                                                                                          Tumwasorn S,
                                                                                                                                                                                                                                      Isolated Porphyromonas gingivalis genes
                                                                                                                                                                                                                                                                                    English
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                                          8BUS-00241640.
91US-00647119.
94US-00353485.
                95US-00570311
                                                                                                                                                                                                                                                                                Claim 1; Col 121-126; 101pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.2%;
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                                                                                                                                                        Lantz
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(UABR-) UAB RES FOUND.
                                                                                                                                                                                      WPI; 1998-582627/49.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                        Patti JM, Han N,
                                                                                                                                                                                                     N-PSDB; AAV58876
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 450 AA;
                                                            25-JAN-1991;
09-DEC-1994;
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Length 1687;

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detection and

- used in the

Patti JM

Lantz M,

Han N,

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1290 DIQFTMGGSPTPTDYTYTVXRDGTKIKEGLTETFEEDGVATGNHEYCVEVKYTAGVSPK 1349
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                                                                                   421
                 302 FEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD
                                                                                 DIOFTMGGSPTPTDYTYTVYRDGTKIKBGLTETTFBEDGVATGNHBYCVEVKYTAGVSPK
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                                                                                                                                                                                                                                                                                                                                                                                                               Arg-gingipain-2, gingivalis, periodontal disease, vaccine, arginine-specific protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228. .719
/label= Protease
/note= "corresponds to Arg-gingipain-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1430. .1704
/label= Hemagglutinin
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/label= Hemagglutinin
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/label= Hemagglutinin
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                                                                                                                                                                                                                                                                  AAR70188 standard; protein; 1704 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                   422 VCVNVTINPTQFNPVQNL 439
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93US-00141324.
94US-00265441.
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                                                                                                                                                                          1350 ECVNVTINPTQFNPVKNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphyromonas gingivalis.
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21-SEP-1995
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Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    935 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASY-INFEGPONPONYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF 121
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    encoding haemagglutinin and/or

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                                                                                                                                                                                                                                 Haemagglutinin protein; periodontal disease; vaccine; hagE.
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88.8%; Pred. No. 5.8e-158
ive 12; Mismatches 31
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                                                                                                 AAW69495 standard; protein; 1687 AA.
88US-00241640.
91US-00647119.
94US-00353485.
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                                                                                                                                                                                                    Haemagglutinin protein hagE
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389; Conservative
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09-DEC-1994;
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Best Local &
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                                                                              121
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                                            62
                                                     PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS
                                                                                        FEETPNGINKGGARFGLSTEADGAKPQSVW1ERTVDLPAGTKYVAFRHYNCSDLNY1LLD
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                                                                              ASY-INFEGPONPDNYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF
                                                                                                                 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD
                                                                                                                                                                                                                                                             DIQPTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFBEDGVATGNHEYCVEVKYTAGVSPK
                                           PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSA1CVSS
                                                                                                                                                    EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNV
                                                                                                                                                                                       VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    Arg-specific gingipain protease; gingivalis; periodontal disease;
                          . 9
        Length 1704;
                                                                                                                                                                                                                                                                                                                                                                                                                  Arg-gingipain high molecular weight prepolyprotein sequence.
                         31; Indels
      86.2%; Score 2058; DB 2;
88.8%; Pred. No. 5.9e-158;
iive 12; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "precursor protein"
                                                                                                                                                                                                                                                                                                                                                              AAW34843 standard; protein; 1704 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYGE-) UNIV GEORGIA RES FOUND INC. (MORE-) MOREHOUSE SCHOOL MEDICINE.
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                         Conservative
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N-PSDB; AAT93872.
                Similarity
     Query Match
Best Local Simil
Matches 389; (
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                                                                                                                                                                                                                                                       The present sequence represents an arginine-specific protease of Porphyromonas gingivalis. The following peptides, derived from Arg- and Lys-specific high molecular weight proteases, offer proteaction against infection: YTYTYYRDGK IKEGIZTATE DECATCHES OFFICE FOR SPROVC (1); YTPVEEKQNG RMIVIVAKKX (II); QLPFIFDVAC VNGDFLFSMP CPAEALMRAQ (III); REPRIVEEKQNG RMIVIVAKKX (II); QLPFIFDVAC VNGDFLFSMP CPAEALMRAQ (III); REPRESCONS NILATTATOGAC VITAMATE TO THE WORDEN K TYAGYSERVC (VI); RAFGREDTRY RMEMNYEDGR KTYTYYRDG (VI); TRAGELTATF REDG (IX); REGILATTF REDG (IX); KIKEGILATTF FEEDGVATGN HEY (X); KIKEGILATTF FEEDGVATGN HEY (XI); KIKEGILATTF (XIII); TATYTYXRDG HEY (XII); KIKEGILATTF (XIII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); TATYTYXRDG HEY (XIII); T
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Porphyromonas gingivalis Arg-specific gingipain protease peptide(s) -
useful for protecting animals and humans from gingivalis and periodontal
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88.8%; Pred. No. 5.9e-158;
ive 12; Mismatches 31;
                                                                                                                                                                             Disclosure; Page 68-73; 95pp; English
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                                                                                             diseases.
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1009 BSFGLGGIGVLTPDNYLITPALDLPNGGKLTFWYCAQDANYASEHYAVYASSTGNDASNF 1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 ASY-INFEGPQNPDNYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a Porphyromonas gingivalis arginine-specific proteinase known as Arg-gingipain/gingipain-2 amino acid sequence. Gingipain-2 consists or a 50kD protease component non-covalently associated with a 44kD haemagolutinin component. The proteinase is stimulated by glycine containing peptides and glycine analogues. It is inhibited by cysteine protease group specific inhibitors. The protease preparation can be used in immunogenic compositions and vaccines against inflammatory response and tissue damage caused by P. gingivalis in periodontal disease. It can also be used to screen for agents that modulate Arg-gingipain proteinase activity inhibitors
                                229. 719 // Annino acids 229-719 are specifically claimed" //note= "Annino acids 720-1185 are specifically claimed" /note= "Amino acids 720-1185 are specifically claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD
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                                                                                                                                                                                                                                                                                                                                                                                                                       New Porphyromonas gingivalis arginine-specific protease preparation useful for preparing vaccines against periodontal disease and for screening for Arg-gingipain inhibitors.
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                 Location/Qualifiers
                                                                                                                                                                                                                                                                                            (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Col 29-42; 55pp; English
                                                                                                                                                                                                                                   93US-00119361.
94US-00265441.
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N-PSDB; AAZ60181.
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                                                                                                                                                                                                  08-NOV-1994;
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24-JUN-1994;
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FEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD 361

181

62

Gaps

9

241

DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 421

362

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302

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Search completed: May 18, 2004, 11:42:44 Job time : 46.2755 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

May 18, 2004, 11:37:00 ; Search time 11.4621 Seconds (without alignments) 3684.135 Million cell updates/sec

2388 1 GTPNPNPNPNPGTTTLSESF.....PKVCVNVTINPTQFNPVQNL 439 US-08-570-311-22 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description   | hemagglutinin | R (EC  | gingipain R (EC 3. | lysine-specific cy | arginyl endopeptid | conserved hypothet | hypothetical prote | autolysin [importe | hypothetical prote | probable RTX famil | hypothetical prote | 80     | e 1,4- | cellulose 1,4-beta | hypothetical prote | Н      | įż     | alkaline serine pr | tail-host specific | prophage pil prote | probable S-layer p | hypothetical prote | conserved hypothet | MGC1 protein precu | in-1   | asin   | cal    |     | etical |
|-----------|---------------|---------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|-----|--------|
| SUMMARIES | ID            | 55            | A55426 |                    | 3                  | ŭ                  | AF2959             | 32                 | C89874             | B75622             | B85547             | F90696             | S10789 | A55976 | S59077             | C86822             | H90975 | B97033 | JC4908             | T13256             | A86685             | D97316             | 876412             | C69503             | T18346             | T10729 | E85822 | AH2515 | 875 | A83412 |
|           | DB            | 7             | 7      | 7                  | ~                  | N                  | 7                  | 0                  | 7                  | ~                  | ~                  | ~                  | ~      | ~      | 7                  | 7                  | ~      | 7      | ~                  | ~                  | ~                  | N                  | N                  | N                  | ~                  | 7      | 7      | ~      | N   | 7      |
|           | Length        | 2628          | 1704   | 1526               | 1732               | 991                | 1052               | 1341               | 1248               | 691                | 5188               | 5291               | 1684   | 596    | 1090               | 1649               | 1345   | 2817   | 715                | 1904               | 1441               | 1939               | 4199               | 607                | 1122               | 1274   | 2660   | 4936   | 702 | 2468   |
| οķο       | Query         | -             |        |                    |                    |                    |                    | 5.7                | 5.4                | 5.4                | 5.2                | 5.2                | 5.2    | 5.2    | 5.1                | 5.1                | 5.0    | 5.0    | 5.0                | 5.0                | 4.9                | 4.9                | 4.9                | 4.9                | 4.9                | 4.9    | 4.9    | 4.9    | 4.8 | 4.8    |
|           | Score         | 2388          | 2058   |                    |                    |                    |                    | 136.5              |                    | 129                | 124                | 124                | 123.5  | 123    | 122.5              | 121                | 120.5  | 119.5  | 119                | 118.5              | 118                | 118                | 118                | 117.5              | 117                | 16.    | 116.5  | -4     | 15. | 114.5  |
|           | Result<br>No. |               | 7      | m                  | 4                  | S                  | Q                  | 7                  | <b>c</b> o         | თ                  | 10                 | 11                 | 12     | 13     | 14                 | 15                 | 16     | 17     | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24                 | 25     | 26     | 27     | 28  | 29     |

2041

180

240

300

2042 DEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTN 2101

1982 FANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINL 181 DEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGIN

PANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINL

121

à g ò d d 2102 VVASFSWAGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTV 2161

241 VVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTV

2162 VFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILL 2221

VPEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILL 360

301

à gg à 임 ò

*8* €

2222 DDIQFTMGGSPTPTDYTYTYVYRDGTXIKEGLIETTFEEDGVATGNHEYCVEVKYTAGVSP 2281

KVCVNVTINPTQFNPVQNL 439

421

361 DDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSP 420

| hypothetical prote | hypothetical prote | cellulase - Cellul | tsh protein - Esch | major surface prot | family 3 glycoside | S-layer protein - | large repetitive p | hypothetical prote | conserved hypothet | probable peptidogl | extracellular seri | hypothetical prote | probable large, mu | internalin-like pr | beta-qalactosidase |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| E90696             | A85547             | S49541             | I54632             | S48754             | H82754             | A47023            | AD0835             | B75489             | AB0204             | AB1180             | AB3528             | A64474             | T36423             | AF1772             | T30551             |
| ~                  | 7                  | ~                  | 7                  | 7                  | 7                  | 7                 | 7                  | 7                  | 7                  | ~                  | 7                  | N                  | ~                  | N                  | ~                  |
| 1461               | 1461               | 872                | 1377               | 702                | 882                | 465               | 3624               | 713                | 1268               | 2044               | 2554               | 987                | 891                | 938                | 1034               |
|                    |                    | 7                  | 7                  | 7                  | 7                  | 9                 | 9                  | 9                  | ø                  | 9                  | 9                  | 9                  | 9                  | 9                  | 9.                 |
| 4.8                | 4.8                | 4                  | 4                  | 4.7                | 4                  | 4                 | 4.                 | 4.                 | 4                  | 4                  | 4                  | 4                  | 4.                 | 4                  | 4                  |
| 114 4.8            | 114 4.8            |                    |                    | 111.5 4.           |                    | 111 4.            |                    |                    |                    | 4.                 | 4                  |                    |                    |                    |                    |

## ALIGNMENTS

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- Porphyromonas gingivalis
                                                                                  A; Description: Cloning, sequence analysis and expression in Escherichia coli of prpRl A;Reference number: S49763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1249 FEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD 1308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1129 EVEIKANGKRADFTETFESSTHGEATAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNV 1188
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A;Ratus: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Cross-references: EMBL:U42210; NID:g1314325; PID:g1314326; PIDN:AAB06565.1
R;Slakeski, N.; Cleal, S.M.; Reynolds, E.C.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z20896
A;Reference number: Z20896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   954 PNPNPNPNPTILISESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 ASY-INFEGPONPONYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VASFSWNGMALNPDNYL1SKDVTGATKVKYYYAVNDGFPGDHYAVM1SKTGTNAGDFTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 PNDNPNPPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAICVSS
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C;Accession: S49763
R;Aduse-Opoku, J.; Muir, J.; Slaney, J.M.; Rangarajan, M.; Curtis, M.A.
submitted to the EMBL Data Library, November 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 87.9%; Pred. No. 1.2e-134;
Matches 385; Conservative 13; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                        A Accession: $49763
A Status: preliminary
A Molecule type: DNA
A Residues: 1-1526 <ADU>
A COSS-references: EMBL:X82680
C Genetics:
C A Genetics:
C Keywords: cysteine proteinase; hydrolase
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A;Residues: 1-1704 <PAV>
A;Cross-references: GB:U15282; NID:g557067; PIDN:AAA69539.1; PID:g557068
B;Pike, N: McGraw, W; Potemps, J:; Travis, J.
J. Biol. Chem. 269, 466-411, 1994
A;Title: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolat
A;Reference number: A53113; MUID:94103245; PMID:8276827
                                                                                                                                                                                                                          Cispecies: Porphyromonas gingivalis
Cispecies: Dorebl-1995 #sequence_revision 10-Feb-1995 #text_change 08-Oct-1999
Cistacession: A55426; D53113
Ripavloff, N.; Potempa, J.; Pike, R.N.; Prochazka, V.; Kiefer, M.C.; Travis, J.; Barr, F. A. Baol. Chem. 270, 1007-1010, 1995
A;Title: Molecular cloning and structural characterization of the Arg-gingipain proteina A;Reference number: A55426; MUID:95138080; PMID:7836351
                                                                                                                                                              gingipain R (EC 3.4.22.37) precursor - Porphyromonas gingivalis
N;Alternate names: 50K high molecular mass arginine-specific cysteine proteinase; HGP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1306
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C;Species: Porphyromonas gingivalis
C;Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 31-Mar-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAICVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 228-249 <PIX>
A;Experimental source: H66
A;Note: sequence extracted from NCBI backbone (NCBIP:141694)
C;Keywords: cysteine proteinase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.2%; Score 2058; DB 2;
88.8%; Pred. No. 4.9e-136;
tive 12; Mismatches 31;
         KVCVNVTINPTQFNPVQNL 2300
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Best Local Similarity 88.8%
Matches 389; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-991 <RES>
A;Cross-references: GB:D26470; NID:g927644; PIDN:BAA05484.1; PID:g927645
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Best Local Similarity 21.1%
Matches 119; Conservative
                                                                                                                                                                Best Local Similarity 25.9*
Matches 120; Conservative
                                                                                                                                                             Similarity
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                                                                                                                                                                                             A.Molecule type: DNA
A.Residues: 1-1350, N', 1352-1363, 'Y', 1365-1447, 'H', 1449-1732 <LEW>
A.Residues: 1-1350, N', 1352-1363, 'Y', 1365-1447, 'H', 1449-1732 <LEW>
A.Residues: 1-1350, N', 1352-1363, 'Y', 1365-1447, 'H', 1449-1732 <LEW>
A.Crose: references: EMBLARCHOSS; NID:g2738802; PID:g2738803; PIDN:AAC26523.1
B.Pike, R.; McGraw, W.; Potempa, J.; Travis, J.
J. Biol. Chem. 269, 406-411, 1994
J. Fiol. Chem. 269, 406-411, 1994
A.Fitle: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolat A;Reference number: A53113; MUID:94103245; PMID:8276627
                                                                                                                  Род
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C; Species: Porphyromonas gingivalis
C; Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 08-Oct-1999
C; Accession: 140229
R; Okamoto, K.; Misumi, Y.; Kadowaki, T.; Yoneda, M.; Yamamoto, K.; Ikehara, Y.
R; Okamoto, K.; Misumi, Y.; Kadowaki, T.; Yoneda, M.; Yamamoto, K.; Ikehara, Y.
R; Okamoto, K.; Misumi, Y.; Kadowaki, T.; Yoneda, M.; Yamamoto, K.; Ikehara, Y.
A; Title: Structural Characterization of argingipain, a novel arginine-specific cysteine
A; Reference number: 140229; MUID:95168884; PMID:7864651
A;Residues: 1-795,'I',797-1389,'N',1391-1478,'Y',1480-1732 <SLA>
A;Crose references: EMBL:U75366; NID:92182811; PID:92182812; PIDN:AAB60809.1
R;Lewis, J.P.; Macrina, F.L.
Infect. Immun. 66, 3035-3042, 1998
A;Title: IS195, an insertion sequence-like element associated with protease genes in A;Reference number: Z20844; MUID:98298016; PMID:9632563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLDEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGG 238
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84.8%; Score 2025.5; DB 2; Length 1732;
Best Local Similarity 87.1%; Pred. No. 9.4e-134;
Matches 384; Conservative 16; Mismatches 34; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: sequence extracted from NCBI backbone (NCBIP:141690)
                                                                                                                                                                                      A, Status: preliminary, translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 229-249 <PIK>
A; Experimental source: H66
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Conserved hypothetical protein Atu3276 [imported] - Agrobacterium tumefaciens (strain C C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: AF2559
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ster, E.W.
Afitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
Afreference number: AB2577; MUID:21608550; PMID:11743193
Afreession: AF2959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 -VWI-----ERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSPTFTDYTYTVY 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        819 KIWIAGQGPTKEDDYVFEAGKKY----HFLMKKMGSGDGTELTISEGGG---SDYTYTVY 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-1052 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL44092.1; PID:g17741659; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 GCTSFAG-----HNSAICVSSASYINFEGPONPDNYLVTPELS-LPGGGTLTFWVCAQD 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            589 INLTDASVNVSCDYNGAIATISANGKMF-GSAVVENGTATINLIGLTNESTLILTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TPPPGGTSFAGHNSAICVSSAS
                                                                                                                                                                   50; Mismatches 171; Indels 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7%; Score 136.5; DB 2; Length 1052;
21.1%; Pred. No. 0.14;
tive 61; Mismatches 148; Indels 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 TVTSGEAIIGRHSASEATV--TGDGSKWTTGDLOVGGDTSDPGG--LAGNGT-
DB 2; Length 991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 RDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKVCVN 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDGTKIKEGLTETTYRDAGMSAQSHEYCVEVKYAAGVSPKVCVD 915
                                                                                                                                                                                                                                                                                                                                      8 NPNPGTTTLSESFENGIPASWKTIDADGDG--NNWT---
10.5%; Score 251.5; DB 2; 25.9%; Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 TTTLSESFENGIPASWKTIDADGDGNNWTT-
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| 00   00   00   00   00   00   00   0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Qy         167 FRHFGCTDFFWINLDEVEIKANGKRADFTETESSTHGEAPAENTTIDADGD         218           1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
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| -VA .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | RESULT 8 C198974 autolysin [imported] - Staphylococcus aureus (strain N315) C1,Species: Staphylococcus aureus C1,Species: Staphylococcus aureus C1,Species: Staphylococcus aureus C1,Species: Staphylococcus aureus C1,Species: Staphylococcus aureus C1,Species: Staphylococcus aureus C1,Species: Staphylococcus aureus C1,Species: C8974 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc C3, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C3, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C3, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C3, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C3, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C3, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C3, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C4, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C4, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C5, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C4, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C5, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C5, Shiba, T.; Kobayashi, I.; Cui, L.; Oguc C3, Shiba, T.; Kobayashi, I.; Cui, L.; Oguc C3, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C5, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C5, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C6, Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; C6, Shiba, T.; Hattori, M.; Modasawara, M.; Hattori, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawara, M.; Modasawa |
| A; Molecule type: DNA A; Readues: 11341 < KUR> A; Readues: 11341 < KUR> A; Readues: 11341 < KUR> A; Cross-references: GB:AE007870; PIDN:AAK90114.1; PID:g15160106; GSPDB:GN00170 C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetic | Query Match   S.4%; Score 129.5; DB 2; Length 1248;     Best Local Similarity   21.9%; Pred. No. 0.53;     Matches   103; Conservative   47; Mismatches   167; Indels   153; Gaps   25;     Qy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |

| THE RELEVENCE SHIPMONE TO CHENT TO CHENTER TO THE RESTRESSIVE OF A                                                                                                                                | DA 692 MUMANANANAN OF UT DIRECANA CERCENTIFICE TO DE MICONOCA MUT VERICA (17.1                                                                                                                                     |
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| 210 WITTIDADGOGOTTISSON MITDAGGORNIACMAINDINISTERIA                                                                                                                                               | 101 INTERNATIONAL OUT OUT OUT OUT OUT OUT THE OOST OF THE OOST OUT OUT OUT OUT OUT OUT OUT OUT OUT OU                                                                                                              |
| 875 WGTKNQVILIGNNIAQGTFNATKQVSVGKDVXLXGTINNRTGWVNAKDL                                                                                                                                             | 642 INTWAAQPTVDANTTWVEVGVDTNNNSQIDSGDVFFPNAVITILQGT                                                                                                                                                                |
| QY 264 IGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPN 307                                                                                                                                           | RESULT 10<br>B85547                                                                                                                                                                                                |
| 308 GINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKY 344                                                                                                                                                     | <pre>probable RTX family exoprotein [imported] - Escherichia coli (strain 0157:H7, substrair<br/>C,Species: Escherichia coli<br/>C,Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001</pre> |
|                                                                                                                                                                                                   | C;Accession: B85547 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca                |
| RESOLT 9<br>PISSO22<br>hypothetical protein - Deinococcus radiodurans (strain R1)                                                                                                                 | Nature 409, 529-533, 2001<br>A.Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.<br>A.Reference number: A85480, MUID:21074935, PMID:11206551                                                   |
| C;Species: Deinococcus radiodurans .<br>C;Dete: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000                                                                               | A,Accession: B85547 A,Status: preliminary                                                                                                                                                                          |
| C.McCession: B/52.2. C.McCession: B. B. B. B. B. B. B. B. B. B. B. B. B.                                                                                                                          | A;Roidectle Type: DNA<br>A;Resides: 1-5188 <sto><br/>A;Cross-references: GB:AE005174; NID:g12513368; PIDN:AAG54838.1; GSPDB:GN00145; UWGP:ZC<br/>A;Experimental source: strain O157:H7, substrain EDL933</sto>     |
| SCIEUCE 200, 1971-1977, 1999<br>A.File: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.<br>A.Beforence number: 275,50, MTTD:20036804. DMTD:1052936                    | Cjeenetius:<br>AjGene: Z0615                                                                                                                                                                                       |
| A.Accession: B75622<br>A.Status: preliminary<br>A.Molecule type: DNA                                                                                                                              | Query Match 5.2%; Score 124; DB 2; Length 5188;<br>Best Local Similarity 23.9%; Pred. No. 8.4;<br>Matches 138; Conservative 63; Mismatches 189; Indels 188; Gaps 35;                                               |
| A,Residues: 1-691 <whi> A,Residues: 1-691 <whi> A,Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12628.1; PID:g6460924; TIGR:DRB00 A,Experimental source: strain R1 C.Genetics:</whi></whi> | QY 10 NPGTTLSESFENGIPASWKTIDADGDGNNWTTTPPPG 47                                                                                                                                                                     |
| A;Gene: DRB0037<br>A;Map position: megaplasmid<br>A;Genome: plasmid<br>A:More: nlasmid MP1                                                                                                        | OY 48 GTSFAGHNSAICVSSASYINFEGPONPDNYLVTPELSLPGGGTLTFW 94  :                                                                                                                                                        |
| Query Match 5.4%; Score 129; DB 2; Length 691; Best Local Similarity 21.3%; Pred. No. 0.27; Matches 113; Conservative 52; Mismatches 192; Indels 174; Gaps 24;                                    | QY 95 VCAQDANYASEHYAVYASSTGNDASNFANALLEEVLTAKTVVTA 138   :                                                                                                                                                         |
| TTTLSESFENGIPASWKTIDADGDGNNWTTTP                                                                                                                                                                  | PEAIRG-TRVQGTWYQKTVOLPAGTKXVAFRHFGCTDFFW-INLDEVEI<br>                                                                                                                                                              |
| OY 52 AGHNSALCVSSASYINFEGPQNDDNYLVTPELS-LPGGGTLTFWVCAQDA 100                                                                                                                                      | ADGDGQ<br> :                                                                                                                                                                                                       |
| QY 101 NYASEHYAVYASSTGNDASNFANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQ 153                                                                                                                                  | QY 221GWLCLSSGQLDWLTAHGGTNVVASFSWN-GM-ALNPDNYLISKDVTGATKVK 270                                                                                                                                                     |
| QY 154 KTVQLPAGTKYVAFRHFGCTDFFWINLDEVEIKANGKRADFT 195                                                                                                                                             | OY 271 YYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFBETPNGINK 311                                                                                                                                                               |
| QY 196ETFESSTHGEAPAEWTTIDADGDQGWLCLSSGQLDWLTAHGGT 239 :                                                                                                                                           | QY 312GGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCS 353<br>                                                                                                                                                           |
| OY 240 NVVASFSWNGMALNPDNYLLISKDVTGATKVKYYYANNDGFPGDHYAVMISKTGTNAGDFT 299                                                                                                                          | Qy 354DINYILLDDIQFTWGGSPT-PTDYTYTVYRDGTKIKEGLFET-FFEEDG 400<br>                                                                                                                                                    |
| CY 300 VVFEETPNGINKGGARFGLSTEADGAKPO-SVWIERTVDLPAGT342   :  :  :  :  :  :  :  :  :  :  :  :  :                                                                                                    | Qy 401 VATGNHEYCVEVKYTA-GVSPKVCVNVTINPTQFNP 435                                                                                                                                                                    |
| 343 KXVAERHYNCSDLNYILLDDIQFTMGGSPTPTDYTYTVYRDYRD                                                                                                                                                  | SULT 11                                                                                                                                                                                                            |

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81

-----HNDIMNKDNEAAWANWWGSD-----

Indels

DB 2;

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-----LIQAGTALLLLFGGVQVFYGDETARPLGDGG-----SDPEQGTRSSMNWANIN 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::|::|
497 QNV-LSHWQKLGQFRNNHIAIGAGAHQKLSDSPYTFARTYESDDIVDEVVVATGAQGTIR 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYTYTVYRDGTKIKEGLT--ETTFEEDGVATGNHEYCVEVKYTAGVSPKVCVNVTINPTQ 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: ||| ::: ||| :: ||| 556 VIVEGVFEDGIVVRDAYTGDEITVTK-GTAIT------FTAGTQGILLIENTAEPVT 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              395 FGFDSVINFEFQNANFNNLEGLFSRYANSINTDFDFNMLSYVSSHDTKL---YSRDD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 EAIRGT-RVQGTWYQKTVQLPAGTKYVAFRHFGCTDFF--WINLDEVEIKANGKRADFTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 PILRNKWNDQASGYEDWF-VPAAEPYRQDLNIAPKDYLIKWITSWVEEFGIDGFRVDTAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 HVEIERWAELKNEAEVALQTWRENNPDKPGANW-----DDNFWMTAEVFGHGLGKSEYFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 GDHYAVMISKTGTN----AGDFTVVF-EETPNGINKGGARFGLSTEADGAKPQSVW--IE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 RTVDLPAGTKYVAFR------HYNCSDLNYI------LLDDIQFTMGGSPTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 ELSLPGGGTLTFWVCAQD-ANYASEHYAVYASSTGNDASNFANALLEEVLTAKTV-VTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 ------WIRADETAGY-----DNCGGSEQTMCIGFLPDIKTEVTTGVDLP
                                                                                                                                                                                                                                                                                                                                                                                                                                23 GIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICV-SSASYINFEGPQNPDNYLVTP
A;Reference number: S10789; MUID:90336627; PMID:1696201
A;Accession: S10789
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1684 <CAN>
A;Cross-references: EMBL:X53373; NID:948305; PIDN:CAA37453.1; PID:948306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 TFESSTHGEAPAE-----WTTIDADGDGQGWLCLSSGQLDWLTA----HG----
                                                                                                                                                                                                                                                                         Query Match 5.2%; Score 123.5; DB 2; Best Local Similarity 20.7%; Pred. No. 2.1; Matches 100; Conservative 52; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 GLPRDWTPNQA--QGQNWHT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 -GTNVVASFSW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433 FNPV 436
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                               R
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                                   hypothetical protein ECs0542 [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
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                                                                                                                          Cjaccession: F90696 "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F90696" "Nation F9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2402 QALG-NGDLTITASVTNANGNTGSGTRDITIDANLPGLRVDTVAGDDIVNSIEHGQALVI 2460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2240 FNAISGDNILNADEKGOPLTISGGSTGLATGAOVTVTLNGHNYSATIDAS--GNWTLTVP 2297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 KANGKRADFIETFESSTHGEAPAEWT---TIDAD------GD-----GQ---- 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 ---DLNYILLDDI-----QFTMGGSPT-PTDYTYTVYRDGTKIKEGLTET-TFEEDG 400
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5291 «HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33965.1; PID:gl3360000; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 VCAQDANYASEHYAVYASST---GNDASNFANALLEEVLTAKTVVT------A 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --GWLCLSSGQLDWLTAHG---GTNVVASFSWN-GM-ALNPDNY---LLSKDVTGATKVK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----KIGINAGDFIVVFEETPNGINK----- 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GGARFGLSTEADGAKPQSVWIERTVDLPAGTKYV-------AFRHYNCS--- 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 GTSFAGHN-----SAICVSSASYINFEGPQ-----NPDNYLVTPELSLPGGGTLTFW 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- VOGTWYOKTVOLPAGTKYVAFRHFGCTDFFW-INLDEVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.2%; Score 124; DB 2; Length 5291; 23.9%; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63; Mismatches 189; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 NPGTTTL--SESFENGIPAS------WKTIDA---DGDGNNWTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: ECs0542
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Cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - Thermomonospora fusca Cispecies: Thermomonospora fusca Cispecies: Thermomonospora fusca Cispecies: Thermomonospora fusca Cispecies: Thermomonospora fusca Cispecies: Thermomonospora fusca Cispecies: Thermomonospora Cispecies: Ascession: A55976

Rizhang, S.; Lao, G.; Wilson, D.B.
Biochemistry 34, 3386-3395, 1995

A;Title: Characterization of a Thermomonospora fusca exocellulase.

A;Title: Characterization of a Thermomonospora fusca exocellulase.

A;Teters: Ascession: A55976

A;Status: preliminary

A;Molecule type: DMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.2%; Score 123; DB 2; Length 596; 23.2%; Pred. No. 0.58; tive 35; Mismatches 112; Indels
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Best Local Similarity
Matches 69; Conserv
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amylace A-180 - alkaliphilic eubacterium 163-26 C;Species: alkaliphilic eubacterium 163-26 C;Date: 21-Nov-1993 #sequence\_revision 01-Dec-1995 #text\_change 15-Oct-1999 C;Accession: S10789 C;Accession: S1078 S;Canduussio, A.; Schmid, G.; Boeck, A. Eur. J. Blochem: 191, 177-185, 1990 A;Title: Blochemical and genetic analysis of a maltopentaose-producing amylase from

us-08-570-311-22.rpr

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| QY 132 AKTVVTAPEAIRGTRVQGTWYQKTVQLP 590<br>CY 132 AKTVVTAPEAIRGTRVQGTWYQKTVQLP 159<br>DD 597 VSAVETRGDYKRFDDTYVANGDGIXIPSGWTGTMPNGDVIKPGVSFLDIRSFYKKDP 653<br>QY 160 AGTKXVAFRHFGCTDFFWINLDEVEIKANGKRADFTETFESSTHGEAPAEWITIDADGDG 219                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Qy 321 EADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILL 360                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |

450 GQALFTGGNAGTGASYAQA------TNSTTAAQGILYANITNYIKSAFTTGTAG 497 Dp

421 KVC------VNVTINPTQF 433 | : | : | : | : | : | 498 AVYGIVGGNGHDSLKISPSQW 518

Sy qq

Search completed: May 18, 2004, 11:47:52 Job time: 13.4621 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

May 18, 2004, 11:35:14 ; Search time 8.0235 Seconds (without alignments) 2848.981 Million cell updates/sec Run on:

US-08-570-311-22 2388 1 GTENPNPNPGTTTLSESF......PKVCVNVTINPTQFNPVQNL 439 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|        |       | ,          |        |    | SUMMAKIES  |                 |             |
|--------|-------|------------|--------|----|------------|-----------------|-------------|
| Result |       | *<br>Query |        |    |            |                 |             |
| No.    | Score | Match      | Length | BB | QI .       | Description     | tion        |
|        | 2388  | 00         | 2628   |    | HGA2 PORGI | 051845          | porphyromon |
| 2      | 2335  | ۲.         | 2164   |    | HGA1 PORGI | P59915          | porphyromon |
| e      | 1431  |            | 686    |    | PRTH_PORGI | P46071          | porphyromon |
| 4      | 251.5 | o.         | 166    |    | CPG1_PORGI | P28784          | porphyromon |
| S      | 132.5 |            | 1256   |    | ATL STAAU  | P52081          | staphylococ |
| y      | 122.5 | 5.1        | 1090   |    | GUXB CELFI | P50899          | cellulomona |
| 7      | 120.5 |            | 2660   |    | YEEJ_ECO57 | Q8x8v7          | escherichia |
| 80     | 117.5 |            | 331    |    | PME ASPAC  | 012535          | aspergillus |
| g,     | 117.5 | 4.9        | 607    |    | YK28 ARCFU | 028251          |             |
| 10     | 117   | 4.9        | 1122   |    | ADP1 MYCGA | 049379          |             |
| 11     | 113   | 4.7        | 1122   |    | ADP2 MYCGA | Q9rem8          | mycoplasma  |
| 12     | 112.5 |            | 1260   |    | ALS1 CANAL | P46590          | candida alb |
| 13     | 112   | 4.7        | 872    |    | GUXA CELFI | P50401          | -           |
| 14     | 111   | 4.6        | 465    |    | SLAP_LACBR | Q05044          |             |
| 15     | 110   | 4.6        | 987    |    | YD94 METUA | 058789          |             |
| 16     | 109.5 | 4.6        | 1385   |    | CSAA_BACUD | 045760          |             |
| 17     | 107.5 | 4.5        | 1034   |    | ITAV_CHICK | P26008          |             |
| 18     | 107.5 | 4.5        | 1200   |    | HYAL STRPU | 076536          |             |
| 19     | 107.5 | 4.5        | 1953   |    | BIGA_SALTY | P25927          |             |
| 20     | 107   | 4.5        | 435    | П  | AM3D_ORYSA | P27933          |             |
| 21     | 105.5 | 4.4        | 282    |    | PRTA_ASPNG | P24665          |             |
| 22     | 105.5 | 4.4        | 669    |    | CHI1 BACCI | P20533          |             |
| 23     | 105.5 | 4.4        | 1609   |    | FIG2_YEAST | P25653          |             |
| 24     | 105   | 4.4        | 524    |    | CHID_BACCI | P27050          | bacil       |
| 25     | 105   | 4.4        | 2812   |    | ZAN HUMAN  | Q9 <b>y</b> 493 | homo sapien |
| 26     | 104.5 | 4.4        | 551    |    | AMYB THETU | P19584          | therm       |
| 27     | 0     | 4.4        | 1034   |    | BGAL_BACME | 052847          |             |
| 28     | 104   | 4.4        |        |    | OGP MOUSE  | 062010          | mus mus     |
| 29     | 104   | 4.4        | Н      |    | NEO1 CHICK | 090610          | _           |
| 30     | 103   | 4.3        | 54     |    | THER_BACST | P06874          | bacill      |
| 31     | 102.5 | 4.3        |        |    | NPRE_BACBR | P43263          | Д           |
| . 32   |       | 4.3        | 122    | Н  | 1          | 5692            |             |
| 33     | 0     | 4.3        | 104    | Т  | ITA8_CHICK | 56              | gallus gall |

1862 GTENPNENPNPGTTILSESFENGIPASWKTIDADGDGNNWTTTEPPGGTSFAGHNSAICV 1921

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1 GIPNPNPNPNPNPGTITLSESFENGIPASWKTIDADGDGNNWTTIPPPGGTSFAGHNSAICV

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Query Match 100.0%; Score 2388; DB 1; Best Local Similarity 100.0%; Pred. No. 1.6e-160; Matches 439; Conservative 0; Mismatches 0;

Length 2628;

9

| P26225 cellulomona<br>Q45753 bacillus th | P10478 clostridium P07897 rattus norv | P76347 escherichia<br>P38059 lactobacill | Q60106 xanthomonas | P15921 rickettsia | Q9xjp3 bacteriopha | P53626 trichoderma | Q45704 bacillus th |
|------------------------------------------|---------------------------------------|------------------------------------------|--------------------|-------------------|--------------------|--------------------|--------------------|
| GUNB_CELFI<br>CSAB_BACUD                 | XYNZ_CLOTM<br>PGCA_RAT                | YEEJ ECOLI<br>SLAP LACHE                 | XANP XANS2         | OMPA_RICRI        | TSPE_BPSFV         | E13B_TRIHA         | C8AA_BACUK         |
|                                          | <b>н</b> н                            |                                          | ٦,                 |                   | Н                  |                    | н                  |
| 1045                                     | 837                                   | 2358<br>439                              | 827                | 2249              | 623                | 762                | 1157               |
| 4.4.                                     | 4.4.<br>E.G.                          | 4. 4.<br>w. s.                           | 4.4                | 4 4               | 4.2                | 4.2                | 4.2                |
| 102                                      | 101.5                                 | 101.5                                    | 101                | 100.5             | 100                | 100                | 100                |
| 3.4                                      | 36                                    | დ რ<br>რ                                 | 40                 | 4 4<br>1 6        | 43                 | 44                 | 45                 |

## ALIGNMENTS

| ARD; PRT; 2628 AA.                                    | , Created)<br>, Last sequence update) |             | ursor.                              | Porphyromonas gingivalis (Bacteroides gingivalis). | tes; Bacteroides (class); Bacteroidales; | Porphyromonas.                     |                 |                           |            | bMed=8926061;                     |                                        | ene A (hagA) of Porphyromonas gingivalis 381 | direct repeats.";                | 00-4007(1996).                    | inates erythrocytes.                     | SIMILARITY: Belongs to peptidase family C25. | 111111111111111111111111111111111111111 |                        | rmatics and the EMBL outstatio | rmatics Institute. There are no restrictions on its | use by non-profit institutions as long as its content is in no way | is not removed.        | license agreement (See http://www.lsb-sib.cn/announce/ | TICENSEGISD-SID . CII) . | 28.1:                     |                      | ence; Hyd              | 24 POTENTIAL. |         | PEPTIDASE | PEPTIDASE | PEPTIDASE | PEPTIDASE | PEPT      | 283324 MW; 61C4DE32540C99DA CRC64; |
|-------------------------------------------------------|---------------------------------------|-------------|-------------------------------------|----------------------------------------------------|------------------------------------------|------------------------------------|-----------------|---------------------------|------------|-----------------------------------|----------------------------------------|----------------------------------------------|----------------------------------|-----------------------------------|------------------------------------------|----------------------------------------------|-----------------------------------------|------------------------|--------------------------------|-----------------------------------------------------|--------------------------------------------------------------------|------------------------|--------------------------------------------------------|--------------------------|---------------------------|----------------------|------------------------|---------------|---------|-----------|-----------|-----------|-----------|-----------|------------------------------------|
| STANDAR                                               | (Rel. 39, Creat<br>(Rel. 39, Last     |             | Hemagglutinin A precursor.<br>HAGA. | omonas gingivalis (Bac                             | Bacteria, Bacteroidetes, Bacteroides     | Porphyromonadaceae; Porphyromonas. | NCBI_TaxID=837; | [1]<br>SPOTTENCE EDOM N A | 381:       | MEDLINE=97047672; PubMed=8926061; | Han N., Whitlock J., Progulske-Fox A.; | "The hemagglutinin gene A (hagA)             | contains four large, contiguous, | Infect. Immun. 64:4000-4007(1996) | -!- FUNCTION: Agglutinates erythrocytes. | <pre>ILLARITY: Belongs to pe</pre>           |                                         | ISS-PROT entry is copy | the Swiss Institute            | the European Bioinformatics Institute.              | non-profit institut                                                | d and this statement 1 | entities requires a license agreement (                | l an email to licenseed  | EMBL: U41807: AAB17128:1: | PIR, T28651; T28651. | utinin; Virulence; Hyd | 1 24          | 25 2628 |           |           |           |           | 2074 2628 | 2628 AA; 283324                    |
| RESULT 1<br>HGA2_PORGI<br>ID HGA2_PORGI<br>AC Q51845; | 30-MAY-2000<br>30-MAY-2000            | 10-OCT-2003 | Hemaggl<br>HAGA.                    | Porphyr                                            | Bacteri                                  | Porphyr                            | NCBI_Ta         | [1]                       | STRAIN=381 | MEDLINE                           | Han N.,                                | "The he                                      | contain                          | Infect.                           | -!- FUN                                  | -!- SIM                                      | 1 1 1 1                                 | This SW                | between                        | the Eur                                             | use by                                                             | modifie                | entitie                                                | or send                  | EMBL: U                   | PIR, T2              | Hemaggl                | SIGNAL        | CHAIN   | DOMAIN    | DOMAIN    | DOMAIN    | DOMAIN    | DOMAIN    | SEQUENCE                           |
| RESULT 1<br>HGA2 FOR<br>ID HGA<br>AC Q51              | 턴                                     | H           | e S                                 | SO                                                 | S                                        | ဗ                                  | ×               | RN<br>o                   | 2          | X.                                | RA                                     | RT                                           | RŢ                               | RL                                | ខ្ល                                      | ပ္ပ                                          | ပ္ပ                                     | ပ္ပ                    | ប្ដ                            | g                                                   | ນ                                                                  | ပ္ပ                    | ပ္ပင္                                                  | 3 5                      | DR.                       | ä                    | ΚW                     | FT            | FT      | FT        | ΕŢ        | FT        | FT        | FE        | ÖS                                 |

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                    1982 FANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLFAGTKYVAFRHFGCTDFFWINL 2041
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FANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINL
                                                         DEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLDWLTAHGGTN
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"Complete genome sequence of the oral pathogenic bacterium Porphyromonas gingivals strain W83.";

J. Bacteriol. 185:5591-5601(2003).

J. Bacteriol. 185:5591-5601(2003).

J. FUNCTION: Agglutinates erythrocytes (By similarity).

-: SIMILARITY: Belongs to peptidase family C25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hemagglutinin; Virulence; Hydrolase; Thiol protease; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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HEMAGGLUTININ A.
PEPTIDASE C25-LIKE 1.
PEPTIDASE C25-LIKE 2.
PEPTIDASE C25-LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                 10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porphyromonadaceae; Porphyromonas.
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P59915;
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Score 2335;

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Query Match

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Infect. Immun. 62:5707-5707(1994).
-!- FUNCTION: CLEAVES HUMAN COMPLEMENT COMPONENT C3. MAY ENABLE
P.GINGTVALIS TO EVADE COMPLEMENT-MEDIATED KILLING DURING THE
IMMUNE RESPONSE. PLAYS AN IMPORTANT ROLE IN SOFT TISSUE INFECTIONS
                                                                                                                                                                                            1460 ASYINFEGPONDDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFA
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                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                          Indels
  Pred. No. 6.9e-157;
2; Mismatches 5;
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- SUBCELLULAR LOCATION: In membrane vesicles.

- SIMILARITY: Belongs to peptidase family C25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Protease prtH (BC 3.4.22.-).
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Infect. Immun. 62:4279-4286(1994).
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       98.4%;
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                          430; Conservative
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Best Local Similarity
Matches 430; Conserv
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AC P46071;
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNPDNYLLSKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGARFGLSTBADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSP 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 TPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKKCVNVTVNST 329
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                                                                                                                                                                                                                                                                                                                                                                                                      89
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                                                                                                                                                                                                                                                                                                                                                                                                      34 VRSPEAIRG-RIQGTWRQKTVDLPAGTEICCFPSLPKAPICST---STLMRLRSKTNAKR
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P28784; Q45168;
01-DEC-1992 [Rel. 35, Last sequence update)
10-OCT-2003 [Rel. 42, Last amnotation update)
11-OCT-2003 [Rel. 42, Last amnotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIJINE=92406812; PubMed=1527017;
Chen Z., Potempa J., Polanowski A., Wikstrom M., Travis J.;
"Purification and characterization of a 50-kDa cysteine proteinase
                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural characterization of argingipain, a novel arginine-specific cysteline proteinase as a major periodontal pathogenic factor from Porphyromonas gingivalis."; Arch. Biochem. Biophys. 316:917-925(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                           Length 989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=381;
MEDLINE=95168884; PubMed=7864651;
Okamoto K., Misumi Y., Kadowaki T., Yoneda M., Yamamoto K.,
                                                                                                                                                                                                                                                                                                                    21; Indels
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                                                                                                                                                                                                                                 989 AA; 110238 MW; FA85FE8A3AC8944C CRC64;
                                                                                                                                                                                                                                                                         59.9%; Score 1431; DB 1;
ilarity 88.0%; Pred. No. 1.9e-93;
Conservative 8; Mismatches 21;
                                                                                                    MEROPS; C25.001; -.
InterPro; IPR002376; formyl transf.
Pfam; PF00551; formyl transf; 1.
Hydrolase; Thiol protease; Repeat; Virulence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (gingipain) from Porphyromonas gingivalis.";
entities requires a license agreement (St
or send an email to license@isb-sib.ch).
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                                                          EMBL, 127483; AAAS1298.1; -.
HSSP; P23882; 1FMT.
MEROPS; C25.001; -.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to licensealeb-sib.ch)
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                                                                                                                                                                                                                                                                                                       and/or Mg(2+) for stabilization. It is stimulated by glycine-containing dipeptides. It is resistant to inhibition by proteinase inhibitors in human plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 GGTSFAG-----HNSAICVSSASYINFEGPQNPDNYLVTPELS-LPGGGTLTFWVCAQD
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FUNCTION: Thiol protease which is believed to participate in intracellular degradation and turnover of proteins. Its proteolytic activity is a major factor in both periodontal tissue destruction and in bacterial host defense mechanisms. Activates
                                                                                                                                                     complement C3 and C5. ATMAINT: Cleavage of proteins, including collagens and immunoglobulins, with a preference for Arg in P1, and hydrophobic residues in P2 and P3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 LPAGTKYVAFRHFGCTDFFWINL-DEVEIKANGKRADFTETFESSTHGEAPAEWTTIDAD
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NUCLBOPHILE (BY SIMILARITY).
RT -> TK (IN REF. 2).
1, 03EB3F44CEBE2544 CRC64;
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InterPro; IPR001769; Peptidase C25.
InterPro; IPR005536; Peptidase C25.
Pfam; PF01364; Peptidase C25, 1.
Pfam; PF01364; Peptidase C25, 1.
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                                                                                                                                                   01-00T-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bifunctional autolyship precursor [Includes: N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28); Mamnosyl-glycoprotein endo-beta-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: ENDOHYDROLYSIS OF THE DI-N-ACETYLCHITOBLOSYL UNIT IN HIGH-MANNOSS GLYCODEPTIDES AND GLYCOPROTEINS CONTAINING THE -[(MAN) 5 (GLORAC) 2] -ASN STRUCTURE. ONE N-ACETYL-D-GLUCOSAMINE RESIDUE REMAINS ATTACHED TO THE PROTEIN; THE REST OF THE CATELOSTOPHRIDE IS RELEASED INTACT.

CATALYTIC ACTIVITY: Hydrolyzes the link between N-acetylmuramoyl residues and L-amino acid residues in certain bacterial cell-wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: Endohydrolysis of the di-N-acetylchitobiosyl curist in high-mannose glycopeptides and glycopteins containing the -[Man(GlcNAc)2]Asn-structure. One N-acetyl-D-glucosamine residue remains attached to the protein; the rest of the oligosaccharide is released intact.
SINGELLULAR LOCATION: Secreted.
FIM: UNDERGOES PROTECLYIIC PROCESSING TO GENERATE THE TWO EXTRACELLULAR LOYLE ENZYMES.
SINILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE N-ACETYLMORAMONI-1-ALAURIB ANIDASE FAMILY 2.
SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO FAMILY 73 OF
                                                                                                                                                                                                                                                                                                                                                                                             "A Staphylococcus aureus autolysin that has an N-acetylmuramoyl-L-alanine amidase domain and an endo-beta-N-acetylglucosaminidase domain: cloning, sequence analysis, and characterization."; Proc. Natl. Acad. Sci. U.S.A. 92:285-289(1995).
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95116542; PubMed=7816834;
Oshida T., Sugai M., Komatsuzawa H., Hong Y.-M., Suginaka H.,
   382 RDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKVCVN 425
                     SEQUENCE FROM N.A., AND SEQUENCE OF 205-214 AND 776-792.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Foster S.J.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                          Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=NCTC 8325-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycopeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                        NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                        STRAIN=RN450;
                                                                                                                                                                                                                                                                                                                                                                                     Tomasz A.;
                                                                                                                ATL STAAU
                                                                                 RESULT 5
ATL_STAAU
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SMRRT; SM00644; Ami 2; 1. SMART; SM00047; LYZZ; 1. CEll wall; Hydrolase; Signal; Multifunctional enzyme; Repeat. SIGNAL 1 29 POTENTIAL.

InterPro; IPR002502; Amidase 2.
InterPro; IPR002901; Amidase 4.
Pfam; PF01510; Amidase 2; 1.
Pfam; PF01835; Amidase 4; 1.

EMBL; D17366; BAA04185.1; -. EMBL; L41499; AAA99982.1; -.

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765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            823 VIKERAHGNETYVILINNTSHNIPLGWFNVKDLNVQNLGKEVKTTQKYTVNKSNNGLSMVP 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 TGATKVK-----YYYAVNDGFPGDHYAVMISKTGT-----NAGDFTVVFEETPN 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                932 TAPTAVKPTTSAAKDYNYTYVIKNG-NGYYYVTPNSDTAKYSLKAFNEQPFAVVKEQVIN 990
                                                                                                                                                                                                                                                                                                                                649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171
                                                                                                                                                                                                                                                                                                                                                                                                                 650 VIKEASLĠĠNKĖYLVKDŶNŠPILIGWVKQGDVIÝNNAKSPVNVMQTŸTVKPGTKLYSVPW 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----- 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 EVLTAKT-----VVTAPEAIR-----GTRVQGTWYQKTVQLPAGTKYVAFRHFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                766 AVAQPKTAVKAYTVTKPQTTQTVSKIAQVKPNNTGIRASVYEKTAK--NGAKY-ADRTFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --DFFWINLDEVEIKANGKRADFTE--TFESSTHGEAPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 WITIDADGDGGGWLCLSSGOLDWLTAHGGTNVVASFSWN-----GMALNPDNYLISKDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       883 WGT-----KNOVILTGNNI----AQGTENATKOVSVGKDVYLYGTINNRTGWVNAKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   710 GTYKQEAGAVSGTGNQTFKATKQQQIDKS----IYLFGTVNGKSGWVSKAYLAVPAAPKK
                                                                                                                                                                                                                                                                                                                                594 PTPTPTPKPSTPTTNNKLTVSSLNGV----AQINAKNNGLFTTVYDKTGKPTKEVQKTFA
                                                                                                                                                                                                                                                                                                                                                                                 47 -----GGTSF---AGHNSAICV----SSASYINFEGPQN-PDNYLVTFELSL----
                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        991 GQTWYYGKLSNGKLAWIKST--DLAKELIKYNQTGMTLNQVAQIQAGLQY 1038
  BIFUNCTIONAL AUTOLYSIN.
N-ACETYLMURAMOYL-L-ALANINE AMIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 G-----INKGGARFGLSTEADGAK-----PQSVWIERTVDLPAGTKY 344
                                                                                                                                                                                                                                   47; Mismatches 167; Indels 153;
                                                                                                                                                                                       Length 1256;
                                                                                                                                                                                                                                                                                  3 PNPNPNPNPNPGTTT----LSESFENGIPASWKTIDADGDG---NNWTTTPPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shen H., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R. "Cellobiohydrolase B, a second exo-cellobiohydrolase from the cellulolytic bacterium Cellulomonas fimi.";
Biothem. J. 311:67-74 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Exoglucanase B precursor (EC 3.2.1.91) (Exocellobiohydrolase
(1.4-beta-cellobiohydrolase B) (CBP120).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Cellulomonadaceae; Cellulomonas:
                                              ENDO-BETA-N-ACETYLGLUCOSAMIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------PGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFAN-
30 1256 BIFUNCTIONAL AUTOLYSIN.
179 775 N-ACETYLMRRAMOYL-L-ALANINE 1
425 589 1.
596 758 2.
770 932 3.
1256 AA; 137384 MW; 2BB76CAA292FDD20 CRC64;
                                                                                                                                                                                     Score 132.5; DB 1;
Pred. No. 0.15;
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MEDLINE=96003898; PubMed=7575482;
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                                                                                                                                                                                          5.5%;
                                                                                                                                                                                                                                          103; Conservative
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                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1708;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996
01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CELFI
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Nature 409:529-533(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=83334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                    CenE, a member of a new family of beta-1,4 glucanases."

Biochem. Biophys. Res. Commun. 199:1223-1228(1994).

-! FUNCTION: Hydrolyze cellohexaose to a mixture of cellotetraose, cellotriose and cellobiose, with only a trace of glucose. It hydrolyzed cellopentaose to cellotriose and cellobiose, and cellotetraose to cellobiose, but it did not hydrolyze cellotriose. Has also wake and cellobiose, but it did not hydrolyze cellotriose. Has also wake and cellobiose, but it did not hydrolyze cellotriose.

-!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages in cellulose and cellotetraose, releasing cellobiose from the non-reducing ends of the chains a fibronectin type III domains.

-!- SIMILARITY: Contains 1 bacterial-type cellulose-binding (CBD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 ASWKT---IDADGDGNNWTTTPPPGGTSFAGHNSAICVSSASYINFEGPQNPDNYLVTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO CELLULASE FAMILY L (FAMILY 48 OF GLYCOSYL
                       SEQUENCE OF 54-78.
MEDLINE=94197708; PubMed=8147863;
Shen H., Tomme P., Meinke A., Gilkes N.R., Kilburn D.G.,
Marren R.J., Miller R.C. Jr.;
"Stereochemical course of hydrolysis catalysed by Cellulomonas fimi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC (BY SIMILARITY).
FIBRONECTIN TYPE-111 1.
FIBRONECTIN TYPE-111 3.
FIBRONECTIN TYPE-111 3.
CELLULOSE-BINDING (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47; Mismatches 157; Indels 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSOUSCI, TECT (EBD BACTERIAL; 1.
Cellulose degradation; Hydrolase; Glycosidase; Repeat; Signal.
strnar.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           515 ASWKVPSELKWTGKPDTWNAAPTG-----NPGLTVEVTSY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
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InterPro; IPR001919; Bac_celose-bind.
InterPro; IPR008965; Cellul bind.
InterPro; IPR008957; FN III—like.
InterPro; IPR008957; FN III.
InterPro; IPR000556; Glyco hydro 48.
InterPro; IPR000556; Glyco hydro 48.
InterPro; IPR008928; Glyco_trans_6hp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD011903; Glyco_hydro_48; 1.
SWART; SM00637; CBD_II; 1.
SWART; SM00060; FN3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00041; fn3; 3.
Pfam; PF02011; Glyco hydro 48; 1.
PRINTS; PR00844; GLHYDRLASE48.
Bacteriol. 175:1910-1918(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L38827; AAB00822.1; -.
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1090
699
785
884
978
1090
1089
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54
700
794
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--TWYQKTVQLP 159
                                                                                                                                                                                         597 VSAVETRGDYKRFDDTYVANGDGIYIPSGWTGTMPNGDVIKPGVSFLDIRSFYKKD---P 653
                                                                                                                                                                                                                                                                                                                                                                                                                   160 AGTKYVAFRHFGCTDFFWINLDEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterchemorrhagic Escherichia coli
"Complete genome sequence of enterchemorrhagic Escherichia coli
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MEDLINE=21074935; PubMed=11205551;
MEDLINE=21074935; PubMed=11205551;
Rose D.J., Maylew G. FI., Bvans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grobeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
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                                                    DNA Res. 8:11-22 (2001).
-!- SIMILARITY: Contains 16 Big-1 domains.
-!- SIMILARITY: Belongs to the intimin/invasin family.
-!- CAUTION: Ref. 2 sequence differs from that shown due to a
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Pfam; PF02369; Big_1; 16.
PRINTS; PR01369; INTIMIN.
SMART; SM00634; BID 1; 16.
SWART; SM00089; PkD; 8.
email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SSTHGEAPAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 -----ASFSWNGMALNPDN--YLISKDVTGA-----TKVKYYYAVNDGFPGDHYAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 RVVEGPTSASITANGRSSETDTSYYVINKSTVAAKEGDDVAEGTYYL---GRPWSEYA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 AIVVAKSGGDYTTIGDAI--DALSTSTTDTQTIFIE----EGT-YDEQVYLPAMTGKVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 ALALSAWADQQGYYGCNFTGYQDTLLAQTGNQLYINSYIEGAVDFIFGQHARAWFQNVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 MISKTGTNAGDFTVVFEET--PNGINKGGARFGLSTEADGAKPOSVWIERTVDLPAGTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Christgau S., Kofod L.V., Halkier T., Andersen L.N., Hockauf M., Dorreich K., Dalboege H., Kauppinen S.;
Dorreich K., Dalboege H., Kauppinen S.;
Pectin methyl esterase from Aspergillus aculeatus: expression cloning in yeast and characterization of the recombinant enzyme.";
Biochem. J. 319:705-712(1996):
Biochem. J. 319:705-712(1996):
--- FUNCTION: Involved in maceration and soft-rotting of plant tisk:
--- FUNCTION: Involved in maceration and soft-rotting of plant tisk:
--- CATALYTIC ACTIVITY: Pectin + N H(2)0 = N methanol + pectate.
--- SIMILARITY: Belongs to the pectinesterase family.
                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pectinesterase precursor (BC 3.1.1.11) (Pectin methylesterase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1F1C81BF1E32174F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 FRHFGCTDFFWINL ---- DEVEIKANGKRADFTETFE ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 WITIDADGDGQGWL-CLSSGQLDWLTAHGGTNVV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.9%; Sco. 22.9%; Pred. No. v..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 117.5; DI
Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY. PECTINESTERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U49378; AAB42153.1; -.
InterPro; IPR0000070; Pectinesterase.
Pfam; PR01095; Pectinesterase; 1.
PROSITE; P800800; PECTINESTERASE 1; 1.
PROSITE; P800503; PECTINESTERASE 2; 1.
Hydrolase; Aspartyl esterase; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----RVVFQQTSMTNVINSLG-
                                                                                                                                                                                                                                                                                                                                                     STRAIN=KSM 510;
MEDLINE=97079238; PubMed=8920970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35681 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70; Conservative
                                                                                                                                                              Aspergillus aculeatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 VAFRHY 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 AA;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               NCBI TaxID=5053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
162
183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285
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YK28\_ARCFU

RESULT 9

331 AA

STANDARD;

PME\_ASPAC Q12535;

RESULT 8
PME\_ASPAC

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  -----NIOL----SGYDTGYWWRIRPINASADGDGA 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keeler C.L. Jr., Hnatow L.L., Whetzel P.L., Dohms J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dohms J.E., Hnatow L.L., Whetzel P., Morgan R., Keeler C.L. Jr.; "Identification of the putative cytadhesin gene of Mycopiasma gallisepticum and its use as a DNA probe."; Avian Dis. 37:380-388 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma gallisepticum.
Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTRAIN-S6;
GOM M.S., Geary S.J.;
Submitted (FEB-1986) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Could be involved in cytadherence.
-!-STMCTION: Could be involved in membrane protein (Probable).
-!-SIMILARITY: Belongs to the adhesin Pl family.
-!-CAUTION: Ref. 4 sequence differs from that shown due to a frameshift in position 159 to 213.
                                                                                                                                                                                    YRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKVCVNVTINP
                                                                  333 ERTVDLPAGIKYVAFRHYNCSDLNYILLDDIQFIMGGSPTPTDYTYTV-
                                                                                                                                                                                                                                                                                                                     ADP1 MYCGA STANDARD; PRT; 1122 AA.
404379; Q49437; Q53351;
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Adhesin P1 precursor (Cytadhesin P1) (Attachment protein).
GAPA OR MGCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hnatow L.L., Keeler C.L. Jr., Tessmer L., Dohms J.E.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY-ILE.
DM -> IW (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (Sont send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, U44804; AAC83385.1; ALT_FRAME.
PIR, T18346; T18346.
Cytadherence; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from Mycoplasma gallisepticum.";
infect. Immun. 64:1541-1547(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96201559; PubMed=8613358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93371270; PubMed=8363503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 159-1122 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 378-570 FROM N.A.
                                                                                                        484 NKSSMLAGGPETIT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-12 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U34842; AAB02987.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1122
1021
1009
314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              997
1002
313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=S6;
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TRANSMEM
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CONFLICT
                     134
                                                                                                                                                            381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                          RESULT 10
ADP1_MYCGA
                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                      g
                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAICVSSASYINFEGPONPDNYLVTPELSLPGGGTLTFWVCAQDAN------YASEH 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----FKVKGNYSTDEAFVS---RLVGFGEAYFOFGPINGNISGTKIIDVFAIGN 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 AGTKYVAFRHFGCTDFFWINLDEVEIKANGKRADFTETFESSTHGEAPAEWTTID---AD 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52
                                                                                                                                                                                                                                                                                                             MEDLINE=98049343; PubMed=380475;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Klenk H.-P., Clayton R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., Morbeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 YAVYASSTGNDASN--FANALLEEVLTAKTVVTAPEAIRGT-----RVQGTWYQKTVQLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 ASIGVNKSGPDNSNQWTGNVTIKNTATGLTYIVKSVKVWATDRNYNEINGARYENTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -------VN---VQI---GRDESFISKDLSFQYDKVPIIWGNVTFRLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 GDGQGWLCLSSGQLDWLTAHGGTNVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGNNWTTTPPPGGTSFAGHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DANYGW-..-GVGQ-DKITDGGNTYIIERI-----YVIGSYLVKVTK-HVESAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of the hyperthermophilic, sulphate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: TO M.JANNASCHII MJ1393 AND MJ1394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.9%; Score 117.5; DB 1; Length 607; 18.3%; Pred. No. 0.64; ative 65; Mismatches 172; Indels 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Transmembrane; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    583 603 POTENTIAL.
607 AA; 66215 MW; F46F116BF2AAFEE1 CRC64;
                                                                                                                                                          Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 PNPGTTTLSESFENGIPASWKTID-ADG------
                                                                  Last sequence update)
Last annotation update)
607 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                               / DSM 4304 / ATCC 49558;
                                                                                                                                                                                  Archaea; Euryarchaeota; Archaeoc
Archaeoglobaceae; Archaeoglobus
                                             (Rel. 36, Created)
(Rel. 36, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000963; AAB89227.1; -.
                                                                                                      Hypothetical protein AF2028
AF2028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; C69503; C69503.
TIGR; AF2028; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                          (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     603 LKLDTLNSLPNKFTQENNIFFSYAMLDGRQWSLGTRKDSTWLT----TNTINNFTYNTQQ 658
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                                                                                                                                                                                                                                                                                                                                                                               659 QLASTAAGENANPRNILNALITAKGFDRRDIGNVDILYSNNTNKFTXYXQVGGAITTWPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                              145 TRVQGTWYQKTVQLP--AGTKYVAFRHFGCTDFFWINLDEVEIK---ANGKRAD--FTET
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10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Adhesin P1 precursor (Cytadhesin P1) (Attachment protein) (Adherence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Papazisi L., Gorton T.S., Kutish G., Markham P.F., Browning G.F., Nguyen D.K., Swartzell S., Madan A., Mahairas G., Geary S.J.; The complete genome sequence of the avian pathogen Mycoplasma gallisepticum strain R(low) ", Microbiology 149:2307-2316 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma gallisepticum.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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Pappazisi L., Troy K.E., Gorton T.S., Liao X., Geary S.J.;
"Analysis of cytadherence-deficient, GapA-negative Mycoplasma
gallisepticum strain R.";
                                                                                                                                                                   DB 1; Length 1122;
Y -> F (IN REF. 3).
I -> T (IN REF. 3).
R -> G (IN REF. 3).
T -> A (IN REF. 3).
DIL -> VYT (IN REF. 4).
55C34DA2D6C3C65 CRC64;
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19.5%; Pred. No. 1.6;
tive 78; Mismatches 195;
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MEDLINE=22830409; PubMed=12949158;
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GAPA OR MYCGA1800 OR MGA 0934.
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SEQUENCE OF 94-1122 FROM N.A.
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1122 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           546 S---GNPQPTSTPMPNSNGNESIPYRWTNSYDYNSVRFAALISKPAGGNTKQVESLFTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 LIFWVCAQDANYASEHYAVYASSTGNDASNFAN----ALLEEVLTAKTVVTAPEAIRG
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Bukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.5%; Pred. No. 3;
tive 77; Mismatches 196; Indels 112;
DB 1; Length 1122;
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15 T -> A (IN REF. 2).

16 V -> A (IN REF. 2).

121387 MW; E57D27A7FBD360AD CRC64;
                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Complete proteome
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01-NOV-1995 (Rel. 32, Last seguence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL. ADHESIN P1.
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Pred. No. 3
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EMBL; AF214004; AAF25381.1; -.
Cytadherence; Signal; Transmembrane; (
26 SIGMAL.
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826 82
1122 AA;
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ALS1_CANAL
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                                                      Hoyer L.L., Scherer S., Shatzman A.R., Livi G.P., "Candida albicans ALS1: domains related to a Saccharomyces cerevisiae sexual agglutinin separated by a repeating motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL).
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2 X 26 AA APPROXIMATE REPEATS.
                                                                                    MOI. MICTODIOI. 15:39-54 [1995].
-!- FUNCTION: MAY PLAY A ROLE IN ADHESION AND PATHOGENESIS.
-!- PTM: N-glycosylated and O-glycosylated (Potential).
-!- SIMILARITY: TO YEAST SAGI.
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            763D1063A2354C24 CRC64;
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10 X 36 AA TANDEM REPEATS.
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11-5.
11-6.
1-8.
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InterPro; IPR008440; Candida ALS.
Pfam; PF05792; Candida ALS; I.
Cell adhesion; Glycoprotein; Repea
                            SEQUENCE FROM N.A.
STRAIN-AICC 11651 / B792;
MEDLINE-95272392; PubMed=7752895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1068 1068 N-L
1260 AA; 132641 MW;
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MEDLINE=9320933; PubMed=8458833;

MEDLINE=9320933; PubMed=8458833;

Meinke A., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;

Meinke A., Gilkes N.B., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;

"Cellulose-binding polypeptides from Cellulomonas fimi: endoglucanase of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of the part of
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532
                                                                                                                                                                                                       90 TLIFWV-----CAQDANYASEHYAVYASSTGNDASNFANALLEEVLITAKTVVTAPEAIR 143
                                                                                                                                                                                                                                                                    565
                                                                                                                                                                                                                                                                                                                        144 GTRVQGTWYQKTVQLPAGTKYVAFR----HFGCTDFFWINLDEVEIKANGKRADFTETFE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    618
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                                                                                                                                                                                                                                                              ----TTTTVTAP----
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                                                                                     --TTTPPPGGTSFAGHNSAICVSSASYINFEGPQNP------DNYLVTPELSLPGGG
                                                                                                                                                --IREPPNPTVTTTEYWSQSFATTTVTAPPGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Exoglucanae A precursor (ES 3.2.1.91) (Exocellobiohydrolase A) (1,4-beta-cellobiohydrolase A) (CBP95).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=ATCC 484;
MEDLINE=94344030; PubMed=8065260;
Meinke A., Gilkes N.R., Kwan E., Kilburn D.G., Warren R.A.J.,
Miller R.C. Jr.;
"Celloblobydrolase A (CbhA) from the cellulolytic bacterium
Cellulomonas fimi is a beta-1,4-exocellobiohydrolase analogous
Trichoderma reesei CBH II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 SKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----PGGTDSVIIREPPNHTVTTTEYW-----
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                                                                                                                                                                                                                                                                 533 TDSVIIREPPNPTVTTTEYWSQSYA-----
                                                                                                                                                187 TTTVTAPPGGT----DSVI----
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P50401;
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16; 40

Gaps

Indels 173;

77;

30; Mismatches 4.7%; Score 112.5; 19.5%; Pred. No. 3.8

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19.5%;

Local Similarity

Query Match

Conservative

68;

Best Loca Matches

DB 1; Length 1260;

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coved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       740 FTVKAKDVAGNVSAASAAVSARTQAATSGGCT------VKYSASSWNTGFTGTVEVK 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THGEAPAEWITID----ADGD---GQGWLCLSSGQLDWLTAHGGTNVVA-SFSWNGMALNPD 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 NYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGI 309
                                                                                                                                                                                                                                                                                                           CATALYTIC.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
CELLUGSE BINDING (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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PROSITE; PS00565; GLYCOSYL HYDROL F6 1; 1.
PROSITE; PS00656; GLYCOSYL HYDROL F6 2; 1.
PROSITE; PS00656; GLYCOSYL HYDROL F6 2; 1.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.7%; Score 112; DB 1; Length 872;
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                                                                                                                                                                                                                                                                                                                                                                                                                          7883B407F995533B CRC64;
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  nodified and this statement is not removed.
             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                               HSSP, P07946, 1EXG.

InterPro; IPR001919; Bac celose-bind.
InterPro; IPR001919; Bac celose-bind.
InterPro; IPR001965; Cellul bind.
InterPro; IPR001961; FN III-like.
InterPro; IPR001961; FN III-like.
InterPro; IPR001962; Pn III-like.
InterPro; IPR001962; Pn III-like.
InterPro; IPR001524; Glycc_hydro_6.
Pfam; PF00141; fn3; 3.
Pfam; PF01341; Glycc_hydro_6; I.
PRINTS; PR00141; FNTYPEIII.
PRINTS; PR001733; GLHYDRIASE6.
ProDom; PD003733; GLHYDRIASE6.
ProDom; PD003733; GLHYDRIASE6.
PROPORT; SM000637; CBD II; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
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SLAP_LACER
SLAP_LACER
AC 005044;
DT 01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                            89300 MM;
                                            EMBL, L25809; AAC36898.1; -. PIR; S49541; S49541.
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nes 85; Conserv
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465 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 EVLTAKTVVTAPEAIRGTRVQGTWYQKTVQ--LPAGTKYVAFRHFGCTDFFWINLDEVEI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 FSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYV-----AFRHYNCSDLN 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------rstdgtkagskvsdkaadQtaleayinankpsgytvtnpnaadat 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---YTVYRDG 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 TTASAKSYATAGAYSTLKTDAATRNVEATGTNALYTKP--GTV----KGAKVVASKATWAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 FEGPONPDNYLVTPELSLFGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 LSTDK-----SVTATNDNSVKIVYRTTD-------GTQVGSNTWV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GKSDTAFAGGI--
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                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAINS-ATC (2287) / DSM 20556;
STRAINS-ATC (2287) / DSM 20556;
WEDLINE-30054358; PubMed-1429463;
Vidgren G., Palva I., Pakkanen R., Lounatmaa K., Palva A.;
Widgren G., Palva Enceting ene of Lactobacillus brevis: cloning by polymerase chain reaction and determination of the nucleotide sequence.";
J. Bacteriol. 174:7419-7427(1992)
-!- FUNCTION: The Slayer is a paracrystalline mono-layered assembly of proteins which coat the surface of bacteria.
-!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.6%; Score 111; DB 1; Length 465;
19.4%; Pred. No. 1.3;
tive 45; Mismatches 187; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-layer with tetragonal symmetry.
                                                                                                                                         Bacteria, Firmicutes, Lactobacillales, Lactobacillaceae,
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-LAYER PROTEIN.
; 2BE2403392E65A2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 LASSKKSADYFRAYGVKTINRGSVYYRVVTMDGKYRGYVYG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
S-layer protein precursor (Surface layer protein).
Lackobacillus brevis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y-----ILLDDIOFTMGGSPTPTDYT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal; Glycoprotein; Cell wall; S-layer.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||: : |: | |: | 1
TKLAQLTTDLTGEKGQVVT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465 AA; 48159 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z14250; CAA78618.1; -. PIR; A47023; A47023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 19.49
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465
                                                                                                                                                                                                                   NCBI_TaxID=1580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 HNSAICVSSASYINFEGPONPDNYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 TGNDASNFANALLEEVIJTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 DFFWINLDEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----YGDKNWKYLEITSANSSEGTAVLFDG--DYF 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234 TAHGGINVVASFSWNGMALNPDNYLISKDVTGATKV----KYYYAVND-----GFPGD 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      607 KKDYNTSNLNAINWTNITLNWSN------DSATLVFNVLGNYSYSERDNILAKYGFA-- 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 HYAVMISKTGTNAGDFTVVFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGT 342
                                                                                                                                                                                                                                                                                     DEPLANDED STRAIN TO STRAIN TO STRAIN THE O. Olsen 261 / ATCC 43067;

MEDLINE=96337999; PubMed=8688087;

MEDLINE=96337999; PubMed=8688087;

Buil C. J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstcok K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 NPNPNPGTTTLSESFENGI-----PASW--KTIDADG-DGNNWTTTPPPGGTSF-AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYS-----NYISIDRRTNGNPTEISPEV-----YWNPPEDEWYYFE-LKIYSNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: TO M.JANNASCHII MJ1393 AND A.FULGIDUS AF2028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
4.6%; Score 110; DB 1; Length 987;
Best Local Similarity 19.8%; Pred. No. 4.1;
Matches 81; Conservative 69; Mismatches 135; Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U67579; AAB99404.1; -.

PIR; A64474; A64474.

TIGR; MJ1394; A1394; A64474.

Hypothetical protein; Transmembrane; Complete proteome. TRANSMEM 12 32 POTENTIAL.

POTENTIAL.

SEQUENCE 997 AA; 112360 MW; DI8628FFB28CA86D CRC64;
                                                                                                                                                         Methanococcus jannaschii.
Archaea, Euryarchaeota, Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                        (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 41, Last annotation update)
987 AA.
  PRT;
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                                                                                                               Hypothetical protein MJ1394
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                              NCBI_TaxID=2190;
  YD94 METJA
                                                                                                                                           MJ1394.
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Search completed: May 18, 2004, 11:43:37 Job time : 10.2235 secs

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May 18, 2004, 11:36:20; Search time 32.094 Seconds (without alignments) 4315.838 Million cell updates/sec
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2388
1 GTENPNPRPPPGTTTLSESF......PKVCVNVTINPTQFNPVQNL 439
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                           1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                               SPTREMBL_25:*
1: Sp archea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
7: sp mammal:*
7: sp mammal:*
7: sp mammal:*
7: sp mammal:*
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sp_virus:*
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sp_wclebrate:*
sp_wclassified:*
sp_rvirus:*
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |    |        | Description | P72197 porphyromon | P72194 porphyromon | P96967 porphyromon |        |        | 09znb5 porphyromon | 051839 porphyromon |        |        | 007442 porphyromon |        |        |        |        |        |        |
|-----------|----|--------|-------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------|--------|--------------------|--------|--------|--------|--------|--------|--------|
| SUMMARIES |    |        | ID          | P72197             | P72194             | P96967             | Q9R9B7 | 051816 | Q9ZNB5             | Q5183 <i>9</i>     | Q51838 | P72196 | 007442             | 051817 | 052050 | Q9F4J0 | Q9KIB3 | 60axeQ | OSUAU1 |
|           |    |        | DB          | 2                  | 7                  | N                  | 7      | 7      | 7                  | ~                  | 7      | 7      | 7                  | 7      | 7      | 7      | ~      | 7      | 16     |
|           |    | Query  | Length      | 1723               | 1723               | 1358               | 1687   | 1704   | 1223               | 1706               | 1706   | 1097   | 1732               | 1732   | 1732   | 925    | 312    | 293    | 1341   |
|           | dę | Query  | Match       | 86.9               | 9.98               | 86.3               | 86.2   | 86.2   | 86.1               | 85.8               | 85.3   | 85.0   | 85.0               | 84.8   | 84.2   | 29.0   | 23.9   | 8.3    | 5.7    |
|           |    |        | Score       | 2074               | 2068               | 2060               | 2058   | 2058   | 2056.5             | 2048               | 2037   | 2030.5 | 2030.5             | 2025.5 | 2011.5 | 691.5  | 571.5  | 199    | 136.5  |
|           |    | Result | No.         | Н                  | 7                  | m                  | 4      | 5      | 9                  | 7                  | 80     | 6      | 10                 | 11     | 12     | 13     | 14     | 15     | 16     |

86.9%; Score 2074; DB 2; Length 1723; 89.1%; Pred. No. 2.9e-129;

Query Match Best Local Similarity

| Q52644 ruminococcu Q9gnu3 paracentrot Q826M1 streptomyce Q8nx96 staphylococc Q8p377 xanthomonas Q82yw8 enterococcu Q7wbn0 borderella Q9yv1 staphylococ Q7wt6 staphylococ Q8e9g6 shewanella Q7wn54 bordetella Q7wn54 bordetella Q9rzs7 deinococcus Q7wn54 bordetella Q9rzs7 deinococcus Q7wn54 bordetella Q9rzs7 deinococcus Q7wn54 bordetella Q9rzs7 deinococcus Q8rs973 bradyrhizob Q8yv10 methanosarc Q8tp21 methanosarc Q8x4hs genteriohia Q8x2t1 escherichia                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       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                | 3 AA.<br>e update)                                                               | [da]<br>Pik                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | RT "Molecular cloning and characterization of Porphyromonas gingivalis RT Lyg-gingipain.";  RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.  BL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.  BR GOS 602.0005524; F:ATP binding; IEA.  BR GO; GO:0006524; F:ATP binding; IEA.  GO; GO:0006310; F:DNA ligase (ATP) activity; IEA.  GO; GO:0006310; F:DNA ligase (ATP) activity; IEA.  BR GO; GO:0006260; P:DNA repair; IEA.  BR GO; GO:0006260; P:DNA replication; IEA.  BR GO; GO:0006588; P:Proteolysis and peptidolysis; IEA.  BR GO; GO:0006588; P:Proteolysis and peptidolysis; IEA.  BR GO; GO:0006588; P:Proteolysis and peptidolysis; IEA.  BR InterPro; IPR001769; Peptidase_C25.  BR InterPro; IPR005354; Peptidase_C25.  BR Ffam; PF01364; Peptidase_C25.  BR Ffam; PF01364; Peptidase_C25.  BR Pfam; PF01364; Peptidase_C25.  BR Pfam; PF01364; Peptidase_C25.  BR Pfam; PF01364; Peptidase_C25.  BR Pfam; PF01364; Peptidase_C25.  BR Pfam; PF01364; Paptidase_C25.  BR Pfam; PF01364; Paptidase_C25.  BR Pfam; PF01364; Paptidase_C25.  BR Pfam; PF01364; Paptidase_C25.  BR Pfam; PF01364; Paptidase_C25.  BR Pfam; PF01364; Paptidase_C25.  BR Pfam; PF01364; Paptidase_C25.  BR Pfam; PF01364; Paptidase_C25.  BR Pfam; PF01364; Paptidase_C25.  BR Pfam; PF01364; Paptidase_C25.  BR Pfam; PF01364; Paptidase_C25.  BR Pfam; PF01364; Paptidase_C25.  BR Pfam; PF01364; Paptidase_C25.  BR Pfam; PF01364; PAPTIGASE_A1; 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
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A., Potempa J.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | cterizz  BMBL/Ge  BMBL/Ge  G; IEA,  YPe Per  (ATP)  'intho  ation;  s and f  s and f  s e C25.  s e C25.  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Porp<br><br>rton P.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | g and c 99) to 999) to 99810.1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
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Porphyromonas gingivalis (Bacteroides gingi Bacteria, Bacteroides (class Borthyromonadaceae; Porphyromonas.  NCBI_TaxID=837;  [1]  SEQUENCE FROM N.A.  Pavloff N., Pemberton P.A., Potempa J., Che Prochazka V., Kiefer M.C., Travis J., Barr                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | "Molecular c<br>Lya gingipai<br>Submitted (15<br>Submitted (25<br>Submitted (25<br>EMBL, U546)<br>MERDE; C25.<br>GO; GO:00082<br>GO; GO:00082<br>GO; GO:00062<br>GO; GO:00062<br>GO; GO:00062<br>GO; GO:00062<br>GO; GO:00062<br>GO; GO:00062<br>GO; GO:00062<br>GO; GO:00062<br>FI InterPro; IPI<br>InterPro; IPI<br>InterPro; IPI<br>InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; IPI<br>FI InterPro; I                                                                                                                                                                                                                                                                                                                   |
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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187261 MW; 5628963D251493EB CRC64;
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01-WAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                     86.6%; Score 2068; DB 2;
88.9%; Pred. No. 7.2e-129;
ive 12; Mismatches 31;
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                                                                                                                                                                                                                                                                          180 LDEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGT
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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R GO; GO: 000524; F:ATP binding; IEA.

R GO; GO: 0006234; F:Cysteine-type peptidase activity; IEA.

R GO; GO: 0006310; F:DNA recombination; IEA.

R GO; GO: 0006281; P:DNA repair; IEA.

R GO; GO: 0006508; P:DNA replication; IEA.

R GO; GO: 0006508; P:DNA replication; IEA.

R GO; GO: 0006508; P:DNA ligase.

R InterPro; IPR001769; Peptidase C25.

R InterPro; IPR001769; Peptidase C25.

R Pfam; PF01785; Peptidase C25.

R Pfam; PF03785; Peptidase C25.

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           11; Mismatches
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J. Biochem. 120:398-406(1996).
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EMBL; D83258; BAA11870.1; -.
MEROPS; C25:002; -... hindin
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               Matches 392; Conservative
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"Cloning and characterization of hage from P. gingivalis 381.";

"Cloning and characterization of hage from P. gingivalis 381.";

"Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.

"EMBL; P$7026946; AADD1810.1; -.

"R GO; GO:0005524; F:ATF binding; IEA.

"GO; GO:0008234; F:ATF binding; IEA.

"GO; GO:0008234; F:DNA ligase (ATP) activity; IEA.

"GO; GO:0006281; P:DNA recombination; IEA.

"GO; GO:0006281; P:DNA repair; IEA.

"GO; GO:0006281; P:DNA replication; IEA.

"GO; GO:0006281; P:DNA replication; IEA.

"R GO; GO:0006281; P:DNA replication; IEA.

"R GO; GO:0006281; P:DNA replication; IEA.

"R GO; GO:0006281; P:DNA replication; IEA.

"R GO; GO:0006281; P:DNA replication; IEA.

"R GO; GO:0006281; P:DNA replication; IEA.

"R InterPro; IPR000977; DNA ligase.

"R InterPro; IPR00110; JG-like.

"R InterPro; IPR00110; JG-like.
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                                                                                        86.3%; Score 2060; DB 2; Length 1358; 88.6%; Pred. No. 1.8e-128; ive 12; Mismatches 32; Indels 6
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                   PROSITE; PS00697; DNA_LIGASE_A1; 1.
SEQUENCE 1358 AA; 147102 WW; 47FCA0B25B06DED8 CRC64;
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 88.6*
Matches 390; Conservative
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STRAIN=381;
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gingipal proteinase of Porphyromonas gingivalis. Biosynthesis
proteinase-adhesin polyprotein.";
J. Biol. Chem. 270:1007-1010(1995).
BEMBL: U15222, AAA69539.1; -.
PIR; A55426; A55426.
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                                                                                                                                                                                                     Length 1687;
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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Travis J., Barr P.J.;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008234; F:OYEtaine-type peptidase activity; IEA.
GO; GO:0003910; F:DNA ligase (ATP) activity; IEA.
GO; GO:0006310; P:DNA ligase (ATP) activity; IEA.
                                                                                                                                                 183702 MW; D085B516A399FE70 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                        Score 2058; DB 2;
Pred. No. 3.2e-128;
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InterPro, IPR005536; Peptidase_C25_
Pfam; PF013164; Peptidase_C25; 1.
Pfam; PP03785; Peptidase_C25 C; 1.
PROSITE; PS00697; DNA_LIGASE_A1; 1.
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NCBI_TaxID=837;
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                                                                                                                                                                                                                     PNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAICVSS
                                                                                                                                                                                                                                          952 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS
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                                                                                                                                                                                              Gaps
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J. Biol. Chem. 274:5012-5020(1999).

EMBL; AB019363; BAA34341.1; -.
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GO; GO:0006281; P:DNA repair; IEA.

GO; GO:0006260; P:DNA replication; IEA.

GO; GO:0006509; P:proteolysis and peptidolysis; IEA.

InterPro; IPR00397; DNA ligase.

InterPro; IPR00110; Ig-like.

InterPro; IPR00110; Ig-like.

InterPro; IPR00159; Peptidase C25.

InterPro; IPR005536; Peptidase C25.

Pfam; PF01364; Peptidase C25; I.

Pfam; PF01364; Peptidase C25, I.

PRO371E; PG00697; DNA LIGASE A1; I.

CHAIN
                                                                                                                                                                      Length 1704;
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                   86.2%; Score 2058; DB 2; Length 1
88.8%; Pred. No. 3.3e-128;
tive 12; Mismatches 31; Indels
                                                                                                                                GINGIPAIN.
1704 AA; 185436 MW; 6A34B40131C2A676 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                     Query Match
Best Local Similarity 88.8
Matches 389; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVVFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYI
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MEDLINE=55160709; PubMed=7857299;
Rinszbaum L., Sotiropoulos C., Jackson C., Cleal S., Slakeski Reynolds B.C.;
"Complete nucleotide sequence of a gene prtR of Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0008234; F:Cysteine-type peptidase activity; IEA.

GO; GO:0008310; F:DNA ligase (ATP) activity; IEA.

R GO; GO:0006310; P:DNA repair; IEA.

R GO; GO:0006281; P:DNA replication; IEA.

R GO; GO:0006508; P:DNA replication; IEA.

R GO; GO:0006508; P:DNA replication; IEA.

R GO; GO:0006508; P:Protacion; IEA.

R InterPro; IPR001769; Peptidase C25.

InterPro; IPR001769; Peptidase C25.

InterPro; IPR01769; Peptidase C25.

R Pfam; PF01364; Peptidase C25.

R Pfam; PF01364; Peptidase C25.

R PROSITE; PS00697; DNA_LIGASE_A1; 1.
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Last annotation update)
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86.1%; Score 2056.5; DB 2;
Best Local Similarity 88.7%; Pred. No. 2.7e-128;
Matches 391; Conservative 11; Mismatches 32;
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422 VCVNVTINPTOFNPVQNL
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                                                                                                           MEDILINE=96311339; PubMed=8713096; Slakeski N., Cleal S.M., Reynolds E.C.; Hordeski N., Cleal S.M., Reynolds E.C.; Charleski N., Cleal S.M., a Porphyrononas gingivalis gene prtR that encodes an arginine-specific thiol proteinase and multiple adhesins."; Biochem. Biophys. Res. Commun. 224:605-610(1996).
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gingivalis W50 encoding a 132 kDa protein that contains an arginine specific thiol endopeptidase domain and a haemagglutinin domain."; Biochem. Biophys. Res. Commun. 207:424-431(1995).
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                                                                                                                                                                                                                                                                                                                                                                     Slakeski N.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; LL6541, AAC18876.1; -.
HSSB; P95493; 1CVR.
                                                                                                                                                                                                                                                                                            Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases
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Pred. No. 1.5e-127;
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                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                        Reynolds E.;
                                                                                                                                                                                                                                                        STRAIN=W50;
                                                                                                                                                                                                                                                                                                                                                     STRAIN=W50;
                                                                                                   STRAIN=W50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 ASY-INFEGPQNPDNYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1011 ESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 ANALLEBULTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rangarajan M., Aduse-Opoku J., Slaney J.M., Young K.A., Curtis M.A.; "The prpR1 and the prR2 arginine-specific protease genes of Porphyromonas gingivalis W50 produce five biochemically distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aduse-Opoku J., Muir J., Slaney J.M., Rangarajan M., Curtis M.A., infaratotrization, genetic analysis, and expression of a protease antigen (PrpRI) of Porphyromonas gingivalis W50."; Infect. Immun. 63:4744-4754(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 1706;
                                                                                                                                                                                                                                                                                                                                                                                              Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; C25.001; -. G0:000524; F:ATP binding; IBA. G0:000524; F:ATP binding; IBA. G0:000524; F:ATP binding; IBA. G0:000524; F:Cytelane-type peptidase activity; IEA. G0:0006210; F:DNA ligase (ATP) activity; IEA. G0:0006210; P:DNA recombination; IEA. G0:0006281; P:DNA repair; IEA. G0:0006280; P:DNA repair; IEA. G0:0006280; P:DNA repair; IEA. G0:0006280; P:DNA replication; IEA. INTERPO; IPR000977; DNA ligase. InterPro; IPR000977; DNA ligase.
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720 1262 BETA-ADHESIN.
1706 AA; 185705 MW; 0E56DCD87FDA8CDD CRC64;
                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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87.9%; Pred. No. 8.2e-127;
ive 13; Mismatches 34;
                                                                                                                                                                                1706 AA.
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InterPro; IPR005536; Peptidase C25 C.
Pfam; PF01364; Peptidase C25, I.
Pfam; PF03785; Peptidase C25 C; I.
                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porphyromonadaceae; Porphyromonas.
NCBI_TaxID=837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96071894; PubMed=7591131;
enzymes.";
Mol. Microbiol. 23:0-0(1997).
EMBL; X82680; CAA57997.1; -.
HSSP; P95493; ICVR.
                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, 01-MAY-1997 (TrEMBLrel. 03, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   385; Conservative
                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                          Protease precursor
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628 358

238 568

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689 Liddigfimggspipidytytvyrdgikikegliffiffebogvatgnheycvevkytagv 748
391 VYSESFGLGGIGVLTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDA 450
                                                                                                                                                                                                                                                                                                                   569 SNVVSSFSWNGMALNPDNYLLSKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDF
                                                                                                                                                                                                                                                                                                                                                                                                                              629 TVVFEETPNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLDDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGV
                                                                                                                                                                  179 NLDEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGOGWLCLSSGQLDWLTAHGG
                                                                                                                                                                                                                                                                                      239 TNVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDF
                                                                                                                                                                                                                                                                                                                                                                                                299 TVVFEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYI
                                                                                                                                                                                                                          509 DLDEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLDWLTAHGG
                                                                                     451 SNFTNALLEETITAKG-VRSPKAIRG-RIQGTWRQKTVDLPAGTKYVAFRHFQSTDMFYI
                                                        SNFANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.0%; Score 2030.5; DB 2; Length 87.3%; Pred. No. 2.3e-126; ive 15; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIGASE_A1; 1.
187914 MW; 45D5B91377391703 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MERCHES; C.25. UU.Z.; -...
GO, GO:0005524; F.ATP binding; IEA.
GO; GO:0005324; F.PTP binding; IEA.
GO; GO:0003310; F.DNA ligase (ATP) activity; IEA.
GO; GO:0006310; P.DNA recombination; IEA.
GO; GO:0006260; P.DNA replication; IEA.
GO; GO:0006281; P.DNA replication; IEA.
R GO; GO:0006508; P.DNA replication; IEA.
R InterPro; IPR0010977; DNA ligase.
R InterPro; IPR001769; Peptidase C25.
InterPro; IPR001536; Peptidase C25.
R Pfam: PF01364; Peptidase C25.
I.
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Lysine-specific cysteine proteinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1732 AA.
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EMBL; U75366; AAB60809.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            749 SPKKCVNVTVNSTQFNPVQNL 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              419 SPKVCVNVTINPTOFNPVQNL 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99235907; PubMed=10219167;
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Best Local Similarity 87.3%
Matches 385; Conservative
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ID 007442
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                                                                               1129 EVEIKANGKRADFTETFESSTHGEATAEWTTIDADGDGGGWLCLSSGQLDWLTAHGGTNV 1188
                                                                                                                                                                           1249 FEETPINGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD 1308
                                                                                                                                                                                                                                                                                                                                                                                                                           DIOFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFREDGVATGNHEYCVEVKYTAGVSPK 1368
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                                                                                                                                                                                                                                                        361
                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                      362 DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTPNPNPNPNPGT-TTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSALC 59
                                                                                                                                                                                                                                                        FEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD
                                182 EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNV
                                                                                                                                           VASFSWNGMAINPDNYLISKDVTGATKVKYYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The tla gene of Porphyromonas gingivalis W50: a homologue of the arginine-specific protease precursor (PrpRI) which shares sequence amiliarity to Tomb-linked receptors.";
J. Bacteriol. 179:4778-4788 (1997).
-i- SUBCELLULAR LOCATION: OUTER MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-97386416; PubMed-9244265;
Aduse-Opoku J., Slaney J.M., Young K.A., Muir J., Rangarajan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.0%; Score 2030.5; DB 2; Length
87.3%; Pred. No. 1.2e-126;
tive 15; Mismatches 34; Indels
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(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Matches 385; Conserv
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01-FEB-1997
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969 GTPNPNPNPNPNPNPGTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---LAGYNSNGC 1025
Slakeski N., Cleal S.M., Bhogal P.S., Reynolds B.C.; "Characterization of a Porphyromonas gingivalis gene prtK that encodes a lysine-specific cysteine proteinase and three sequence-related
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NCBI_TaxID=837;
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ANDLINE-96213011; PubMed-8631659;

Barkocy-Gallagher G.A., Han N., Patti J.M., Whitlock J.,

Progulsk-Fox A., Lantz M.S.;

Analysis of the prtP gene encoding porphypain, a cysteine proteinase of Porphyromonas gingivalis.";

Of Porphyromonas gingivalis.";

U. Bacteriol. 178 1234-2741(1996).

B. Bacteriol. 178 1234-2741(1996).

B. Brill: U42210; AAB06565.1; -..

B. Brill: U42210; AAB06565.1; -..

B. Brill: U42210; AAB06565.1; -..

B. GO; GO:000524; F.ATP binding; IEA.

GO; GO:000524; F.ATP binding; IEA.

GO; GO:000524; F.ATP binding; IEA.

GO; GO:0006280; F.INA lagase (ATP) activity; IEA.

GO; GO:0006280; P.INA repair; IEA.

GO; GO:0006280; P.INA repair; IEA.

GO; GO:0006280; P.INA repair; IEA.

GO; GO:0006280; P.INA repair; IEA.

RO; GO:0006280; P.INA repair and peptidolysis; IEA.

InterPro; IPR001766; Peptidase C25.

InterPro; IPR00176; Peptidase C25.

B. Pfam; PF03184; Peptidase C25.

B. Pfam; PF03184; Peptidase C25.

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60 VSSASY-INFEGPONPDNYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDA
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                                                                                                                                                SNFANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWI
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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SEQUENCE 1732 AA; 187875 WW; 654271DBEF7BCAE4 CRC64;
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01-OCT-2003
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                                                                                                                                                                                                                                                                                             119 SNFANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWI 178
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Tals195, an insertion sequence-like element associated with protease genes in Porphyromonas gingivalis.";

Infect. Immun. 66:3035-3042(1998).

REMEL; AP017059; AAC26523.1;

REMEL; AP017059; AAC26523.1;

REMEL; AP017059; AAC26523.1;

RO; GO:000524; F.ATP binding; IEA.

RO; GO:000524; F.ATP binding; IEA.

RO; GO:000524; F.DA Ingase (ATP) activity; IEA.

RO; GO:000528; F.DA recombination; IEA.

RO; GO:0006281; P.DNA recombination; IEA.

RO; GO:0006281; P.DNA repair; IEA.

RO; GO:0006281; P.DNA repair; IEA.

RO; GO:0006281; P.DNA repair; IEA.

RO; GO:0006281; P.DNA repair; IEA.

RO; GO:0006281; P.DNA repair; IEA.

RO; GO:0006281; P.DNA repair; IEA.
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1 GTPNPNPNPNPGT-TTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSALC
                                                                                                                                            60 VSSASY-INFEGPONPONYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNVVASFSWNGMALINPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDF
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Lysine specific cysteine protease.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria, Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187931 MW; B2337463D5CB5EA5 CRC64;
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GO; GO:0008214; F.Cysttine-type peptidae
GO; GO:000310; F.DNA ligase (ATP) activ
GO; GO:0006281; P.DNA recombination; IEA.
GO; GO:0006281; P.DNA repair; IEA.
GO; GO:0006286; P.DNA replication; IEA.
GO; GO:0006286; P.DNA replication; IEA.
GO; GO:0006286; P.DNA replication; IEA.
GO; GO:0006288; P.DNA replication; IEA.
GO; GO:0006288; P.DNA replication; IEA.
GO; GO:0006288; P.DNA peptidase.
InterPro; IPRO01769; Peptidase.
CZ5.
InterPro; IPRO01769; Peptidase.
CZ5.
Pfam; PF03384; Peptidase.
CZ5. C.
Pfam; PF03385; Peptidase.
CZ5. C.
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Local Similarity

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                                                                                            364 IGPVTPDNYLITPKVE--GAKRVKYWVSTQDANWAAEHYAVMASTTGTAVGDFV-ILFEE
                                                                                                                                                                                                                                                                                                                                                                      528 DPTVLEYIDETYSSRDDQVEVEVEYCVTAVYNDNIESQSVCDKLIYDSQSDIILYEGFEAGS
                                                                                                                                                                                                                                                                                                                                                                                                              206 APAEWITIDADGDGQGWLCLSSGQLDW-LTAHGGTNVVASFSWNGM--ALNPDNYLISKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -------KIKEGLTETTE
                                                                   69 EGPQNPDNYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALLEE
                                                                                                                                                                                                                                                                                                                                ---FESSTHGE
                                                                                                                                                                             ------GAWYERTINLPEGTKYIAWRHYNCTDIYFLKLDDITVFGT
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"P. gingivalis polypeptides and nucleic acids.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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Best Local Similarity 33.3%; Pred. No. 3e-30;
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Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical outer membrane protein PG27.
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Ross B.C.;
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                                                                                                                                                    VSSASY-INFEGPQNPDNYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDA
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Ross B.C., Barr I., Patterson M., Agius C., Rothel L., Margetts M., Hocking D., Webb E.;
"P. gingivalis polypeptides and nucleic acids.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.0%; Score 691.5; DB 2; Length 925; 30.0%; Pred. No. 1.3e-37; tive 63; Mismatches 138; Indels 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative outer membrane protein PG57.
Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                      Indels
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AY007522; AAG24228.1;
-Interpro; IPR003961; FN III.
SMART; SM0060; FN3; I.
SEQUENCE 925 AA; 103632 MW; 5FF2198D6914DAE8 CRC64:
  al Similarity 86.6%; Pred. No. 4.2e-125; 382; Conservative 16; Mismatches 36;
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                                                                                                                 134 TVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDEVEIKANGKRAD 193
                                                                                                                                                                                194 FIETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASFSWNGMALN 253
                                                                                                                                                                                                                                                254 PDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETPNGINKGG 313
                                                                                                                                                                                                                                                                                ----- YTP---- 172
                                                                                                                                                                                                                                                                                                             314 ARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFTMGGSPTP 373
                                                                                                                                                                                                                                                                                                                                             ------PHP 182
                                                    NYLVTPELSLPGGG--TLTFWVCAQDANYASEHYAVYASSTGNDASNFANALLEEVLTAK 133
374 IDYTYTVYRDGIKIKEGLIETIFEEDGVAIGNHEYCVEVKYIAGVSPKVCVNVII 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOC-2002 (TrEMBLrel. 22, Last sequence update)
Immunoreactive 32 kDa antigen PG25.
Porphyromonas gingivalis (Bacteroides gingivalis)
Bacteria; Bacteroidetes; Bacteroides
Porphyromonadaceae; Porphyromonas.
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77 YIYIVYRDGVKIASGLTEPTFLDEDVPAGEHTYCVEVQYQGGVSDKVCVDVEVK--DFKP 376 YIYIVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKVCVNVTINPIQFNP Gaps Ross B., Barr I., Patterson M., Agius C., Rothel L., Margetts M., Hocking D., Webb E.;
Hocking D., Webb E.;
"P. gingivalis polypeptides and nucleic acids.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFIS5351; AAD38410.1; -.
SEQUENCE 293 AA; 32272 MW; CC03EAC241F7F6F1 CRC64; 2; Length 293; Score 199; DB 2; Length 29: Pred. No. 1.7e-05; 5; Mismatches 18; Indels Query Match
Best Local Similarity 60.9%;
Matches 39; Conservative VONL 439 436 SOCCES SERVING SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES SOCCES S ð qq ð D

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2388
1 GTENPNPNPGTTTLSESF.....PKVCVNVTINPTQFNPVQNL 439
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Copyright (c) 1993 - 2004 Compugen Ltd.
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| Sequence 6, Appli<br>Sequence 19, Appl<br>Sequence 14, Appl<br>Sequence 14, Appl<br>Sequence 34, Appl<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 3, Appli<br>Sequence 10, Appli<br>Sequence 10, Appli<br>Sequence 20, Appli<br>Sequence 33, Appli<br>Sequence 33, Appli<br>Sequence 33, Appli<br>Sequence 33, Appli<br>Sequence 33, Appli<br>Sequence 33, Appli<br>Sequence 33, Appli<br>Sequence 33, Appli<br>Sequence 33, Appli<br>Sequence 33, Appli<br>Sequence 33, Appli<br>Sequence 36, Appli | G Genes<br>F Periodontal Disease                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
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| 4 US-09-066-330-6 3 US-08-822-324-19 4 US-09-071-035-264 4 US-08-82-324-14 4 US-08-821-567B-34 4 US-08-821-944A-4 4 US-08-945-567D-4 4 US-08-945-567D-3 5 US-08-945-567D-3 5 US-08-945-567D-3 5 US-08-945-567D-3 5 US-08-945-567D-3 5 US-08-945-567D-3 5 US-08-945-567D-3 5 US-08-945-567D-3 5 US-08-945-567D-3 6 US-08-945-567D-3 7 US-08-913-942-4 7 US-08-913-942-4 7 US-08-535-230A-2                                                                                                                      | ALIGNMENTS  SULT 1  -08-570-311-22  Berenn 22, Application US/08570311  Berenn No. 2824791  GENERAL INFORMATION:  APPLICANT: Progulske-Fox, Ann APPLICANT: Herogulske-Fox, Ann APPLICANT: Herogulske-Fox, Ann APPLICANT: Herogulske-Fox, Ann APPLICANT: Hen, Waining APPLICANT: Hen, Waining APPLICANT: Hentz, Marilyn APPLICANT: Hentz, Marilyn APPLICANT: Betti, Joseph TITLE OF INVENTION: Cloned Porphyromonas gingivalis Ge NUMBER OF SEQUENCES: 29 CORRESPONDENCE ADDRESS: ADDRESSEE: Ted W Whitlock STREET: 2421 N.N. 41st Street, Suite A-1 CITY: Gainerville STREET: 2421 N.N. 41st Street, Suite A-1 CITY: Gainerville STREET: 2421 N.N. 41st Street, Suite A-1 COUNTRY: USA ZIP: 3266 COMPUTER READABLE FORM: MEDIOM TYPER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: BATCHION DATA: APPLICATION NUMBER: US (08/570,311 FLING DATE: 09-DESC-1994 CLASSIFICATION NUMBER: US 07/647,119 FILING DATE: 08-DATA: APPLICATION NUMBER: US 07/647,119 FILING DATE: RESPERIATION: 424 RAPLICATION NUMBER: US 07/647,119 FILING DATE: RESPERIATION: A24 RAPLICATION NUMBER: US 07/647,119 FILING DATE: RESPERIATION: A24 RAPLICATION NUMBER: US 07/647,119 FILING DATE: RESPERIATION: A24 RAPLICATION NUMBER: US 07/647,119 FILING DATE: RESPERIATION: A24 RAPLICATION NUMBER: US 07/647,119 FILING DATE: RESPERIATION: A24 RAPLICATION NUMBER: US 07/647,119 FILING DATE: RESPERIATION: A24 RAPLICATION NUMBER: US 07/647,119 FILING DATE: RESPERIATION: USBER: 36,965 REFERENCE POCCAET NUMBER: US 07/647,119 FILING DATE: RELECOMMUNICATION: USBER: 36,965 REFERENCE POCCAET NUMBER: US 07/647,119 FILING DATE: RELECOMMUNICATION: USBER: US 08/353,485 FILING DATE: RELECOMMUNICATION: USBER: 36,965 REFERENCE POCCAET NUMBER: US 07/647,119 FILING DATE: RELECOMMUNICATION: USBER: 36,965                                                                                                                                                                                                                                                                                                                  |
| 2 2 3 2 3 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | TI  -570-311-22  wence 22, Application US/08570311  wence 22, Application US/08570311  wence 22, Application US/08570311  wence 22, Application US/08570311  wence 22, Application US/08570311  APPLICANT: Tumwasorn, Somying  APPLICANT: Tumwasorn, Somying  APPLICANT: Lenix, Marilyn  APPLICANT: Han, Naiming  APPLICANT: Han, Naiming  APPLICANT: Patti, Joseph  TITLE OF INVENTION: Cloned Porphy  TITLE OF INVENTION: Cloned Porphy  TITLE OF INVENTION: Cloned Porphy  TITLE OF INVENTION: Cloned Porphy  TITLE OF INVENTION: Cloned Porphy  TITLE OF INVENTION: Cloned Porphy  TITLE OF INVENTION: Cloned Porphy  TITLE OF INVENTION: Cloned Porphy  TITLE OF INVENTION: Alst Street,  STATE: 2421 N.W. 41st Street,  CLIX: Gainesville  COUNTRY: USA  ZIP: 32606  COMPUTER: IBM PC compatible  COMPUTER: IBM PC compatible  COMPUTER: IBM PC compatible  COMPUTER: IBM PC compatible  COMPUTER: Batenin Release #1.0  COMPUTER: Batenin Release #1.0  COMPUTER: IBM PC compatible  COMPUTER: 1BM PC compatible  COMPUTER: 1BM PC compatible  COMPUTER: 1BM PC compatible  COMPUTER: 1BM PC compatible  COMPUTER: 1BM PC compatible  COMPUTER: 1BM PC compatible  CLASSIFICATION NUMBER: US 08/353,4  FILING DATE: 25-JAN-1991  CLASSIFICATION: 424  PRIOR APPLICATION NUMBER: US 07/241,6  FILING DATE: 25-JAN-1991  CLASSIFICATION NUMBER: US 18-SEP-1988  ATTORNEY AGENTA INFORMATION:  REGISTRATION NUMBER: 36,965  REGISTRATION NUMBER: 36,965  REGISTRATION NUMBER: 36,965  REGISTRATION INFORMATION:  TELEPRANEE WORNEY NUMBER: 1915.6  TELECOMMUNICATION INFORMATION:  TELEPRANEE PORTON NUMBER: 1915.6  TELECOMMUNICATION INFORMATION:  TELEPRANEE PORTON NUMBER: 1915.6  TELECOMMUNICATION INFORMATION:  TELEPRANEE PORTON NUMBER: 1915.6  TELECOMMUNICATION INFORMATION:  TELEPRANEE PORTON NUMBER: 1915.6  TELECOMMUNICATION NUMBER: 1915.6                                                                                                                                                                                                                                                                |
| 28 128<br>29 128<br>29 128<br>31 125.5<br>32 123.5<br>34 120<br>35 120<br>37 120<br>38 118<br>40 118<br>41 118<br>42 118<br>44 1118                                                                                                                                                                                                                                                                                                                                                                            | RESULT 1 US-08-570-311-22 Sequence 22, Applicat Sequence 22, Applicat Sequence 22, Applicat APPLICANT: Progul APPLICANT: Progul APPLICANT: Lantz, APPLICANT: Lantz, APPLICANT: Lantz, APPLICANT: Lantz, APPLICANT: APTLICANT TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION NUMBER OF SEQUENCE CORRESPONDENCE ADD ADDRESSEE: Fd COUNTRY: Gainesvil STATE: COUNTRY: USA STATE: COUNTRY: Gainesvil STATE: COUNTRY: USA COMPUTER: FL COMPUTER: FL COMPUTER: FL COMPUTER: FL COMPUTER: FL COMPUTER: DATE: COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPUTER: DATE COMPU |
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       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: WALLLOCK, TEM W.
REFERENCE/DOCKET NUMBER: UF15.C3
TELEPHONE: (904) 372-5800
TELEPHONE: (904) 372-5800
TELEFRAN: (904) 372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/08570311; Patent No. 5824791 GENERAL INFORMATION:
APPLICANT: Progulake-Fox, Ann APPLICANT: Tumwasorn, Somying APPLICANT: Lepine, Guylaine; APPLICANT: Han, Naiming APPLICANT: Lantz, Marilyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2282 KVCVNVTINPTOFNPVQNL 2300
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amino acid
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US-08-570-311-18
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Patent No. 5824791
GENERAL INFORMATION
APPLICANT: Tunwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Lantz, Marilyn
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF ERQUENCES: 29
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                                                                                                                                                        Length 439;
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Best Local Similarity 100.0%; Pred. No. 2.7e-204;
Matches 439; Conservative 0; Mismatches 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
FILING DATE:
CLASSIFICATION: 424
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LENGTH: 439 amino acids
TYPE: amino acid
TOPOLOGY: linear
HOLECULE TYPE: protein
US-08-570-311-22
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US-08-570-311-14
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361 DDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSP 420
                             361 DDIQFIMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSP 420
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APPLICANT: Prognulske-Fox, Ann
APPLICANT: Tumwascur, Somying
APPLICANT: Hen, Naiming
APPLICANT: Hen, Naiming
APPLICANT: Hen, Naiming
APPLICANT: Hen, Oseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOPTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                 US-08-570-311-20
; Sequence 20, Application US/08570311
; Patent No. 5824791
                                                                                                                                                            421 KECVNVTVDPVQFNPVQNL 439
                                                                                                                               421 KVCVNVTINPTOFNPVONL 439
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REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (904) 372-5800 INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  456 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-570-311-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 FANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINL
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                                                                                                                                                                                                                                                 ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                            E: Ted W. Whitlock
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDABE: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION HAS:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION: 424
PRIOR APPLICATION OF ATA
PRIORAPHICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAMME: WhitLock, Ted W.
NAMME: WhitLock, Ted W.
PREGISTRATION NUMBER: 36,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UF: TELECOMMUNICATION INFORMATION: TELEPHONE: (904) 372-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 456 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 98.2
Matches 431; Conservative
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                                                                                                                                                    STREET: 2421 N.W. CITY: Gainesville
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                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                              COUNTRY:
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us-08-570-311-22.rai

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APPLICANT: Travis, James
APPLICANT: Travis, James
APPLICANT: Travis, Janes
APPLICANT: Inmamura, Jan
TITLE OF INVENTION: MITHODS AND COMPOSITIONS FOR CONTROL OF BLOOD COAGULATION
FILE REFERENCE: 235.00160101
CURRENT APPLICATION NUMBER: US/09/482,500A
CURRENT FILING DATE: 2001-12-17
PRIOR FILING DATE: 1999-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 BEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLDDVEIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NFEGPQNPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASNFANALL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 MGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKVCVNV 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 MGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKECVNV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 WNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVVFEETP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 NGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLDDIQFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 ANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNVVASFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 WNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVKISKTGTNAGDFTVVFEETP
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                                                                                                                                                                                                                                                                                                                 Length 450;
                                                                                                                                                                                                                                                                                                            97.2%; Score 2321; DB 2;
98.4%; Pred. No. 2.6e-198;
tive 3; Mismatches 4;
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                 REFERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09482500A; Patent No. 6627193; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Porphyromonas gingivalis
36,965
                                                                                    TELEFAX: (904) 372-5800
INFRMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acide
TYPE: amino acid
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SOFTWARE: Patentin version 3.0
SEQ ID NO 1
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421 TVDPVQFNPVQNL 433
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Matches 426; Conservative
                                                                                                                                                                                                                                       MOLECULE TYPE: protein
REGISTRATION NUMBER:
                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                                                                                                                 Query Match
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                      61 SSASYINFEGPONPDNYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASN 120
                                                                                                                                                                                                                                                                                                                 241 VVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Progulske-Fox, Ann
APPLICANT: Tunwasorn, Somying
APPLICANT: Tunwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Ted W. Whitlock
STREET: 2421 N. W. 41st Street, Suite A-1
                                                                  61 SSASYINFEGPONPDNYLVTPELSLPNGGTLTFWVCAQDANYASEHYAVYASSTGNDASN 120
                                                                                                                                                                                                                                               181 DDVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLGWLTAHGGTN
                                                                                                                                                                                                                                                                                                                                                241 VVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGPPGDHYAVMISKTGTNAGDFTV
                                                                                                                                                                                                                      DEVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSP
                                                                                                                     FANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINL
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock maximum.
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-570-311-16; Sequence 16, Application US/08570311; Patent No. 5824791
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1110 EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLDWLTAHGGTNV 1169
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Sequence 10, Application US/08336308A
Sequence 10, Application US/08336308A
Sequence 10, Application US/0836308A
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S.
APPLICANT: Parioff, Nadine
TITLE OF INVENTION: Porphyromonas gingivalis
TITLE OF INVENTION: Arginine-specific Proteinase Coding Sequences
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
9
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                                                                                                                                                                                                                                                                                                                                                                                                                           86.2%; Score 2058; DB 2;
88.8%; Pred. No. 5.2e-174;
iive 12; Mismatches 31;
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTOCNEY,FAGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE,DOCKET NUMBER: 1015.C3
TELECOMMUNICATION INFORMATION:
TELEFAK: (904) 375-8100
TELEFAK: (904) 372-5800
TELEFAK: (904) 372-5800
TELEFAK: (904) 372-5800
TELEFAK: (904) 372-5800
SEQUENCE CHARACTERISTICS:
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Matches 389; Conservative
                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                            781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application US/08570311
Patent No. 5824791
Patent No. 5824791
GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
APPLICANT: Tunwasorn, Somying
APPLICANT: Lepine, Guylaine
APPLICANT: Lepine, Guylaine
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Useph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
                                                                                                                                                                                               782 BSFGLGGIGULTPDNYLITPALDLPNGGKLTFWVCAQDANYASEHYAVYASSTGNDASNF
                                                                                                                                                                                                                                                                                 122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD
                                                                                                                                                                                                                                                                                                                                             EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNV
                                                                                                                                                                      63 ASY-INFEGPONPONYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF
                                                                                    3 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSALCVSS
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                                            Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                        4.3e-174;
                      Pred. No. 4.3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNDRER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-OJN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
      VCVNVTINPTOFNPVQNL 439
                                            Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                    Best Local Similarity
Matches 389; Conser
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NAME: Ferber, Donna M.
REGISTRATION UNDHER: 33,978
REFRENCE/DOCKET NUMBER: 103-
TELECOMMUNICATION INFORMATION:
TELEFAME: (303) 489-8089
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                 Genco, Caroline A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.2%;
88.8%;
GENERAL INFORMATION:
APPLICANT: Potenmya, Jan S.
APPLICANT: Travis, James
APPLICANT: Genco, Caroline
TITLE OF INVENTION: IMMUNO
TITLE OF INVENTION: METHOD
NUMBER OF SEQUENCES: 24
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Greenlee, Win
                          Jan S.
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                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 389; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLDWLTAHGGTNV 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGGGWLCLSSGQLDWLTAHGGTNV 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 VASFSWNGMAINPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV 301
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; Pred. No. 5.3e-174;
12; Mismatches 31; Indels 6
                                                                              COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAME: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,308A
FILING DATE: 08-NOV-1994
CLASSIFICATION NUMBER: US 08/119,361
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/119,361
FILING DATE: 10-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/265,441
FILING DATE: 24-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: FECTSET.
NAME: FECTSET.
TELECOMMUNICATION NUMBER: 31,878
REFERENCE/DOCKET NUMBER: 21-93C
TELECOMMUNICATION NUMBER: 21-93C
TELECOMMUNICATION NUMBER: 21-93C
TELECOMMUNICATION NUMBER: 21-93C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.2%;
88.8%;
                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.8*
Matches 389; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1704 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                       ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-336-308A-10
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; Sequence 6, Application US/08822324 ; Patent No. 6129917

RESULT 9 US-08-822-324-6

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1307 DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTBTTFEBDGVATGNHEYCVEVKYTAGVSPK 1366
IMMUNOGENIC COMPOSITIONS COMPRISING
PORPHYROMONAS GINGIVALIS PROTEINS AND/OR PEPTIDES AND
METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       952 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1127 EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNV 1186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1247 FEETPNGINKGGARRGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 PNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAICVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 ASY-INFEGPONPONYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGÖGWLCLSSGQLDWLTAHGGTNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEETPNGINKGGARFGLSTEADGAKPOSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31; Indels
                                                                                                                                                                                                                                                                                                                                                          WEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,324
FLILNG DATE: 21-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,945
FLILNG DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                           P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 2058; DB 3;
; Pred. No. 5.3e-174;
12; Mismatches 31;
                                                                                                                                                        3: Greenlee, Winner and Sullivan, 5370 Manhattan Circle, Suite 201
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1187 VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV 1246
                                                                                                                                                                       1247 FEETPNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD 1306
                                                                                                                                                                                                                                                                            1127 EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNV 1186
                                                                                                                                            302 FEETPNGINKGGARFGLSTEADGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYILLD 361
                                                                                                                                                                                                                                              362 DIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGVSPK 421
                                               242 VASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFTVV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Progulske-Pox, Ann
APPLICANT: Tumwasorn, Somying
APPLICANT: Lepine, Gaylaine
APPLICANT: Han, Naiming
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION WUMBER: US 07/647,119
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-JAN-1991
CLASSIFICATION: 424
PROR APPLICATION: 424
PROR APPLICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION: 424
PRIOR DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UF15.C3
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 8, Application US/08570311; Patent No. 5824791; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  1367 ECVNVTINPTQFNPVKNL 1384
                                                                                                                                                                                                                                                                                                                                        422 VCVNVTINPTOFNPVQNL 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (904) 375-8100
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-570-311-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 ASY-INFEGPQNPDNYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNV 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSALCVSS
                                                                                                                                                                                                                                                             APPLICANT: Travis, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff hadine
TITLE OF INVENTION: Porphyromonas gingivalis
TITLE OF INVENTION: Arghine-specific Proteinase Coding Sequences
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Greenlee, Winner and Sullivan, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.2%; Score 2058; DB 3; Length 1704;
88.8%; Pred. No. 5.3e-174;
cive 12; Mismatches 31; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/265,441
FILING DATE: 24-UDN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/336,308
FILING DATE:
                                                                                                                                                                                         Sequence 10, Application US/09490931
Patent No. 6274718
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ferber, Donna M.
REGISTRATION UNDRER: 33,878
REFERENCE/DOCKET UNDRER: 21-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8080
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1704 amino acids
TYPE: amino acid
                                                       422 VCVNVTINPTOFNPVQNL 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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CITY: Boulder
STATE: Colorado
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Matches 389; Conser
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                                                                                                                                                                       US-09-490-931-10
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120 NFANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWIN 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: TURWAGEOTH, SOMYING
APPLICANT: Lepine, Guylaine
APPLICANT: Han, Naiming
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: and Probes for the Detection of Periodontal Disease
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 GTPNPNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SSASY-INFEGPQNPDNYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 NVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          568 NVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GIPNPNPNPNPNPGTITLSESFENGIPASWKTIDADGDGNNWTTTPPPGGTSFAGHNSAICV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 86.1%; Score 2055; DB 2;
Best Local Similarity 88.4%; Pred. No. 4.9e-174;
Matches 389; Conservative 13; Mismatches 32;
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2421 N.W. 41st Street, Suite A-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: U8-SPP-1988
ATTONEV/AGENT INFORMATION:
NAME: WhitLock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF15.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1087 amino acids
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Patent No. 5824791
GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 PKVCVNVTINPTOFNPVONL 439
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Sequence 8. Application US/08353485
Secuent No. 5830710
GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
APPLICANT: Lepine, Guylaine
APPLICANT: Lantz, Marilyn
APPLICANT: Patti, Joseph
TITLE OF INVENTION: Cloned Porphyromonas gingivalis Genes
TITLE OF INVENTION: 12 and Probes for the Detection of Periodontal Disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               568 NVVASFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGPPGDHYAVMISKTGTNAGDFT
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                                                                    Length 1087;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: BR PC compatible
COMPAGE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION DATA:
APPLICATION DATA:
FILING DATE: 25-JAN-1991
CLASSIFICATION: 424
                                                               Query Match

86.1%; Score 2055; DB 2;
Best Local Similarity 88.4%; Pred. No. 4.9e-174;
Matches 389; Conservative 13; Mismatches 32;
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ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
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                  JS-08-570-311-8
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85.8%; Score 2048; DB 4;
llarity 88.1%; Pred. No. 4.1e-173;
Conservative 14; Mismatches 32;
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                                                               Sequence 10, Application US/09066330A Patent No. 6511666
                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Porphyromonas gingivalis
US-09-066-330-10
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Matches 386; Conserv
                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 10
LENGTH: 1706
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                                     RESULT 14
US-09-066-330-10
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                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/570,311
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; Pred. No. 6.9e-174;
13; Mismatches 32;
                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/353,485
FILING DATE: 09-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
FILING DATE: 25-UAM-1991
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Whitlock, Ted W. REGISTRATION NUMBER: 36,965 REFERENCE/DOCKET NUMBER: UF15.C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1019 PKVCVNVTINPTQFNPVKNL 1038
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                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.1%;
88.4%;
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LENGTH: 1358 amino acids
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Best Local Similarity 88.4%
Matches 389; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-570-311-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: limination
                                                                                     COMPUTER: IBM PC
OPERATING SYSTEM:
FL
USA
                                                                                                                                                                        FILING DATE
                                       32606
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1011 ESFGLGGIGVLIPDNYLIIPPALDLPNGGKUTFWVCAQDANYASEHYAVYASSTGNDASNF 1070
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Reynolds, Eric C.

APPLICANT: Reynolds, Eric C.

APPLICANT: Bhogal, Peter S.

APPLICANT: Bhogal, Peter S.

APPLICANT: BLakeski, Nada

TITLE OP INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE

TITLE OP INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE

CURRENT APPLICATION NUMBER: US/09/066,330A

CURRENT APPLICATION NUMBER: W6275

EARLIER PILING DATE: 1995-10-30

BARLIER FILING DATE: 1995-10-30

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PALENTIN OF: 2.0
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APPLICANT: Reynolds, Eric C.
APPLICANT: Bhogal, Peter S.
APPLICANT: Blakeski, Nada
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
FILE REFERENCE: Reynolds
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                                                                                                                                                                                        Query Match
Best Local Similarity 87.3%; Pred. No. 1.5e-171;
Matches 385; Conservative 15; Mismatches 34; Indels 7;
CURRENT APPLICATION NUMBER: US/09/066,330A;
CURRENT FILING DATE: 1998-09-15;
EARLIER APPLICATION WUMBER: PN 6275
EARLIER FILING DATE: 1995-10-30;
EARLIER FILING DATE: 1996-10-30;
NUMBER OF SEQ ID NOS: 15;
SEQ ID NO 11
LENGTH: 1732
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                                                                                                                                                   ORGANISM: Porphyromonas gingivalis US-09-066-330-11
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Perfect score:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Appli Appli Appli Sequence 10, App] Sequence Sequence Sequence Sequence Sequence Sequence Sequence Description Sequence Sequence Sequence Sequence Sequence US-10-229-066-10 US-10-174-695-3 US-10-174-695-5 US-10-174-695-6 US-10-174-695-6 US-10-387-977-18 US-10-387-977-23 US-10-387-977-23 US-10-387-977-23 US-10-387-977-24 US-10-387-977-24 US-10-387-977-25 US-10-387-977-81 US-10-387-977-20 US-10-387-977-17 SUMMARIES Query Match Length DB Score 2030.5 711.5 303 233.5 153 153 153 153 153 153 2048 Result

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| Sequence 14592, A Sequence 14592, A Sequence 83, Appl Sequence 84, Appl Sequence 85, Appl |                     |                                                      | Sequence 6, Appli<br>Sequence 23473, A<br>Sequence 264, App<br>Sequence 76, Appl<br>Sequence 79, Appl | 9 9 H 4 4 4                                                        | Sequence 3, Appliance Sequence 9, Appliance Sequence 3, Appliance 3, Appliance 4, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appliance 19, Appl |
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| -10-282-122A-<br>-10-156-761-1<br>-10-387-977-8<br>-10-387-977-8                          |                     | 0-282-122A<br>0-282-122A<br>0-387-977-<br>0-387-977- | US-10-229-066-6<br>US-10-369-493-23473<br>US-10-206-576-264<br>US-10-387-977-76<br>US-10-387-977-79   |                                                                    | US-10-175-275-3<br>US-10-175-275-3<br>US-10-282-122A-55546<br>US-09-813-214A-9<br>US-10-2797-862-33<br>US-10-229-066-4<br>US-10-387-977-19                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| 12<br>15<br>15<br>15                                                                      | 42222               | 152                                                  | 14<br>12<br>12<br>15<br>15<br>15                                                                      | 4 C C A 4 4                                                        | 11.0<br>9 11.4<br>11.5<br>11.5<br>11.5<br>11.5<br>11.5<br>11.5<br>11.5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| 8472<br>555<br>255<br>255<br>25                                                           | 960<br>1638<br>1638 | 2435<br>2435<br>25<br>25                             | 6 6 9 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                               | 1095<br>1095<br>1833<br>1833                                       | 1992<br>1992<br>1333<br>2122<br>2353<br>22<br>22<br>29                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
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| 132.5<br>132.5<br>132<br>132<br>132                                                       | $\omega$            | 131<br>131<br>130<br>130                             | 129<br>125.5<br>125.5<br>125                                                                          | 123.5<br>123.5<br>121<br>120<br>120                                | 120<br>120<br>118<br>118.5<br>118                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| 16<br>17<br>19<br>20                                                                      | 22<br>23<br>24<br>4 | 25<br>26<br>27<br>28                                 | 80 H R R                                                                                              | . ധ ധ ധ ധ ധ<br>4 സ ര ഗ . ജ ഗ                                       | भ व व व व व व<br>भ व व व व व व व<br>भ व व व व                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |

## ALIGNMENTS

1010 4, 63 ASY-INFEGPONPDNYLVTPELSLPGGGTLTFWVCAQDANYASEHYAVYASSTGNDASNF 121 62 Sequence 10. Application US/10229066
| Publication No. US2003015/637A1
| GENDERAL INFORMATION:
| APPLICANT: Reynolds, Eric C.
| APPLICANT: Reynolds, Eric C.
| APPLICANT: Slakeski, Nada
| TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
| TITLE REPERENCE: Reynolds
| CURRENT APPLICATION NUMBER: US/10/229,066
| CURRENT FILING DATE: 1998-09-15
| PRIOR PILING DATE: 1998-09-15
| PRIOR APPLICATION NUMBER: PN 6275
| PRIOR FILING DATE: 1996-10-30
| PRIOR FILING DATE: 1996-10-30
| NUMBER OF ESQ ID NOS: 15
| SEQ ID NO 10
| LENGTH: 1706
| LENGTH: 1706
| LENGTH: 1706 954 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS 3 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGNNWTTTPPPPGGTSFAGHNSAICVSS Gaps 6; Length 1706; Indels 85.8%; Score 2048; DB 14; 88.1%; Pred. No. 1e-177; tive 14; Mismatches 32; ORGANISM: Porphyromonas gingivalis Query Match Best Local Similarity 88.1% Matches 386; Conservative US-10-229-066-10

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1204 SNVVSSFSWNGMALNPDNYLISKDVTGATKVKYYYAVNDGFPGDHYAVMISKTGTNAGDF 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 PNPNPNPNPGTTTLSESFENGIPASWKTIDADGDGHGWKPGNAPG---IAGYNSNGCVYS 291
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                                                                     1264 TVVPEETPNGINKGGARFGLSTEANGAKPQSVWIERTVDLPAGTKYVAFRHYNCSDLNYI
                                                                                                                                 359 LLDDIQFTMGGSPTPTDYTYTVYRDGTKIKEGLTETTFEEDGVATGNHEYCVEVKYTAGV
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                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10174695
; Sequence 3, Application US/2003023202A1
; General INFORMATION;
APPLICANT: Reynolds, Eric Charles
; APPLICANT: Reynolds, Eric Charles
; APPLICANT: Glakeski, Nada
; APPLICANT: Glakeski, Nada
; APPLICANT: Ghen, Chao Guang
; APPLICANT: Ghen, Chao Guang
; APPLICANT: Ghen, Chao Guang
; TILLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
; FILE REFERENCE: 529282000700
; CURRENT FILING DATE: 2002-06-18
; PRIOR FILING DATE: 2000-12-21
; PRIOR FILING DATE: 1999-112-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE FEASEQ for Windows Version 4.0
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Publication No. US20030232022A1
GENERAL INFORMATION:
APPLICANT: Slakeski, Nada
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
APPLICANT: Barr, Ian George
TITLE OF INTENTION: P. GINGTVALIS ANTIGENIC COMPOSITION
FILE REFERENCE: 529282000700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.4%; Score 727; DB 15; 75.8%; Pred. No. 1.1e-57; tive 10; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/174,695
                                                                                                                                                                                                                                               419 SPKVCVNVTINPTOFNPVQNL 439
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ORGANISM: Porphyromonas gingivalis
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    ANALLEEVLTAKTVVTAPEAIRGTRVQGTWYQKTVQLPAGTKYVAFRHFGCTDFFWINLD 181
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Sequence 11, Application US/10229066
Sequence 11, Application US/10229066
Publication No. US20030157637A1
GENERAL INFORMATION:
APPLICANT: Bhogal, Peter S.
APPLICANT: Bhogal, Peter S.
APPLICANT: Bhogal, Peter S.
APPLICANT: Bhogal, Peter S.
APPLICANT: Bhogal, Peter S.
APPLICANT: STAKESH, Nada
TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
FILE REFERENCE: Reynolds
CURRENT FILING DATE: 2002-08-28
FRIOR PELICATION NUMBER: US/09/066,330
PRIOR PLICATION NUMBER: US/09/066,330
PRIOR PLICATION NUMBER: PN 6275
PRIOR PLICATION NUMBER: PN 6275
PRIOR PLICATION NUMBER: PT/AU96/00673
PRIOR FILING DATE: 1996-10-30
PRIOR FILING DATE: 1996-10-30
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                 EVEIKANGKRADFTETFESSTHGEAPAEWTTIDADGDGQGWLCLSSGQLDWLTAHGGTNV
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US-10-229-066-11
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Sequence 18, Application US/10387977
Publication No. US20040005276A1
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ORGANISM: Porphyromonas gingivalis
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Publication No. US20030232022A1
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric Charles
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Best Local S:
Matches 44,
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12.7%; Score 303; DB 15; Length 231;
Best Local Similarity 37.5%; Pred. No. 2.9e-19;
Matches 87; Conservative 30; Mismatches 69; Indels 4
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Sequence 6, Application US/10174695

Publication No. US2003023202A1

GENERAL INFORMATION:
APPLICANT: Reynolds, Eric Charles
APPLICANT: Slakeski, Nada
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
APPLICANT: Barr, Ian George
TITLE OF INVENTION: P. GINGIVALIS ANTIGENIC COMPOSITION
FILE REPERBNCE: 529282000700
CURRENT APPLICATION NUMBER: US/10/174,695
CURRENT APPLICATION NUMBER: PCT/AU00/01588
PRIOR APPLICATION NUMBER: PCT/AU00/01588

PRIOR PLING DATE: 2000-12-21

PRIOR PLING DATE: 1999-12-24

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                             32; Indels
                                                                                                                                                                                                                                                                    Query Match 29.8%; Score 711.5; DB 1
Best Local Similarity 74.1%; Pred. No. 2.8e-56;
Matches 143; Conservative 11; Mismatches 32
CURRENT FILING DATE: 2002-06-18

PRICR APPLICATION NUMBER: PCT/AU00/01588

PRIOR FILING DATE: 2000-12-21

PRIOR APPLICATION NUMBER: AU PQ 4859

PRIOR FILING DATE: 1999-12-24

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 419
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US-10-174-695-5
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LENGTH: 231
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| FUDITICATION NO. USZUU400052/6A1 |
| GENERAL INFORMATION: Exic Charles |
| APPLICANT: Reynolds, Exic Charles |
| APPLICANT: Reynolds, Exic Charles |
| APPLICANT: Blakeski, Nada |
| APPLICANT: Blakeski, Nada |
| TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE |
| TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH |
| TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH |
| TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH |
| TITLE OF INVENTION: DATE: 2003-07-18 |
| PRIOR APPLICATION NUMBER: US 09/423,056 |
| PRIOR PILING DATE: 1990-03-22 |
| PRIOR PILING DATE: 1990-04-30 |
| PRIOR PILING DATE: 1997-04-30 |
| NUMBER OF SEQ ID NOS: 105 |
| SEQ ID NO 18 |
| LENGTH: 29 |
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--- DSPASYTYTVYRDGTKIK 141
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                                                                                                         389 EGLTETTFEEDGVATGNHEYCVEVKYTAGVSPKVCVNVTI-NPTQFNPVQNL 439
                                                                                                                                                                              142 EGLTATTFEEDGVAAGNHEYCVEVKYTAGVSPKVCKDVTVEGSNEFAPVQNL 193
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APPLICANT: Chen, Chao Guang
APPLICANT: Chen, Chao Guang
APPLICANT: Barr, Ina George
TITLE OF INVENTION: P. GINGTVALIS ANTIGENIC COMPOSITION
FILE REFERENCE: 529262000700
CURRENT PELLING NATE: 2002-06-18
PRIOR APPLICATION NUMBER: PCT/AU00/01588
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASCESQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 196
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6.4%; Score 153; DB 15;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 29; Conservative 0; Mismatches 0;
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1 Similarity 75.9%; Pred. No. 5.2e-13;
44; Conservative 2; Mismatches 9
               92 RYDDFTFE--AGKKYTFTMRRAGMGDGTDMEVED-
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375 DYTYTVYRDGTKIKEGLTETTFEEDGVAT 403
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Best Local Similarity 100.0
Matches 29; Conservative
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Best Local Similarity
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US-10-387-977-26
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US-10-387-977-21
Sequence 21, Application US/10387977
Sequence 21, Application US/10387977
Sequence 21, Application US/10387977
Sequence 21, Application No. US20040005276A1
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric Charles
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: DIAGNOSIS AND TREATHENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DIAGNOSIS AND TREATHENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DIAGNOSIS AND TREATHENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DATE: 2003-07-18
CURRENT APPLICATION NUMBER: US 09/423.056
PRIOR FILING DATE: 1998-04-30
PRIOR PELLING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 29
TYPE: PRI
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, End Charles
APPLICANT: O'Brief-Simpson, Neil Martin
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
FILE REFERENCE: 5.29282000301
CURRENT APPLICATION NUMBER: US/10/387,977
CURRENT APPLICATION NUMBER: US 09/423,056
PRIOR APPLICATION NUMBER: POT/AU98/00311
PRIOR APPLICATION NUMBER: PUS/200-03-22
PRIOR APPLICATION NUMBER: AU PO 6528
PRIOR PELING DATE: 1999-04-30
PRIOR PELING DATE: 1997-04-30
PRIOR PELING DATE: 1997-04-30
SPOID NOS: 105
SEQ ID NO 23
LENGTH: 29
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6.4%; Score 153; DB 15; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 29; Conservative 0; Mismatches 0; Indel8
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375 DYTYTVYRDGTKIKEGLTETTFEEDGVAT 403
                                                     DYTYTVYRDGTKIKEGLTETTFEEDGVAT 29
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Sequence 26. Application US/10387977

Sequence 26. Application US/2004005276A1

GENERAL INFORMATION:
APPLICANT: Reynolds. Eric Charles
APPLICANT: Reynolds.
TITLE OF INVENTION: SYNTHETIC PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
FILE REFERENCE: 529282001001

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
FILE REFERENCE: 52928200101

CURRENT FILING DATE: 2003-07-18
PRIOR PILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 1998-04-30
PRIOR FILING DATE: 1998-04-30

PRIOR FILING DATE: 1998-04-30

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SPRIOR FILING DATE: 1998-04-30

SPRIOR FILING DATE: 1998-04-30
Sequence 24, Application US/10387977

Sequence 24, Application US/10387977

Sequence 24, Application US/10387977

Publication No. US20040005276A1

GENERAL INFORMATION:

APPLICANT: Starbards Starbards

APPLICANT: Slakeki, Nada

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH

TITLE OF INVENTION: DORPHYROMONAS GINGIVALIS

FILE REFERENCE: 52928200301

CURRENT APPLICATION NUMBER: US/10/387,977

CURRENT FILING DATE: 2000-03-22

PRIOR APPLICATION NUMBER: AU PO 6528

PRIOR APPLICATION NUMBER: AU PO 6528

PRIOR APPLICATION NUMBER: AU PO 6528

PRIOR APPLICATION NUMBER: AU PO 6528

PRIOR FILING DATE: 1998-04-30

PRIOR FILING DATE: 1998-04-30

PRIOR FILING DATE: 1998-04-30

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100.0%; Pred. No. 7.3e-07;
tive 0; Mismatches 0; Indels
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; ORGANISM: Porphyromonas gingivalis
US-10-387-977-26
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Sequence 20, Application US/10387977

Sequence 20, Application US/10387977

Sequence 20, Application US/0040005276A1

GENERAL INFORMATION:
APPLICANT: RegroldS, Exic Charles
APPLICANT: Grands, Nada
TITLE OF INVENTION: SYNTHERIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION UNMBER: US 09/423.056

PRIOR APPLICATION NUMBER: US 09/423.056

PRIOR FILING DATE: 2000-03-22

PRIOR FILING DATE: 1998-04-30

PRIOR FILING DATE: 1998-04-30

PRIOR FILING DATE: 1997-04-30

NUMBER OF SEQ ID NOS: 105

SOCTWARE: FastSEQ for Windows Version 4.0

LEAGURE OF DATE: 29

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APPLICANT: Reynolds, Eric Charles
APPLICANT: Reynolds, Eric Charles
APPLICANT: Slakeski, Nada
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: O'Brien-Simpson, Neil Martin
TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH
TITLE OF INVENTION: DORAPHYROMONAS GINGIVALIS
TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS
FILE REPRENCE: 529282000301
CURRENT APPLICATION NUMBER: US 09/423,056
PRIOR FILING DATE: 1998-04-30
PRIOR PLING DATE: 1998-04-30
PRIOR PELING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 105
SEQ ID NOS: 105
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Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 25; Conservative 0; Mismatches 0;
  Pred. No. 3.9e-06;
                                0; Mismatches
                                                                                     375 DYTYTVYRDGTKIKEGLTETTFEEDGVAT 403
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US-10-387-977-20
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                                                                                                                                                                                                                                                       US-10-387-977-81; Sequence 81, Application US/10387977; Publication No. US20040005276A1; GENERAL INFORMATION:
  96.6%;
Best Local Similarity 96.6
Matches 28; Conservative
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GENERAL INFORMATION

APPLICANT: Reynolds, Eric Charles

APPLICANT: Reynolds, Neil Martin

APPLICANT: Slakeski, Nada

APPLICANT: Slakeski, Nada

TITLE OF INVENTION: SYNTHETIC PEPTIDE CONSTRUCTS FOR THE

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PERIODONTITIS ASSOCIATED WITH

TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS

FILE REPERENCE: 5.29282000301

CURRENT APPLICATION NUMBER: US/10/387,977

CURRENT APPLICATION NUMBER: US 09/423,056

PRIOR APPLICATION NUMBER: PSCT/AU98/00311

PRIOR APPLICATION NUMBER: AU PO 6528

PRIOR PILING DATE: 1997-04-30

NUMBER OF SEQ ID NOS: 105

SEQ ID NO 25

LENGTH: 29

LENGTH: 29

LENGTH: 29

LENGTH: 29
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APPLICANT: Reynolds, Eric Charles
APPLICANT: O'Brien-Simpson, Neil Martin
APPLICANT: Slakeski, Nada
TITLE OF INVENTION: SYNTHERIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: SYNTHERIC PEPTIDE CONSTRUCTS FOR THE
TITLE OF INVENTION: DORPHYROMONAS GINGIVALIS
FILE REPERENCE: 529282000301
CURRENT APPLICATION NUMBER: US 09/423,056
PRIOR PILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: PCT/AU98/00311
PRIOR APPLICATION NUMBER: PCT/AU98/00311
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 105
SOFTHARE: FasteSEQ for Windows Version 4.0
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                                                                         375 DYTYTVYRDGTKIKEGLTETTFEEDGVAT 403
                                                                                                                              1 DYTYTVYRDGTKIKEGLTETTFEEDGVAT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/10387977; Publication No. US20040005276A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Porphyromonas gingivalis
                                                                                                                                                                                                                                                                      Sequence 17, Application US/10387977 Publication No. US20040005276A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28; Conservative
                    Conservative
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Best Local Similarity
Matches 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-387-977-17
                                                                                                                                                                                                                       RESULT 12
US-10-387-977-17
                          29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 17
LENGTH: 29
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                          Matches
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0; Gaps Query Match 5.7%; Score 136; DB 15; Length 29; Best Local Similarity 96.3%; Pred. No. 2.6e-05; Matches 26; Conservative 0; Mismatches 1; Indels

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ð Д Search completed: May 18, 2004, 11:52:22 Job time : 35.0043 sece